

AC005339

F-MAMMA1000824//Homo sapiens 12p13.3 BAC RPC111-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//4.2e-104:503:99//AC005912

F-MAMMA1000831//Homo sapiens clone UWCG:g1211a139, complete sequence.//0.76:302:58//AC005502

5 F-MAMMA1000839//Human BAC clone RG013L03 from 7q21, complete sequence.//1.9e-54:322:68//AC002456

F-MAMMA1000841//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//6.7e-140:647:92//AL023755

F-MAMMA1000842//, complete sequence.//0.0068:499:59//AC005817

10 F-MAMMA1000843//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.13:439:59//AC004710

F-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//2.2e-05:208:64//AL034557

F-MAMMA1000851//Gallus domesticus flamin gene 5' region, partial cds.//0.86:193:63//U00146

15 F-MAMMA1000855//Human minisatellite region detected by myoglobin 33-repeat probe, clone lambda 33.10.//0.081:229:62//M30549

F-MAMMA1000856//B. taurus microsatellite marker ETH8 (D6S3) DNA.//0.0024:253:60//Z2747

F-MAMMA1000859//Sequence 6 from Patent WO9722695.//2.3e-79:533:82//A63553

F-MAMMA1000862

20 F-MAMMA1000863//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//1.0e-28:439:64//AP000050

F-MAMMA1000865

F-MAMMA1000867//CIT-HSP-2385J8.TR.1 CIT-HSP Homo sapiens genomic clone 2385J8, genomic survey sequence.//0.00017:158:70//AQ240906

25 F-MAMMA1000875//Homo sapiens DNA sequence from PAC 232G24 on chromosome Xq27.1-q27.3. Contains two exons similar to MAGE gene family, EST, CA repeat, STS, complete sequence.//1.0:121:68//AL022152

F-MAMMA1000876//Homo sapiens clone HS19.6 Alu-Ya5 sequence.//8.4e-41:185:90//AF015152

F-MAMMA1000877//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//8.3e-57:522:75//AL022336

30 F-MAMMA1000880//Homo sapiens full-length insert cDNA clone ZD54A10.//5.2e-26:143:100//AF086327

F-MAMMA1000883//Human DNA sequence from clone 786D3 on chromosome 22q13.31-33 Contains GSS, complete sequence.//0.99:225:63//AL023801

F-MAMMA1000897//R. norvegicus mRNA for plasma protein.//4.8e-07:479:58//Y11283

35 F-MAMMA1000905//F26L5TRB IGF Arabidopsis thaliana genomic clone F26L5, genomic survey sequence.//0.94:115:66//B61433

F-MAMMA1000906//HS\_3110\_B2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=22 Row=B, genomic survey sequence.//2.5e-63:548:78//AQ182819

F-MAMMA1000908//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//5.2e-80:480:90//AL033397

40 F-MAMMA1000914//Plasmodium falciparum MAL3P8, complete sequence.//7.6e-09:596:58//AL034560

F-MAMMA1000921//CIT-HSP-2171D8.TR CIT-HSP Homo sapiens genomic clone 2171D8, genomic survey sequence.//6.6e-07:249:66//B89575

F-MAMMA1000931//Homo sapiens clone DJ0892G19, complete sequence.//2.9e-43:415:66//AC004917

45 F-MAMMA1000940//HS-1056-A2-E02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=4 Row=I, genomic survey sequence.//6.1e-44:235:78//B47296

F-MAMMA1000941//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 complete genomic sequence, complete sequence.//9.4e-48:443:75//AC002299

F-MAMMA1000942//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.8e-14:175:76//AL031117

50 F-MAMMA1000943//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0082:684:56//AC005308

F-MAMMA1000956//Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.//3.3e-30:530:67//AC004643

55 F-MAMMA1000957//HS\_3039\_A2\_C08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//1.3e-72:390:94//AQ155121

F-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-58:318:86//AC006001

F-MAMMA1000968//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the

- TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4, 5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.4e-18:396:65//AL022394
- 5 F-MAMMA1000975//Human DNA sequence from clone 34417 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence.//1.4e-79:690:77//AL024458
- F-MAMMA1000979//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//0.089:214:66//AC004991
- 10 F-MAMMA1000987//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.1e-58:458:82//AC000114
- F-MAMMA1000998//Human DNA sequence from PAC 997K18 on chromosome 20p12. Contains ESTs and CA repeat.//1.1e-05:439:62//AL021406
- F-MAMMA1001003//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.24:166:68//AL022401
- 15 F-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.6e-103:139:99//AJ011929
- F-MAMMA1001021//Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds.//6.5e-48:465:76//AF070567
- 20 F-MAMMA1001024//CITBI-E1-2501L21.TF.1 CITBI-E1 Homo sapiens genomic clone 2501L21, genomic survey sequence.//1.0:175:62//AQ241701
- F-MAMMA1001030//Homo sapiens G protein-coupled receptor LGR5 (LGR5) mRNA, complete cds.//1.1e-30:753:6//1AF061444
- 25 F-MAMMA1001035//Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complete sequence.//7.9e-24:256:76//AC002990
- F-MAMMA1001038//CIT-HSP-2284N21.TF CIT-HSP Homo sapiens genomic clone 2284N21, genomic survey sequence.//0.96:78:75//AQ000903
- F-MAMMA1001041//chicken mRNA for alpha-actinin, complete cds.//2.8e-09:355:63//D26597
- 30 F-MAMMA1001050//Homo sapiens BAC clone RG060P12 from 7q21, complete sequence.//2.6e-40:378:76//AC002457
- F-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//4.8e-97:661:83//L25125
- F-MAMMA1001067//Homo sapiens genomic intron breakpoint sequence of MLL rearrangement, 285 bp.//2.8e-18:110:100//AJ000169
- 35 F-MAMMA1001073//HS\_3046\_A2\_G08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=16 Row=M, genomic survey sequence.//1.0:142:68//AQ098420
- F-MAMMA1001074//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.2e-23:386:70//AL031733
- 40 F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence.//1.1e-27:559:65//L09749
- F-MAMMA1001078//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//2.2e-22:334:69//AC006120
- F-MAMMA1001080//Human immunoglobulin heavy chain variable region (VH III family) from IgM rheumatoid factor.//6.4e-58:327:92//L29155
- 45 F-MAMMA1001082//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//3.8e-87:695:77//AC004087
- F-MAMMA1001091//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//7.0e-05:594:60//AC005256
- F-MAMMA1001092//Human DNA sequence from PAC 49C23 on chromosome X contains malate dehydrogenase pseudogene and STS.//1.6e-91:174:87//Z93019
- 50 F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds.//6.4e-23:507:66//AF016045
- F-MAMMA1001110//Homo sapiens chromosome 19, cosmid F16815, complete sequence.//0.77:316:60//AC004637
- 55 F-MAMMA1001126//Homo sapiens PAC 50H2 in the CUTL1 locus, complete sequence.//3.3e-21:237:73//AF047825
- F-MAMMA1001133//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//0.97:202:63//Z95116

- F-MAMMA1001139//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt]//1.6e-84:406.82//S70011  
 F-MAMMA1001143//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//1.3e-14:182.76//AL022339  
 F-MAMMA1001145//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//5.2e-87:714:78//Z71187  
 5 F-MAMMA1001154//CIT-HSP-2341D13.TF CIT-HSP Homo sapiens genomic clone 2341D13 genomic survey sequence.//0.00051:249.61//AQ055735  
 F-MAMMA1001161//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//2.2e-30:410.70//AC004518  
 10 F-MAMMA1001162//Homo sapiens full-length insert cDNA clone ZA79C01.//2.4e-13:87:100//AF086123  
 F-MAMMA1001181//Mus musculus C2C12 unknown mRNA, partial cds.//9.3e-15:432:60//U31629  
 F-MAMMA1001186//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//6.8e-57:670:72//AC005696  
 F-MAMMA1001191  
 15 F-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//1.5e-117:759:84//U29156  
 F-MAMMA1001202  
 F-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.5e-161:764:98//AC005412  
 F-MAMMA1001206//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//5.1e-30:535:65//AC004099  
 20 F-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//8.4e-182:860:98//AC005393  
 F-MAMMA1001220//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.7e-58:690:70//AC004875  
 25 F-MAMMA1001222//Mouse Ioridin mRNA, complete cds.//2.7e-07:624:58//M34398  
 F-MAMMA1001243//Homo sapiens chromosome 17, clone hRPK.192\_H\_23, complete sequence.//0.91:177:66//AC005726  
 F-MAMMA1001244  
 F-MAMMA1001249//Human 28S ribosomal RNA pseudogenes and alu repeat region sequence.//6.7e-09:502:58//U67616  
 30 F-MAMMA1001256//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//5.0e-37:342:80//Z99495  
 F-MAMMA1001259  
 F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//8.7e-40:659:64//AB014561  
 35 F-MAMMA1001268//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//4.9e-43:265:81//AC004453  
 F-MAMMA1001271//Salmo salar DNA for a cryptic repeat.//2.6e-06:311:63//AJ012206  
 F-MAMMA1001274//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.6e-70:327:83//AC004840  
 40 F-MAMMA1001280//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-05:276:66//AC003035  
 F-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//3.6e-98:199:98//AL022314  
 45 F-MAMMA1001296//RPC111-38B4.TV RPC11-11 Homo sapiens genomic clone RPC11-11-38B4, genomic survey sequence.//4.7e-33:292:71//AQ030084  
 F-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.6e-182:860:98//AC005703  
 50 F-MAMMA1001305//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D2ZS1168 and a CA repeat polymorphism, complete sequence.//1.9e-70:163:97//Z93244  
 F-MAMMA1001322//Human DNA sequence from clone 774I24 on chromosome 1q24.1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and GSS, complete sequence.//2.6e-19:379:68//AL031290  
 55 F-MAMMA1001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 197L1, WORKING DRAFT SEQUENCE.//4.5e-131:751:90//AL031390  
 F-MAMMA1001330

- F-MAMMA1001341//Sus scrofa.//1.6e-36:420:73//Z46906  
 F-MAMMA1001343//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//1.1e-05:818:58//AL031744  
 F-MAMMA1001346  
 5 F-MAMMA1001383//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.0e-44:505:74//AC004086  
 F-MAMMA1001388//Human IGF binding protein complex acid-labile subunit a mRNA, complete cds.//1.5e-07:415:58//M86826  
 10 F-MAMMA1001397//Human DNA sequence from clone 462D8 on chromosome 22q11.21-12.1 Contains EST, STS and GSS, complete sequence.//1.6e-23:209:75//AL022332  
 F-MAMMA1001408//HS\_3242\_A1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=21 Row=O, genomic survey sequence.//2.7e-07:181:69//AQ207300  
 F-MAMMA1001411//Homo sapiens autosomal dominant polycystic kidney disease type II protein (PKD2) gene, exon 14.//0.98:120:68//AF004872  
 15 F-MAMMA1001419//HS\_2053\_B1\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=23 Row=L, genomic survey sequence.//1.9e-75:424:93//AQ244585  
 F-MAMMA1001420//Homo sapiens chromosome 4 clone B203C23 map 4q25, complete sequence.//2.4e-09:199:70//AC004049  
 20 F-MAMMA1001435//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-201104, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-42:558:69//AC004529 F-MAMMA1001442//Plasmodium falciparum chromosome 2, section 37 of 73 of the complete sequence.//0.0019:516:56//AE001400  
 F-MAMMA1001446//Homo sapiens Xp22 BAC GSHB-519ES (Genome Systems Human BAC library) complete sequence.//3.6e-42:486:70//AC003684  
 25 F-MAMMA1001452//RPC111-48022.TJ RPC111 Homo sapiens genomic clone R-48022, genomic survey sequence.//5.3e-87:423:98//AQ199294  
 F-MAMMA1001465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING DRAFT SEQUENCE.//0.00038:114:75//AL033543  
 F-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//4.1e-99:604:87//L31783  
 30 F-MAMMA1001487//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0e-13:158:77//AC005486  
 F-MAMMA1001501//Human mRNA for calcium activated neutral protease large subunit (muCANP, calpain, EC 3.4.22.17).//9.6e-52:438:81//X04366  
 F-MAMMA1001502//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B7, WORKING DRAFT SEQUENCE.//3.7e-152:720:99//AL031714  
 35 F-MAMMA1001510//Human PAC clone DJ34804 from 22q12.1-qter, complete sequence.//1.1e-05:371:61//AC002378  
 F-MAMMA1001522  
 F-MAMMA1001547  
 40 F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.3e-128:614:98//AB007931  
 F-MAMMA1001575//Human chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//0.97:154:68//AF001548  
 F-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//1.8e-95:529:91//M61764  
 F-MAMMA1001590//Human DNA sequence from clone 125H2 on chromosome 22q11-12 Contains part of myosin heavy chain gene, EST, CA repeat, STS, GSS, complete sequence.//1.8e-07:104:84//Z98949  
 45 F-MAMMA1001600//HS\_3022\_A2\_H01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=2 Row=O, genomic survey sequence.//1.6e-66:405:90//AQ163791  
 F-MAMMA1001604//Human DNA sequence from clone 1114G22 on chromosome 1q24-25 Contains EST, CA repeat, Ninenin like sequence, complete sequence.//0.00043:715:58//AL008626  
 50 F-MAMMA1001606//Jd114 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 2G6, genomic survey sequence.//0.19:266:62//B13685  
 F-MAMMA1001620//Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds.//9.7e-54:442:69//AF053630  
 F-MAMMA1001627//X.borealis ribosomal spacer DNA, with a DNaseI-hypersensitive site.//0.14:221:62//M29833  
 55 F-MAMMA1001630//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.0e-47:611:71//AC005412  
 F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds.//1.1e-42:611:67//U57796  
 F-MAMMA1001635//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//4.0e-35:407:70//AC000118



F-MAMMA1001649//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.44:245:63//AL022577

F-MAMMA1001654//Mouse transcriptional control element.//0.0025:189:63//M17284

F-MAMMA1001663//CIT-HSP-2165E16.TR CIT-HSP Homo sapiens genomic clone 2165E16, genomic survey sequence.//9.7e-05:146:66//B95491

F-MAMMA1001670//HS\_3136\_A1\_G06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=11 Row=M, genomic survey sequence.//3.1e-28:237:85//AQ148779

F-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//3.3e-181:863:98//AC005614

F-MAMMA1001679//HS\_3054\_A1\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=O, genomic survey sequence.//1.0:89:70//AQ106118

F-MAMMA1001683//Spermatogenesis similis mRNA for 90 kD basal apparatus-protein.//8.3e-07:480:62//AJ224970

F-MAMMA1001686//HS\_3219\_B1\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=5 Row=B, genomic survey sequence.//0.00072:180:65//AQ180345

F-MAMMA1001692//HS\_3047\_B1\_B10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=D, genomic survey sequence.//2.5e-94:459:98//AQ134228

F-MAMMA1001711//Homo sapiens clone DJ0635005, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-42:316:82//AC004845

F-MAMMA1001715//CIT-HSP-2347A14.TF CIT-HSP Homo sapiens genomic clone 2347A14, genomic survey sequence.//1.1e-60:413:87//AQ059125

F-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//1.8e-133:646:97//AF095687

F-MAMMA1001735//chicken brain tubulin beta chain mma.//3.5e-110:740:84//J00913

F-MAMMA1001740//Human DNA sequence from PAC 136017 on chromosome X contains ESTs and STS.//0.98:416:57//Z72001

F-MAMMA1001743//Homo sapiens clone DJ0981007, complete sequence.//3.2e-16:194:75//AC006017

F-MAMMA1001744//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//0.0036:181:66//AL030998

F-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//1.2e-60:822:68//AF070718

F-MAMMA1001751//Human potassium channel KCNO1 mRNA, complete cds.//1.2e-35:583:65//U90065

F-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//8.4e-102:627:87//AF041338

F-MAMMA1001757//HS\_2058\_B2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=8 Row=F, genomic survey sequence.//1.7e-24:173:88//AQ243865

F-MAMMA1001760//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man9)-alpha-mannosidase, EC 3.2.1.113, a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//6.6e-76:349:87//AL022722

F-MAMMA1001764//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.23:633:57//M97514

F-MAMMA1001768//Bovine herpesvirus 1 complete genome.//2.3e-11:547:60//AJ004801

F-MAMMA1001769//Homo sapiens 12q13.1 PAC RPC1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-76:509:78//AC004801

F-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.7e-106:744:82//X85991

F-MAMMA1001783//Human PAC clone 127H14 from 12q, complete sequence.//6.0e-20:228:75//AC002563

F-MAMMA1001785

F-MAMMA1001788//Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene. Contains ESTs, STSs and GSSs, complete sequence.//5.0e-05:152:74//Z99129

F-MAMMA1001790//Homo sapiens chromosome 12p13.3 clone RPC13-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//4.5e-53:318:80//AC005845

F-MAMMA1001806//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//1.0:131:67//AC004262

F-MAMMA1001812//Human Chromosome X clone bWXD187, complete sequence.//3.0e-34:257:83//AC004383

5 F-MAMMA1001815//Homo sapiens PAC clone DJ0850G01 from 7q21.2-q22, complete sequence.//5.2e-61:516:79//AC004128

F-MAMMA1001817//Homo sapiens 12q24 PAC RPC11-261P5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.1e-32:295:78//AC004031

F-MAMMA1001818//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1.333303.//0.71:179:67//AJ011930

10 F-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//3.0e-91:726:79//Y13148

F-MAMMA1001824//HS\_3108\_A1\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=23 Row=M, genomic survey sequence.//3.4e-05:119:74//AQ107508

F-MAMMA1001836//Homo sapiens chromosome 18, clone hRPK.537\_E\_1, complete sequence.//3.4e-45:312:85//AC006211

15 F-MAMMA1001837//Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA, complete cds.//4.5e-51:480:75//AF052042

F-MAMMA1001848//CITBE1-2516P17.TF CITBE1-Homo sapiens genomic clone 2516P17, genomic survey sequence.//1.0e-100:486:98//AQ279620

F-MAMMA1001851//Human DNA from overlapping chromosome 19-specific cosmids R30072 and R28588, genomic sequence, complete sequence.//5.1e-07:197:67//AC002390

20 F-MAMMA1001854

F-MAMMA1001858//RPC11-11L22.TP RPC11-Homo sapiens genomic clone RPC11-11L22, genomic survey sequence.//0.091:161:65//B75631

F-MAMMA1001864//Human PAC clone DJ0205E24 from Xq23, complete sequence.//2.6e-09:397:61//AC003013

25 F-MAMMA1001868//HS\_2196\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=24 Row=B, genomic survey sequence.//5.8e-13:86:100//AQ032455

F-MAMMA1001874//H.sapiens CpG island DNA genomic MseI fragment, clone 63h5, reverse read cp63h5.rta.//1.0:127:63//Z62129

F-MAMMA1001878//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//1.7e-19:372:67//Z94802

30 F-MAMMA1001880//RPC11-90K3.TJ RPC11-Homo sapiens genomic clone R-90K3, genomic survey sequence.//6.6e-11:362:62//AQ283465

F-MAMMA1001890//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508115, WORKING DRAFT SEQUENCE.//1.8e-45:317:86//AL021707

35 F-MAMMA1001907//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//2.7e-23:255:77//Z82207

F-MAMMA1001908//HS\_2225\_A1\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2225 Col=5 Row=A, genomic survey sequence.//5.4e-08:264:62//AQ301597

40 F-MAMMA1001931//HS\_3049\_B2\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=18 Row=H, genomic survey sequence.//1.7e-47:295:90//AQ100157

F-MAMMA1001956//H.sapiens DNA sequence.//0.056:233:66//Z22493

F-MAMMA1001963//Homo sapiens adenylosuccinate lyase gene, complete cds.//0.99:173:68//AF106656

F-MAMMA1001969//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//5.3e-63:479:78//Z73986

45 F-MAMMA1001970//Homo Sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.4e-126:699:93//AC003071

F-MAMMA1001992//HS\_3078\_A1\_A09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=17 Row=A, genomic survey sequence.//3.3e-08:257:65//AQ143646

50 F-MAMMA1002009//Homo sapiens chromosome 17, clone hRPK.214\_O\_1, complete sequence.//1.5e-07:244:62//AC005224

F-MAMMA1002011//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//1.3e-07:170:69//AQ304711

F-MAMMA1002032//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//2.1e-34:315:79//AC004803

55 F-MAMMA1002033//HS\_3023\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=8 Row=M, genomic survey sequence.//4.3e-69:366:94//AQ105493

F-MAMMA1002041//Genomic sequence from Human 9q34, complete sequence.//5.3e-85:439:82//AC001227

F-MAMMA1002042//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//1.4e-20:314:70//

AC005669

F-MAMMA1002047//Homo sapiens 12p13.3 BAC RPC11-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//6.8e-14:526:62//AC005906

F-MAMMA1002056//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.1e-47:648:71//AL030996

F-MAMMA1002058//Homo sapiens PAC clone DJ0732C22 from 7p11.2-p13, complete sequence.//2.4e-19:256:74//AC04869

F-MAMMA1002068//Homo sapiens, clone hRPK.2\_A\_1, complete sequence.//5.4e-41:407:78//AC006197

F-MAMMA1002078//Human DNA sequence from PAC 106I20 on chromosome 22q12 Contains ESTs and STS, complete sequence.//0.021:333:64//Z81313

F-MAMMA1002082

F-MAMMA1002084//Caenorhabditis elegans cosmid F28C12, complete sequence.//0.032:469:58//Z93380

F-MAMMA1002093//HS\_3050\_B1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=11 Row=L, genomic survey sequence.//1.0:77:71//AQ105997

F-MAMMA1002108//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//8.3e-10:464:60//AF017308

F-MAMMA1002118

F-MAMMA1002125//Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.//1.0e-35:619:68//AC003962

F-MAMMA1002132//RPC11-78F11.TJ RPC11 Homo sapiens genomic clone R-78F11, genomic survey sequence.//1.0e-90:357:97//AQ286460

F-MAMMA1002140//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-45:583:64//AC004216

F-MAMMA1002143//Human serum constituent protein (MSE55) mRNA, complete cds.//6.0e-11:192:70//M88338

F-MAMMA1002145//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//0.0028:570:59//AL021391

F-MAMMA1002153//HS\_3005\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=7 Row=G, genomic survey sequence.//4.9e-41:213:99//AQ132213

F-MAMMA1002155//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462O23, WORKING DRAFT SEQUENCE.//1.2e-45:303:78//AL031431

F-MAMMA1002156

F-MAMMA1002158//CITBI-E1-2508P18.TR CITBI-E1 Homo sapiens genomic clone 2508P18, genomic survey sequence.//7.1e-42:255:92//AQ266165

F-MAMMA1002170//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//2.0e-81:604:81//AC004448

F-MAMMA1002174//Homo sapiens clone UWGC:y67c126 from 6p21, complete sequence.//3.2e-43:333:83//AC004212

F-MAMMA1002198//H.sapiens thiol-specific antioxidant protein mRNA.//1.0e-34:121:98//Z22548

F-MAMMA1002209//HS\_2197\_B1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2197 Col=13 Row=J, genomic survey sequence.//9.6e-18:163:84//AQ210058

F-MAMMA1002215//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//6.3e-08:435:60//AF017308

F-MAMMA1002219//Rattus norvegicus roxo70 mRNA, complete cds.//1.8e-124:752:87//AF032667

F-MAMMA1002230//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.67:356:59//AC004710

F-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//9.3e-140:836:87//U38253

F-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//1.4e-145:691:98//AC005666

F-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//6.0e-138:660:98//AC005600

F-MAMMA1002267//Homo sapiens chromosome 2, P1 clone 777H5 (LBNL H27), complete sequence.//0.066:333:60//AC003676

F-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a)mRNA, partial cds.//1.1e-39:404:74//AF068748

F-MAMMA1002269//HS\_3163\_B1\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

- nomic clone Plate=3163 Col=5 Row=H, genomic survey sequence.//1.0.150:63//AQ171576  
 F-MAMMA1002282//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.5e-22:315:67//AC003108  
 F-MAMMA1002292//B. garinii (strain T1s1) p83/100 gene (partial).//0.73:200:64//X81533  
 5 F-MAMMA1002293//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//1.6e-56:408:75//AC006023  
 F-MAMMA1002294//Sequence 2 from Patent WO9516779.//1.8e-06:401:62//A45258  
 F-MAMMA1002297  
 F-MAMMA1002298//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.0056:525:61//AC004221  
 10 F-MAMMA1002299//CIT-HSP-2345B2.TR CIT-HSP Homo sapiens genomic clone 2345B2, genomic survey sequence.//1.2e-90:446:98//AQ053994  
 F-MAMMA1002308//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//1.3e-35:329:78//AL031680  
 15 F-MAMMA1002310//Human gastric (H\* \* K\*)-ATPase gene, complete cds.//0.0060:301:60//J05451  
 F-MAMMA1002311//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.6e-50:327:69//AC004737  
 F-MAMMA1002312//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and STS.//1.3e-09:741:58//Z86064  
 20 F-MAMMA1002317  
 F-MAMMA1002321//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//1.9e-158:746:99//AC005756  
 F-MAMMA1002322//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//5.3e-52:617:70//AC004796  
 25 F-MAMMA1002329//Homo sapiens RaP2 interacting protein 8 (RPIP8) mRNA, complete cds.//0.22:143:67//U93871  
 F-MAMMA1002332//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//1.6e-31:287:74//AL034402  
 F-MAMMA1002333//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//2.5e-09:674:59//AL022022  
 30 F-MAMMA1002339//Homo sapiens chromosome 21q22.3, cosmid clone Q4H9 complete sequence bases 1.41604.//2.1e-57:522:77//AJ011932  
 F-MAMMA1002347//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.0e-14:258:69//AC004129  
 35 F-MAMMA1002351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1059H15, WORKING DRAFT SEQUENCE.//7.8e-132:723:91//AL022100  
 F-MAMMA1002352//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 128O3, WORKING DRAFT SEQUENCE.//5.8e-17:326:70//Z98742  
 F-MAMMA1002353//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.1e-14:399:63//AC004825  
 40 F-MAMMA1002355//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 109G6, WORKING DRAFT SEQUENCE.//3.7e-43:420:75//AL023879  
 F-MAMMA1002356//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:534:59//AC004153  
 45 F-MAMMA1002359//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.3e-18:156:75//AC005831  
 F-MAMMA1002360//Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST.//4.9e-43:353:69//Z68885  
 F-MAMMA1002361//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//1.8e-22:282:74//AL008719  
 50 F-MAMMA1002362//Platymys spixii CR1-like LINE, partial sequence.//0.00058:83:79//D82938  
 F-MAMMA1002380//CIT-HSP-2383K24.TF CIT-HSP Homo sapiens genomic clone 2383K24, genomic survey sequence.//4.4e-10:85:92//AQ196889  
 F-MAMMA1002384//RPCI11-80J20.TV RPCI11 Homo sapiens genomic clone R-80J20, genomic survey sequence.//2.7e-56:286:98//AQ284134  
 55 F-MAMMA1002385//CIT-HSP-2328G13.TF CIT-HSP Homo sapiens genomic clone 2328G13, genomic survey sequence.//5.5e-46:335:84//AQ043985  
 F-MAMMA1002392//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-29:273:78//

AC004888

F-MAMMA1002411//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//8.2e-09:287:63//AL023 875

F-MAMMA1002413//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var1) gene, complete cds.//9.6e-08:730:57//L40608

F-MAMMA1002417//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//4.1e-06:181:72//AL034402

F-MAMMA1002427//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//1.3e-51:593:72//AC004604

F-MAMMA1002428

F-MAMMA1002434//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//7.3e-56:388:81//Z93023

F-MAMMA1002446//CIT-HSP-2324O22.TR CIT-HSP Homo sapiens genomic clone 2324O22, genomic survey sequence.//2.3e-56:302:95//AQ027479

F-MAMMA1002454//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.1e-54:190:94//AC005229

F-MAMMA1002461//Rattus norvegicus calcium channel alpha-1 subunit gene, partial cds.//0.00045:457:60//U14005

F-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//9.7e-33:709:60//U10556

F-MAMMA1002475//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.092:506:58//AC004671

F-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2-unordered pieces.//0.025:100:76//AC005077

F-MAMMA1002485//Homo sapiens stannocalcin-2 (STC-2) mRNA, complete cds.//2.9e-118:560:98//AF055460

F-MAMMA1002494//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//1.5e-22:297:73//AC005913

F-MAMMA1002498//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//7.2e-10:330:64//AC002477

F-MAMMA1002524//Homo sapiens huntingtin gene, partial exon.//0.0080:124:72//L49359

F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.4e-160:775:97//AF065214

F-MAMMA1002545//Homo sapiens chromosome 17, clone hRPC74\_E\_22 complete sequence.//1.9e-41:345:80//AC005696

F-MAMMA1002554

F-MAMMA1002556

F-MAMMA1002566

F-MAMMA1002571//CIT-HSP-2296N17.TR CIT-HSP Homo sapiens genomic clone 2296N17, genomic survey sequence.//1.7e-07:76:90//AQ006579

F-MAMMA1002573//Homo sapiens DNA, trinucleotide repeats region, clone GAA C27.//2.7e-08:195:70//AB018507

F-MAMMA1002585

F-MAMMA1002590//Homo sapiens BAC clone GS250A16 from 7p21-p22, complete sequence.//2.1e-26:361:69//AC005019

F-MAMMA1002597//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1103G7, WORKING DRAFT SEQUENCE.//1.3e-34:550:69//AL034548

F-MAMMA1002598//H. sapiens mRNA for ribosomal protein L7.//1.1e-21:123:100//X57958

F-MAMMA1002603//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//0.0018:358:61//AC005220

F-MAMMA1002612//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//2.1e-13:336:63//AC004861

F-MAMMA1002617//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.14:229:64//AC005486

F-MAMMA1002618

F-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.5e-71:319:85//AJ010598

F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds.//1.5e-20:157:90//AF041449

F-MAMMA1002623//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//8.3e-06:137:72//AE000660

F-MAMMA1002625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1056L3, WORKING

DRAFT SEQUENCE.//1.9e-171:819:98//AL031727

F-MAMMA1002629//Human BAC clone RG385F02 from 7p15, complete sequence.//4.8e-85:478.78//AC003093

F-MAMMA1002636//Human POU domain factor (Brn-3a) gene, exon 2, complete cds.//5.6e-09:499:62//U10063

F-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//3.6e-115:785.82//AF055666

5 F-MAMMA1002646//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.5e-45:291:90//AC002038

F-MAMMA1002650//Homo sapiens candidate tumor suppressor HIC-1 (HIC-1) gene, complete cds.//6.6e-06:661:59//L41919

10 F-MAMMA1002655//HS\_2003\_A2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2003 Col=22 Row=A, genomic survey sequence.//9.0e-15:198:74//AQ224233

F-MAMMA1002662

F-MAMMA1002665//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.4e-37:235.84//AC005029

15 F-MAMMA1002671//Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.//0.00027:272:64//U22398

F-MAMMA1002673

F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//3.7e-161:752:99//D86987

F-MAMMA1002685//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39417, WORKING DRAFT SEQUENCE.//6.2e-45:510:70//AL023585

F-MAMMA1002698//HS\_3024\_B1\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3024 Col=11 Row=F, genomic survey sequence.//1.7e-10:155:75//AQ072214

20 F-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//5.9e-75:509:83//AF018261

F-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//1.2e-159:749:99//AB011399

25 F-MAMMA1002708//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//3.0e-57:347:79//AL031053

F-MAMMA1002711//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//3.4e-31:484:69//AC005030

F-MAMMA1002721//CIT-HSP-2350M5.TR CIT-HSP Homo sapiens genomic clone 2350M5, genomic survey sequence.//1.4e-06:265.63//AQ061245

30 F-MAMMA1002727//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAT repeat polymorphism, complete sequence.//0.18:386:58//AL023584

F-MAMMA1002728//Human DNA sequence from PAC 296K21 on chromosome X contains cytokerin exon, delta-aminolevulinic synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37), 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//3.2e-05:362:63//Z83821

35 F-MAMMA1002744//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//0.00010:535.58//AE001368

F-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//1.2e-182:880:97//AC005856

40 F-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-175:829:98//AC006055

F-MAMMA1002754//Homo Sapiens Chromosome X clone BWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.1e-31:372:75//AC004676

F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds.//3.3e-26:151:98//AB007902

45 F-MAMMA1002764//Human Chromosome 11 Cosmid cSRL166a1, complete sequence.//5.2e-49:355:81//U73636

F-MAMMA1002765//RPCI11-20A22.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20A22, genomic survey sequence.//6.7e-13:155:76//B92153

F-MAMMA1002769//CIT-HSP-2323G1.TF CIT-HSP Homo sapiens genomic clone 2323G1, genomic survey sequence.//9.7e-21:151:90//AQ028244

50 F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//5.6e-105:179:99//U07561

F-MAMMA1002780//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-08, complete sequence.//0.071:277:58//Z98546

F-MAMMA1002782//HS\_3213\_B2\_B08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=16 Row=D, genomic survey sequence.//0.00018:219:63//AQ175845

55 F-MAMMA1002796

F-MAMMA1002807//Human Chromosome X PAC RPCI1-290C9 from the Pieter de Jong Human PAC library; complete sequence.//6.9e-22:332:69//AC002404

- F-MAMMA1002820//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.5e-11:483:62//AC003035
- F-MAMMA1002830//Homo sapiens chromosome 17, clone hCIT529110, complete sequence.//1.0e-64:320:83//AC002553
- 5 F-MAMMA1002833//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//2.8e-47:413:80//AC004875
- F-MAMMA1002835
- F-MAMMA1002838//A-916H10.TP CIT978SK Homo sapiens genomic clone A-916H10, genomic survey sequence.//1.1e-39:164:83//B14462
- 10 F-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//1.9e-62:373:81//U58883
- F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds.//1.7e-135:635:99//AB018353
- F-MAMMA1002844//F1707-T7 IGF Arabidopsis thaliana genomic clone F1707, genomic survey sequence.//6.7e-17:383:66//B11616
- F-MAMMA1002858
- 15 F-MAMMA1002868//RPCI11-54F9.TJ RPCI11 Homo sapiens genomic clone R-54F9, genomic survey sequence.//8.3e-81:392:99//AQ081566
- F-MAMMA1002869//Sequence 1 from patent US 5552529.//2.2e-86:696:78//I25863
- F-MAMMA1002871//Lupinus angustifolius nodulin-45 gene, complete cds.//0.029:370:59//L12388
- F-MAMMA1002880//RPCI11-23M23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-23M23, genomic survey sequence.//1.8e-20:271:74//B86518
- 20 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds.//1.2e-28:680:61//D45027
- F-MAMMA1002886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380A1, WORKING DRAFT SEQUENCE.//0.00040:505:57//Z97653
- F-MAMMA1002887//HS\_3238\_B2\_G08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=16 Row=N, genomic survey sequence.//5.5e-79:401:97//AQ219814
- 25 F-MAMMA1002890//Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes.//4.6e-35:136:73//AF109906
- F-MAMMA1002892//Mouse Cosmid ma66a100 from 14D1-D2, complete sequence.//5.7e-14:450:60//AC004096
- 30 F-MAMMA1002895//H.sapiens CpG island DNA genomic MseI fragment, clone 46b6, forward read cpg46b6.ft1a.//3.7e-36:190:100//Z58616
- F-MAMMA1002908//Penaeus monodon microsatellite locus Pmo27.//1.1e-05:195:62//AF068828
- F-MAMMA1002909//Human Chromosome 11 pac pDJ205d23, complete sequence.//1.0e-13:457:61//AC002402
- F-MAMMA1002930//Homo sapiens Xp22 BAC GSHB-512P14 (Genome Systems Human BAC library) complete sequence.//0.25:260:62//AC004467
- 35 F-MAMMA1002937//H.sapiens ZNF74-1 mRNA.//6.3e-13:577:59//X71623
- F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds.//5.1e-193:910:98//AB014598
- F-MAMMA1002941//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 in BCRL2-GGT Region, complete sequence.//2.7e-23:174:77//AC004032
- 40 F-MAMMA1002947//Rhodococcus capsulatus strain SB1003, partial genome.//1.3e-09:475:61//AF010496
- F-MAMMA1002964//Human thiopurine methyltransferase (TPMT) gene, exon 5.//0.0029:314:60//AF019366
- F-MAMMA1002970//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//4.0e-10:194:71//Z94056
- 45 F-MAMMA1002972//H.sapiens CpG island DNA genomic MseI fragment, clone 2g10, forward read cpg2g10.ft1a.//0.3e:156:66//Z55272
- F-MAMMA1002973//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//2.9e-41:234:79//AC005919
- F-MAMMA1002982//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//1.7e-05:322:63//AL022098
- 50 F-MAMMA1002987//CITBI-E1-2514J12.TR CITBI-E1 Homo sapiens genomic clone 2514J12, genomic survey sequence.//0.0064:135:66//AQ275871
- F-MAMMA1003003//cSRL-145D12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-145D12, genomic survey sequence.//2.8e-31:201:89//B01998
- 55 F-MAMMA1003004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y237C10, WORKING DRAFT SEQUENCE.//1.6e-10:180:73//AL031601
- F-MAMMA1003007//Homo sapiens (clone cosmid c11q-8D1) tetranucleotide repeat polymorphism at the D11S488 locus.//3.5e-12:435:61//U04732

F-MAMMA1003011//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//2.3e-50:734:67//U79139  
 F-MAMMA1003013//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.2e-86:341:79//AC003694

5 F-MAMMA1003015//Homo sapiens Chromosome 16 BAC clone CIT987SK-591M7, complete sequence.//2.6e-13:443:61//AC003661  
 F-MAMMA1003019//HS\_3221\_A1\_A01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=1 Row=A, genomic survey sequence.//2.8e-51:299:92//AQ184271  
 F-MAMMA1003026  
 F-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//0.0037:134:73//AC005214

10 F-MAMMA1003035//RPCI-11-11P4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11P4, genomic survey sequence.//1.1e-07:66:100//B74936  
 F-MAMMA1003039//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.1e-19:220:76//AC004671  
 F-MAMMA1003040//Human DNA sequence from PAC 340N1 on chromosome 1p35-36.2. Contains ESTs, polymorphic CA repeat, trna and endogenous retrovirus.//9.5e-91:469:78//Z98257

15 F-MAMMA1003044//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//0.21:289:61//AL031321  
 F-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//1.7e-139:663:98//AF077952

20 F-MAMMA1003049  
 F-MAMMA1003055//HS\_3014\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=20 Row=L, genomic survey sequence.//4.2e-05:215:64//AQ164940  
 F-MAMMA1003056//HS\_3221\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=24 Row=H, genomic survey sequence.//1.4e-16:206:74//AQ302772

25 F-MAMMA1003057//M.domesticus MD6 mRNA.//8.5e-128:654:94//X54352  
 F-MAMMA1003066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 273F20, WORKING DRAFT SEQUENCE.//1.0:142:71//AL034371  
 F-MAMMA1003089//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.7e-42:373:78//AC004796

30 F-MAMMA1003099//Homo sapiens beta-filamin mRNA, complete cds.//2.6e-42:288:88//AF042166  
 F-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//1.6e-12:477:64//U72634  
 F-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//3.4e-121:789:85//AF071316

35 F-MAMMA1003127//R.norvegicus MYR1 mRNA for myosin I heavy chain.//9.4e-58:423:83//X68199  
 F-MAMMA1003135//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.62:676:58//U67916  
 F-MAMMA1003140

40 F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//2.2e-80:397:97//Y15062  
 F-MAMMA1003150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING DRAFT SEQUENCE.//7.3e-123:266:88//AL021579  
 F-MAMMA1003166//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SEQUENCE.//1.6e-33:143:82//Z99716

45 F-NT2RM1000001//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//0.50:216:61//Z95400  
 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//4.8e-65:385:92//D31886  
 F-NT2RM1000032  
 F-NT2RM1000035//Cricetus griseus SREBP cleavage activating protein (SCAP) mRNA, complete cds.//6.3e-135:565:84//U67060

50 F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.1e-106:542:95//AB014590  
 F-NT2RM1000039//Mouse genetic suppressor element mRNA.//0.080:239:60//L27155  
 F-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//8.4e-96:535:91//D87671  
 F-NT2RM1000059//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600

55 F-NT2RM1000062//Nephila clavipes dragline silk protein spidroin 1 gene, partial cds.//0.54:306:63//U37520  
 F-NT2RM1000080//Sequence 2 from patent US 5763589.//1.5e-115:566:97//AR012692  
 F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//1.8e-114:550:97//AB014561



F-NT2RM1000092//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.63:180:65//AC005594

F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.027:126:70//AF007155

5 F-NT2RM1000119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//0.022:644:58//Z97630

F-NT2RM1000127//RPC11-44E5.TJ RPC11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//1.6e-45:254:94//AQ195884

F-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete cds.//5.5e-153:778:95//AB018335

10 F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUF56 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1e-90:448:97//AF044959

F-NT2RM1000153//Human NotI linking clone 924A081D, genomic survey sequence.//5.9e-07:66:96//U49890

F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.025:126:70//AF007155

F-NT2RM1000187//CITB1-E1-2510J4.TR CITB1-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.1e-05:56:98//AQ261184

15 F-NT2RM1000199//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//1.6e-38:711:65//D64009

F-NT2RM1000242

F-NT2RM1000244//HS\_2229\_A1\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2229 Col=7 Row=E, genomic survey sequence.//2.0e-13:95:95//AQ298474

20 F-NT2RM1000252//Homo sapiens chromosome 17, clone hRPK\_206\_C\_20, complete sequence.//0.023:225:61//AC006070

F-NT2RM1000256//Caenorhabditis elegans cosmid F22B3, complete sequence.//8.5e-24:473:64//Z68336

F-NT2RM1000257//Homo sapiens MAGOH mRNA, complete cds.//6.4e-69:455:85//AF035940

F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds.//6.5e-57:460:80//D50920

25 F-NT2RM1000271

F-NT2RM1000272

F-NT2RM1000280//Bos gaurus vacuolar H-ATPase subunit D (VATD) mRNA, complete cds.//6.7e-97:430:92//U11927

F-NT2RM1000300//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//2.1e-96:170:100//Z93097

30 F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds.//8.1e-127:708:92//D63880

F-NT2RM1000318//Homo sapiens mRNA for ribosomal protein L39, complete cds.//5.7e-34:182:99//D79205

F-NT2RM1000341//Homo sapiens full-length insert cDNA clone YP11F06.//1.3e-100:504:97//AF085879

F-NT2RM1000354//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//1.6e-11:201:73//AQ218494

35 F-NT2RM1000355//Mus musculus E25B protein mRNA, complete cds.//1.8e-77:578:82//U76253

F-NT2RM1000365//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.4e-113:367:97//AC004821

F-NT2RM1000377//H.sapiens mRNA for MAP kinase phosphatase 4.//6.1e-14:362:62//Y08302

40 F-NT2RM1000388//Azospirillum brasilense lateral flagellin (laf1) gene, complete cds.//1.0e-482:58//U26679

F-NT2RM1000394//M.musculus mRNA for histone H3.3A.//1.7e-94:549:89//Z85979

F-NT2RM1000399

F-NT2RM1000421//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//3.6e-08:195:72//AQ032737

45 F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//3.7e-84:418:97//AF084928

F-NT2RM1000499//Human mRNA for KIAA0167 gene, complete cds.//1.3e-35:525:69//D79989

F-NT2RM1000539//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//4.6e-73:533:83//AC004993

50 F-NT2RM1000553

F-NT2RM1000555//Homo sapiens clone 24514 unknown mRNA.//2.3e-110:555:97//AF070542

F-NT2RM1000563//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-123:477:100//AC004873

F-NT2RM1000623//HS\_2213\_B1\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//8.2e-06:75:89//AQ032737

55 F-NT2RM1000648//Halobium cutitubrum L11, L1, L10 and L12 equivalent ribosomal protein gene cluster.//1.3e-06:414:61//X15078

F-NT2RM1000661//Homo sapiens cap-binding protein 4EHP mRNA, complete cds.//9.3e-54:275:97//AF047695

F-NT2RM1000666//HS\_2016\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=P, genomic survey sequence.//5.7e-13:199:73//AQ227865

F-NT2RM1000669//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//2.7e-94:499:94//AL031133

5 F-NT2RM1000672

F-NT2RM1000691//Homo sapiens HRIHFB2060 mRNA, partial cds.//2.2e-119:582:98//AB015348

F-NT2RM1000699//Caenorhabditis elegans cosmid Y41C4A, complete sequence.//0.95:284:61//AL032627

10 F-NT2RM1000702//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.073:290:58//AQ089514

F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase.//4.8e-65:435:85//AJ004832

F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds.//8.0e-126:690:92//AB011139

F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//2.5e-66:524:83//AF027208

15 F-NT2RM1000746//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 22S15, BAC clone 7B7, complete sequence bases 1.333303.//0.92:395:58//AJ011930

F-NT2RM1000770//Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds.//2.1e-70:407:92//L39210

F-NT2RM1000772//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.6e-36:98:93//AC000380

20 F-NT2RM1000780//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//9.3e-22:126:99//X52233

F-NT2RM1000781//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.1e-09:540:59//AC004153

25 F-NT2RM1000800//Mus musculus mRNA for B-IND1 protein.//4.0e-81:497:88//Z97207

F-NT2RM1000802

F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//3.7e-63:490:84//AF027208

F-NT2RM1000826//Homo sapiens clone 24514 unknown mRNA.//7.2e-153:749:96//AF070542

F-NT2RM1000829//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.74:215:67//AQ099134

30 F-NT2RM1000833//Canis familiaris sec61 homologue mRNA, complete cds.//5.1e-114:683:88//M96629

F-NT2RM1000850//F.rubripes GSS sequence, clone 163A22aF11, genomic survey sequence.//1.1e-26:279:74//AL018762

F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//9.3e-148:726:97//AJ010840

35 F-NT2RM1000857//Rattus norvegicus gene for cytochrome P450/6 beta B, exon 2.//0.97:124:65//AB008378

F-NT2RM1000867//H.sapiens DNA sequence surrounding NotI site, clone NRLA143D.//1.2e-31:172:98//K95834

F-NT2RM1000874//Homo sapiens KE05 protein mRNA, complete cds.//2.8e-131:632:97//AF064605

F-NT2RM1000882//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519a13 containing human gene for ferritin heavy chain (FTH), complete sequence.//1.2e-98:214:99//AC004228

40 F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//2.7e-156:762:97//AF082516

F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds.//2.0e-17:310:67//AB014561

F-NT2RM1000894//Mus musculus second largest subunit of RNA polymerase I (RPA2) mRNA, complete cds.//3.2e-95:469:83//U58280

45 F-NT2RM1000898

F-NT2RM1000905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//1.8e-74:188:98//Z97630

F-NT2RM1000924//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-148:601:98//AC004873

50 F-NT2RM1000927//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.071:392:60//AC004846

F-NT2RM1000962//H.sapiens CpG Island DNA genomic MseI fragment, clone 140d1, forward read cpq140d1.ft1a.//4.1e-35:187:99//Z56803

F-NT2RM1000978//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-23:266:77//AC005959

55 F-NT2RM1001003//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//4.0e-160:760:98//U97067

F-NT2RM1001008//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//1.7e-11:602:61//U52064

F-NT2RM1001043//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//3.9e-93:645:86//Z95125

F-NT2RM1001044//S.pombe chromosome III cosmid c320.//0.90:128:66//AL022245

5 F-NT2RM1001059//Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.//3.8e-53:261:80//AC005915

F-NT2RM1001066//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.64:285:59//B94391

F-NT2RM1001072//HS\_3115\_B1\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=13 Row=H, genomic survey sequence.//7.3e-23:140:95//AQ147905

10 F-NT2RM1001074//Homo sapiens chromosome 19, cosmid F20489, complete sequence.//5.0e-50:186:98//AC005263

F-NT2RM1001082//Sequence 1 from Patent WO9718303.//2.1e-144:736:95//A62731

F-NT2RM1001085//CIT-HSP-2310F21.TR CIT-HSP Homo sapiens genomic clone 2310F21, genomic survey sequence.//8.8e-45:235:97//AQ020757

15 F-NT2RM1001092//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.1e-89:471:95//AQ155489

F-NT2RM1001102//Human HEM45 mRNA, complete cds.//1.2e-28:482:63//U88964

F-NT2RM1001105//Homo sapiens hRED1 gene, exon 1 (5'UTR).//0.0014:349:61//Z95973

20 F-NT2RM1001112//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//0.060:429:58//AC004678

F-NT2RM1001115//Plasmodium falciparum merozoite surface protein 3 (MSP-3) gene, partial cds.//0.93:156:62//AF024624

F-NT2RM1001139//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//1.2e-10:466:59//AC004755

25 F-NT2RM2000006//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//5.3e-150:724:98//AL031291

F-NT2RM2000013//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.5e-58:749:69//X58826

F-NT2RM2000030//Homo sapiens clone DJ0708P22, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.1e-97:270:77//AC004863

30 F-NT2RM2000032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-25:172:76//AL034379

F-NT2RM2000042//Human DNA sequence from cosmid U55E4, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//5.0e-05:325:65//Z73418

35 F-NT2RM2000092//Homo sapiens (D8S321 locus) DNA sequence, tetranucleotide repeat polymorphism.//0.63:117:68//L12269

F-NT2RM2000093//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//0.38:312:62//AF109905

40 F-NT2RM2000101

F-NT2RM2000124//Mouse cAMP-dependent protein kinase catalytic subunit mRNA, complete cds.//3.8e-58:297:97//M12303

F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A2 (PDE9A) mRNA, complete cds.//3.8e-138:653:98//AF067224

45 F-NT2RM2000192//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//2.2e-33:191:95//B93289

F-NT2RM2000239//F.rubripes GSS sequence, clone 156P04aG12, genomic survey sequence.//8.9e-44:445:69//AL018549

50 F-nnnnnnnnnnn//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds.//0.00020:380:61//AF075292

F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds.//3.1e-128:615:98//AB011162

F-NT2RM2000259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310C13, WORKING DRAFT SEQUENCE.//0.0013:305:63//AL031658

F-NT2RM2000260//Mus musculus WW domain binding protein 15 mRNA, partial sequence.//3.0e-14:645:61//AF073934

55 F-NT2RM2000287//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SE-

QUENCE, 50 unordered pieces.//1.3e-11:96:86//AC003656

F-NT2RM2000322//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//8.5e-115:233:97//AL031864

F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//8.8e-175:805:99//AB011132

F-NT2RM2000363//RPC111-90B10.TJ RPC111 Homo sapiens genomic clone R-90B10, genomic survey sequence.//6.7e-15:96:98//AQ285300

F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//1.2e-94:599:86//U48251

F-NT2RM2000371//RPC111-5714.TJ RPC111 Homo sapiens genomic clone R-5714, genomic survey sequence.//1.1e-52:312:91//AQ083343

F-NT2RM2000374//M. musculus nodal gene, a TGF-beta-like gene.//6.7e-31:196:91//X70514

F-NT2RM2000395//Leishmania major chromosome 1, complete sequence.//0.9:345:58//AE001274

F-NT2RM2000402//Arabidopsis thaliana BAC T19D16 genomic sequence.//2.1e-23:414:63//U95973

F-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//1.4e-131:439:88//AF030430

F-NT2RM2000420//HS\_3063\_B2\_F11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//3.2e-25:154:95//AQ103204

F-NT2RM2000422//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//1.7e-128:782:86//L22022

F-NT2RM2000452//HS\_3009\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=10 Row=H, genomic survey sequence.//1.2e-16:122:90//AQ130794

F-NT2RM2000469//HS\_2019\_A1\_G02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2019 Col=3 Row=M, genomic survey sequence.//9.6e-22:176:85//AQ229041

F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds.//7.5e-15:386:63//AB018290

F-NT2RM2000502

F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//5.1e-171:824:97//AF061243

F-NT2RM2000522

F-NT2RM2000540

F-NT2RM2000556//Homo sapiens 12q13.1 PAC RPC15-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.9e-42:344:82//AC004466

F-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//2.8e-154:751:97//AF072132

F-NT2RM2000567//Pseudomonas aeruginosa enoyl-CoA hydratase gene, partial cds; pilin biosynthetic protein (fimL) gene, complete cds; and unknown gene.//3.0e-06:664:58//AF083252

F-NT2RM2000569//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//1.3e-15:348:67//AL031681

F-NT2RM2000577//RPC111-43G22.TJ RPC111 Homo sapiens genomic clone R-43G22, genomic survey sequence.//1.6e-14:155:80//AQ199391

F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.4e-174:820:98//D86987

F-NT2RM2000588//Homo sapiens 12q13.1 PAC RPC15-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-60:344:82//AC004466

F-NT2RM2000594//Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.//4.9e-118:761:85//AF068626

F-NT2RM2000599//O. sativa osr40g3 gene.//0.30:585:56//Y08988

F-NT2RM2000609

F-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.8e-102:709:83//U35776

F-NT2RM2000623//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//3.4e-17:450:65//AC005952

F-NT2RM2000624

2.9e-06:231:64//Z82061

F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//6.3e-142:664:98//AB018272

F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//7.4e-138:664:98//AB014558

F-NT2RM2000639//RPC111-69E5.TJ RPC111 Homo sapiens genomic clone R-69E5, genomic survey sequence.//3.7e-14:97:97//AQ267491

F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-167:518:99//AB014576

F-NT2RM2000669

F-NT2RM2000691//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.1e-106:748:82//AC002038

F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds.//6.8e-49:748:64//D86984

F-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//2.4e-124:594.98//AB015342  
 F-NT2RM2000735//Human ZNF43 mRNA.//8.4e-111:756.82//X59244  
 F-NT2RM2000740//Mus musculus lymphocyte specific helicase mRNA, complete cds.//1.3e-141:815.89//U25691  
 F-NT2RM2000795//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING  
 5 DRAFT SEQUENCE.//1.0e-78:723.76//AL021392  
 F-NT2RM2000821//Rat mRNA for beta COP.//2.0e-150:879.88//X57228  
 F-NT2RM2000837//Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.//1.1e-05:361.62//  
 AC005017  
 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//8.7e-184:847.99//AB015046  
 10 F-NT2RM2000952  
 F-NT2RM2000984//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-  
 RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//  
 7.6e-41:239.76//AF109905  
 F-NT2RM2001004//CIT-HSP-2333N18.TR CIT-HSP Homo sapiens genomic clone 2333N18, genomic survey se-  
 15 quence.//1.1e-11:298.66//AQ035862  
 F-NT2RM2001035//Mus musculus mCAF1 protein mRNA, complete cds.//1.4e-120:627.91//U21855  
 F-NT2RM2001065//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//6.8e-118:690.88//  
 AF071314  
 F-NT2RM2001100//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.3e-  
 20 145:614.99//AC004873  
 F-NT2RM2001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING  
 DRAFT SEQUENCE.//2.7e-95:461.99//AL034380  
 F-NT2RM2001131//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//7.2e-  
 24:726.62//U52064  
 25 F-NT2RM2001141  
 F-NT2RM2001152//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the  
 CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase com-  
 ponent A 1, Choroideremia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, com-  
 30 plete sequence.//0.98:300.62//AL022401  
 F-NT2RM2001177//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//  
 1.2e-147:741.96//AC005488  
 F-NT2RM2001194//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial  
 cds.//0.026:408.59//U66829  
 F-NT2RM2001196//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-  
 35 135:627.98//AC004987  
 F-NT2RM2001201//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503.86//AF046700  
 F-NT2RM2001221//Chimpanzee (P. paniscus) involucrin, complete cds.//0.53:670.55//M26514  
 F-NT2RM2001238//Rat glutaminase mRNA, complete cds.//3.4e-128:719.90//M65150  
 F-NT2RM2001243  
 40 F-NT2RM2001247//CITBI-E1-2521M18.TR CITBI-E1 Homo sapiens genomic clone 2521M18, genomic survey  
 sequence.//0.0011:274.59//AQ276184  
 F-NT2RM2001256//M. musculus mRNA for 200 kD protein.//2.3e-129:742.90//X80169  
 F-NT2RM2001291//CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey se-  
 quence.//4.6e-09:156.72//B57734  
 45 F-NT2RM2001306//RPCI11-28I5.TP RPCI11 Homo sapiens genomic clone RPCI11-28I5, genomic survey se-  
 quence.//0.069:234.64//B84850  
 F-NT2RM2001312//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.1e-22:111:  
 81//AC005919  
 F-NT2RM2001319//Borrelia burgdorferi (section 4 of 70) of the complete genome.//0.99:340.58//AE001118  
 50 F-NT2RM2001324//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 209H1, WORKING  
 DRAFT SEQUENCE.//3.7e-44:340.85//Z84465  
 F-NT2RM2001345//HS\_3005\_A1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.042:290.58//AQ089514  
 F-NT2RM2001360//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-60:365.87//  
 55 U56429  
 F-NT2RM2001370//Homo sapiens PAC clone DJ0815D20 from 7p11-p13, complete sequence.//0.98:415.58//  
 AC004899  
 F-NT2RM2001393//Homo sapiens Chromosome 22q11.2 PAC Clone p\_m11 In BCRL2-GGT Region, complete

sequence.//4.0e-54:394:75//AC004033  
 F-NT2RM2001420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//2.8e-169:789:99//AL033520  
 F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.1e-96:453:99//AJ007509  
 5 F-NT2RM2001499//Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.//7.1e-91:601:83//AB000113  
 F-NT2RM2001504//Homo sapiens chromosome 19, cosmid R30017, complete sequence.//0.81:200:69//AC005624  
 10 F-NT2RM2001524//Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2.//3.8e-16:316:65//Z91708  
 F-NT2RM2001544  
 F-NT2RM2001547//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//3.3e-24:318:67//AL032657  
 F-NT2RM2001575//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//2.1e-26:582:64//M34551  
 F-NT2RM2001582//M.musculus red-1 gene.//1.4e-102:581:90//X92750  
 15 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds.//7.0e-10:282:65//AB007902  
 F-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//9.6e-131:736:90//AF032667  
 F-NT2RM2001605//RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre-B cell leukemia, mRNA, 6455 nt].//2.3e-85:749:75//S66431  
 F-NT2RM2001613//Rattus rattus sec61 homologue mRNA, complete cds.//8.6e-118:779:85//M96630  
 20 F-NT2RM2001632//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//1.5e-50:561:71//AC004691  
 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//9.2e-153:740:98//AB014518  
 F-NT2RM2001637//E.nubripes GSS sequence, clone 155D22bD8, genomic survey sequence.//2.5e-13:224:64//Z91020  
 25 F-NT2RM2001641//CIT-HSP-2347F23. CIT-HSP Homo sapiens genomic clone 2347F23, genomic survey sequence.//1.3e-67:340:98//AQ060913  
 F-NT2RM2001648//Canis familiaris sec61 homologue mRNA, complete cds.//1.4e-110:459:89//M96629  
 F-NT2RM2001652//Bos taurus guanine nucleotide-exchange protein (ARF-GEPI) mRNA, complete cds.//1.2e-153:807:93//AF023451  
 30 F-NT2RM2001659//nxbx0002e071 CUGI Rice BAC Library Oryza sativa genomic clone nxbx0002J13f, genomic survey sequence.//1.0:485:56//AQ051653  
 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//3.7e-172:802:99//AF044195  
 F-NT2RM2001668  
 35 F-NT2RM2001670//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.2e-18:279:70//AJ003147  
 F-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein-3 mRNA; complete cds.//1.6e-137:683:94//U21157  
 40 F-NT2RM2001675//RPC111-51J16.TJ RPC111 Homo sapiens genomic clone R-51J16, genomic survey sequence.//1.0:394:58//AQ053677  
 F-NT2RM2001681//Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project).//0.87:220:61//AL021890  
 F-NT2RM2001688//B.parapertussis bvg locus (transcription regulators of virulence factors) with bvgA and bvgS genes.//1.0:286:62//X52948  
 45 F-NT2RM2001695//CIT-HSP-345H13.TVB CIT-HSP Homo sapiens genomic clone 345H13, genomic survey sequence.//3.2e-53:241:82//B59854  
 F-NT2RM2001696//Mouse DNA with homology to EBV IR3 repeat, segment 2, clone Mu2.//1.2e-05:306:58//M10668  
 F-NT2RM2001698//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//6.0e-06:548:59//AL021920  
 50 F-NT2RM2001699//HS\_3195\_8B2\_DO1\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3195 Col=2 Row=H, genomic survey sequence.//2.7e-07:322:61//AQ189056  
 F-NT2RM2001700//Mycobacterium tuberculosis H37Rv complete genome; segment 109/162.//7.8e-05:354:58//Z95556  
 55 F-NT2RM2001706//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//7.5e-42:335:81//AC004469  
 F-NT2RM2001716

- F-NT2RM2001718//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//4.2e-08:536:58//AC004290
- F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence.//1.4e-26:163:95//AF052123
- F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//6.2e-11:530:98//AB007931
- 5 F-NT2RM2001730//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//3.1e-102:248:95//AJ010598
- F-NT2RM2001743
- F-NT2RM2001753//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.11:138:86//Z68117
- F-NT2RM2001760//Canis familiaris sec61 homologue mRNA, complete cds.//9.4e100:418:88//M96629
- 10 F-NT2RM2001768//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993
- F-NT2RM2001771//Homo sapiens chromosome 19, BAC CIT-B-39315 (BC301323), complete sequence.//1.3e-66:680:72//AC006116
- F-NT2RM2001782
- F-NT2RM2001784//Bovine herpesvirus type 1 (Cooper) DNA (30 kb).//0.027:384:60//Z48053
- 15 F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770
- F-NT2RM2001797//HS\_3045\_AT\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3045 Col=1 Row=G, genomic survey sequence.//1.4e-74:381:97//AQ129456
- F-NT2RM2001800
- 20 F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.3e-178:827:99//AF044195
- F-NT2RM2001805//Malus domestica leucine-rich receptor-like protein kinase (LRPKm1) gene, 5' flanking region and 5' UTR.//1.0:290:58//AF053126
- F-NT2RM2001813//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//3.3e-16:109:95//B89870
- 25 F-NT2RM2001823//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//5.8e-62:819:68//AC004274
- F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//3.6e-131:738:90//AF013759
- F-NT2RM2001840//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.1e-57:422:79//AC002347
- 30 F-NT2RM2001855//HS\_3224\_A1\_H07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3224 Col=13 Row=O, genomic survey sequence.//0.00012:68:91//AQ205285
- F-NT2RM2001867//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.068:102:70//AL031177
- 35 F-NT2RM2001879//Human DNA sequence from cosmid cU72E5, between markers DXS366 and DXS87 on chromosome X.//0.0029:500:59//Z68328
- 40 F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//1.9e-187:866:97//AB014610
- F-NT2RM2001896//S. cerevisiae chromosome III complete DNA sequence.//8.6e-30:613:63//X59720
- F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.9e-176:859:97//AB007931
- F-NT2RM2001930//M. musculus mRNA for semaphorin G.//4.7e-117:730:85//X97818
- F-NT2RM2001935//Sequence 11 from Patent WO9610637.//1.0:356:60//A50028
- 45 F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence.//6.9e-138:653:98//AF091080
- F-NT2RM2001950//RPCI11-24L12.TP RPCI-11 Homo sapiens genomic clone RPCI11-24L12, genomic survey sequence.//2.7e-19:188:81//B86700
- F-NT2RM2001982//Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence.//0.42:179:65//AC005825
- 50 F-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//3.8e-20:123:98//AF089816
- F-NT2RM2001989//Sequence 3 from patent US 5747317.//1.9e-167:786:98//AR004981
- F-NT2RM2001997//Human HepG2 partial cDNA, clone hmd1b08m5.//9.6e-25:160:95//D16955
- F-NT2RM2001998//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//0.88:380:60//AB003151
- 55 F-NT2RM2002004//Human Chromosome X, complete sequence.//5.0e-88:831:77//AC002407
- F-NT2RM2002014
- F-NT2RM2002030//Mus musculus glutamine-fructose-6-phosphate amidotransferase mRNA, complete cds.//

1.5e-89:822:74//U00932  
 F-NT2RM2002049//Bovine elastin mRNA, partial cds.//8.8e-11:125.81//M26132  
 F-NT2RM2002055  
 F-NT2RM2002088//Mus musculus WW domain binding protein 17 mRNA, partial sequence.//1.4e-15:421.63//  
 5 AF073936  
 F-NT2RM2002091//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING  
 DRAFT SEQUENCE.//4.6e-160:771.98//AL034380  
 F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//7.7e-164:776.98//AJ010840  
 10 F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//  
 2.4e-143:684.98//AF030435  
 F-NT2RM2002128//Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete  
 cds.//7.0e-27:330.73//U13152  
 F-NT2RM2002142//Danio rerio gastrulation specific (G12) mRNA, complete cds.//6.3e-10:135.80//U27121  
 15 F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//4.2e-143:800:  
 92//AF084928  
 F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds.//5.2e-164:787.97//AB007936  
 F-NT2RM2002580//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//7.4e-  
 13:337.62//AC004423  
 F-NT2RM4000024//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.2e-62:  
 20 801:70//X58826  
 F-NT2RM4000027//Caenorhabditis elegans cosmid F09E5.//0.36:336.60//U37429  
 F-NT2RM4000030//H.sapiens CpG island DNA genomic MseI fragment, clone 56h10, forward read  
 cpq56h10.ft1a.//9.3e-22:127.100//Z55685  
 F-NT2RM4000046//Curcubita maxima 25S - 18S rDNA intergenic spacer.//4.1e-05:386.60//X13059  
 25 F-NT2RM4000061  
 F-NT2RM4000085//B.taurus mRNA for nuclear DNA helicase II.//1.9e-10:485.59//X82829  
 F-NT2RM4000086  
 F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds.//  
 4.2e-23:345.69//AF060865  
 30 F-NT2RM4000139//R.norvegicus trg mRNA.//1.4e-56:708.69//X68101  
 F-NT2RM4000155//CIT-HSP-228N15.TR CIT-HSP Homo sapiens genomic clone 228N15, genomic survey se-  
 quence.//3.0e-09:88.90//AQ000070  
 F-NT2RM4000156//H.sapiens HPBR11-7 gene.//2.0e-21:586.60//X67336  
 F-NT2RM4000167//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.7e-143:810:  
 35 90//D12646  
 F-NT2RM4000169//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//0.0054:746.57//AC004157  
 F-NT2RM4000191//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//0.00018:468:  
 60//AF051726  
 40 F-NT2RM4000197  
 F-NT2RM4000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING  
 DRAFT SEQUENCE.//0.67:461.60//AL031667  
 F-NT2RM4000200  
 F-NT2RM4000202//H.sapiens CpG island DNA genomic MseI fragment, clone 34c2, forward read cpq34c2.ft1a.//  
 45 1.7e-27:190.90//Z65361  
 F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//1.4e-182:856.98//AB018255  
 F-NT2RM4000215//S.cerevisiae MAK16 protein gene, complete cds, and LTE1 protein gene, 3' end.//3.1e-31:731:  
 62//J03852  
 F-NT2RM4000229//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//  
 50 4.6e-102:233.94//AC005383  
 F-NT2RM4000233//Mus musculus semaphorin V1a mRNA, complete cds.//1.6e-135:835.86//AF030430  
 F-NT2RM4000244//RPC11-24P15.TV RPC1-11 Homo sapiens genomic clone RPC1-11-24P15, genomic survey  
 sequence.//5.5e-08:422.62//B86757  
 F-NT2RM4000251//Mus musculus clone UWGC:mbac92 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete  
 55 sequence.//0.98:207.60//AC005855  
 F-NT2RM4000265//Homo sapiens Chromosome 11q12.2 PAC clone pJD1081b4 containing human mRNA for T-  
 cell glycoprotein CD6, complete sequence.//5.2e-41:707.65//AC003689  
 F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//7.9e-153:609.93//



M99438

F-NT2RM4000324

F-NT2RM4000327//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//3.9e-44:727:68//AF022085

5 F-NT2RM4000344//Mus musculus ATP-dependent metalloprotease FtsH1 mRNA, complete cds.//1.0e-143:801:90//AF090430

F-NT2RM4000349//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700

F-NT2RM4000354//HS\_2221\_A2\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221 Col=14 Row=E, genomic survey sequence.//1.0e-20:180:83//AQ253449

10 F-NT2RM4000356

F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//1.6e-133:628:99//AB014542

F-NT2RM4000368//RPC111-91B5.TJ RPC111 Homo sapiens genomic clone R-91B5, genomic survey sequence.//5.0e-12:431:61//AQ283217

15 F-NT2RM4000386//Mus musculus DOC4 (Doc4) mRNA, complete cds.//7.4e-86:845:72//AF059485

F-NT2RM4000395//Saccharomyces cerevisiae chromosome VI cosmid 9965.//2.5e-34:767:61//D44597

F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.5e-15:114:94//AB015046

F-NT2RM4000421

F-NT2RM4000425//Homo sapiens chromosome 17, clone hRPK.294\_U\_22, complete sequence.//1.5e-37:295:82//AC005921

20 F-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//3.9e-94:740:78//AF062476

F-NT2RM4000457//CIT-HSP-2346B17.TR CIT-HSP Homo sapiens genomic clone 2346B17, genomic survey sequence.//1.5e-22:149:92//AQ062111

F-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//1.3e-76:386:97//AJ010952

25 F-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22A, //1.1e-22:356:67//AB000459

F-NT2RM4000494//Homo sapiens 12p13.3 BAC RPC111-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.53:198:70//AC005908

F-NT2RM4000511

F-NT2RM4000514

30 F-NT2RM4000515//CIT-HSP-2285L3.TR CIT-HSP Homo sapiens genomic clone 2285L3, genomic survey sequence.//0.0012:200:66//AQ000113

F-NT2RM4000520

F-NT2RM4000531//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//2.9e-31:732:64//M58297

35 F-NT2RM4000532//HS\_3231\_B1\_C05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3231 Col=9 Row=F, genomic survey sequence.//1.3e-59:362:90//AQ192093

F-NT2RM4000534

F-NT2RM4000585//CITBI-E1-250818.TR CITBI-E1 Homo sapiens genomic clone 250818, genomic survey sequence.//1.1e-34:208:93//AQ260706

40 F-NT2RM4000590//CIT-HSP-2291M14.TF CIT-HSP Homo sapiens genomic clone 2291M14, genomic survey sequence.//8.3e-34:180:99//AQ004125

F-NT2RM4000595//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete sequence.//1.2e-09:203:66//AC005288

F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds.//5.3e-14:305:68//AB002390

45 F-NT2RM4000611//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870

F-NT2RM4000616//D.melanogaster mRNA for acetyl-CoA synthetase.//2.3e-59:721:68//Z46786

F-NT2RM4000674

F-NT2RM4000689//CIT-HSP-2381O13.TF CIT-HSP Homo sapiens genomic clone 2381O13, genomic survey sequence.//2.6e-31:174:97//AQ110303

50 F-NT2RM4000698

F-NT2RM4000700

F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.1e-89:744:77//AF022789

F-NT2RM4000717

55 F-NT2RM4000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.1e-140:299:99//AL034379

F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//3.8e-158:743:98//AB018033

F-NT2RM4000741

F-NT2RM4000751//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//7.1e-95:754:77//M99593

F-NT2RM4000764

F-NT2RM4000778//Caenorhabditis elegans cosmid F36H12.//0.30:523:60//AF078790

5 F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//5.5e-172:810:98//AB007920

F-NT2RM4000787//Human DNA sequence from PAC 370M22 on chromosome 22q12-qter. contains GRB2 ADAPTOR LIKE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (UQCRFS1) exon, ESTs, STS, CA repeat and CpG island.//0.0057:163:69//Z82206

10 F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//6.9e-39:237:94//AC005306

F-NT2RM4000795//Rattus norvegicus neuroigin 3 mRNA, complete cds.//5.9e-97:857:74//U41663

F-NT2RM4000796//HS\_3214\_B1\_F11\_T7 C1T Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=21 Row=L, genomic survey sequence.//1.1e-14:254:68//AQ175988

15 F-NT2RM4000798//Bos taurus guanine nucleotide-exchange protein (ARF-GEPI) mRNA, complete cds.//6.2e-78:816:72//AF023451

F-NT2RM4000813//Leishmania major glycoprotein 96-92 (GP 96-92) gene, partial cds.//0.33:276:63//M63109

F-NT2RM4000820//, complete sequence.//2.6e-142:450:97//AC005406

F-NT2RM4000833//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//1.9e-52:501:71//AC004373

20 F-NT2RM4000848//Homo sapiens chromosome 17, clone hRPK.167\_N\_20, complete sequence.//1.0:477:56//AC005940

F-NT2RM4000852

F-NT2RM4000855//Homo sapiens chromosome 17, clone hCIT.457\_L\_16, complete sequence.//3.4e-29:229:83//AC003957

25 F-NT2RM4000887

F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds.//2.1e-20:407:64//AB011004

F-NT2RM4000950//Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.//0.41:311:64//AC004929

30 F-NT2RM4000971//RPC11-53H3.TJ RPC11 Homo sapiens genomic clone R-53H3, genomic survey sequence.//1.0:208:64//AQ053735

F-NT2RM4000979//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//1.3e-19:207:78//AC005245

35 F-NT2RM4000996//CITBI-E1-2506B10.TF CITBI-E1 Homo sapiens genomic clone 2506B10, genomic survey sequence.//1.4e-73:361:98//AQ263651

F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//5.1e-170:803:98//AB018272

F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//3.3e-125:584:99//AB014539

F-NT2RM4001032//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.00034:777:58//U47276

40 F-NT2RM4001047//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.5e-92:776:74//S51858

F-NT2RM4001054//Canis familiaris sec61 homologue mRNA, complete cds.//3.1e-102:859:76//M96629

F-NT2RM4001084//CIT-HSP-2330F9.TR CIT-HSP Homo sapiens genomic clone 2330F9, genomic survey sequence.//4.6e-78:379:99//AQ044479

F-NT2RM4001092//cSRL-71b1-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone cSRL-71b1, genomic survey sequence.//1.1e-12:152:75//B05776

45 F-NT2RM4001116

F-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.9e-136:717:93//AC004593

F-NT2RM4001151//Streptomyces antibioticus ATP-binding protein and membrane protein (oleC-ORF1, oleC-ORF2, oleC-ORF3, oleC-ORF4, and oleC-PRF5) genes, complete cds; 3427 base-pairs.//0.0083:368:60//L06249

50 F-NT2RM4001155//Bos taurus 50 kDa protein (adp50) mRNA, complete cds.//3.9e-120:764:85//U04706

F-NT2RM4001160

F-NT2RM4001187

F-NT2RM4001191//CIT-HSP-2010E7.TF CIT-HSP Homo sapiens genomic clone 2010E7, genomic survey sequence.//6.2e-12:181:72//B53378

55 F-NT2RM4001200//H.sapiens HZF10 mRNA for zinc finger protein.//1.3e-66:799:69//X78933

F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//4.2e-152:707:99//AF004828

F-NT2RM4001204

F-NT2RM4001217//Homo sapiens ectoderm-neural cortex-1 protein (ENC-1) mRNA, complete cds.//1.6e-62:715:70//AF005381

F-NT2RM4001256//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884

5 F-NT2RM4001258//HS\_3171\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=18 Row=N, genomic survey sequence.//2.5e-18:215:77//AQ149676

F-NT2RM4001309//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//4.9e-28:526:66//AL022163

10 F-NT2RM4001313//H. sapiens mRNA for phosphatidylinositol 3-kinase.//2.5e-77:474:89//Z46973

F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11.//1.2e-16:230:73//U97002

F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.1e-41:642:66//D89016

F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.//0.0040:141:68//AQ025127

15 F-NT2RM4001344//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORKING DRAFT SEQUENCE.//5.5e-06:469:60//AL021388

F-NT2RM4001347

F-NT2RM4001371//Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence.//0.10:400:61//AC004786

20 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.2e-167:790:98//AF098799

F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//0.99:255:99//AL021393

F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//0.027:336:58//AP000023

25 F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//5.9e-124:783:85//AF020526

F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete cds.//2.2e-34:418:71//AF050183

F-NT2RM4001414//Homo sapiens full-length insert cDNA clone ZE16C11.//9.1e-76:363:100//AF086563

30 F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBNL H146), complete sequence.//2.0e-47:623:69//AC004226

F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH), cell division protein DivIVA (divIVA), and isoleucine-tRNA synthetase (IleS) genes, complete cds; and unknown gene.//3.6e-09:566:58//AF068901

35 F-NT2RM4001454

F-NT2RM4001455

F-NT2RM4001483//Human zinc finger protein ZNF136.//3.2e-36:329:78//U09367

F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//1.2e-155:724:99//AB014585

40 F-NT2RM4001519//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00019:418:59//AC004688

F-NT2RM4001522//Human HepG2 3' region Mbol cDNA, clone hmd6a08m3.//1.4e-16:130:88//D17274

F-NT2RM4001557

F-NT2RM4001565

45 F-NT2RM4001566

F-NT2RM4001569//HS\_2050\_B1\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2050 Col=15 Row=F, genomic survey sequence.//2.7e-09:109:84//AQ234720

F-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.2e-127:740:89//AF071317

50 F-NT2RM4001592//M. musculus mRNA of enhancer-trap-locus 1.//7.3e-117:710:88//X69942

F-NT2RM4001594//Homo sapiens chromosome 9q34, clone 107G20, WORKING DRAFT SEQUENCE, 2 ordered pieces.//0.34:386:59//AC002355

F-NT2RM4001597//M. musculus red-1 gene.//6.2e-139:788:90//X92750

F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//3.3e-162:750:99//AB018334

55 F-NT2RM4001611//Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592.//2.5e-05:490:58//D90910

F-NT2RM4001629//Mus musculus palmytoylated protein p55 mRNA, complete cds.//0.65:186:64//U38196

F-NT2RM4001650//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0435P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.99:422:59//AC004689

F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds.//2.6e-81:449:93//AB002320  
 F-NT2RM4001666  
 F-NT2RM4001682//Mus musculus clone OST9187, genomic survey sequence.//3.2e-35:240:87//AF046699  
 F-NT2RM4001710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING  
 5 DRAFT SEQUENCE.//1.9e-151:564:97//AL031447  
 F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds.//7.0e-85:748:74//D86957  
 F-NT2RM4001715//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,  
 complete sequence.//1.2e-91:488:94//AL034430  
 F-NT2RM4001731//Orang-utan in volucrin gene, complete cds.//0.40:530:59//M25312  
 10 F-NT2RM4001741//Mouse mRNA for talin.//1.1e-129:737:90//X56123  
 F-NT2RM4001746//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316G12, WORKING  
 DRAFT SEQUENCE.//2.3e-49:320:89//AL031709  
 F-NT2RM4001754//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Li-  
 brary) complete sequence.//6.3e-64:379:76//AC005831  
 15 F-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//3.7e-146:871:87//Z83868  
 F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.3e-173:803:99//AB018270  
 F-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence.//2.0e-165:593:99//AC006017  
 F-NT2RM4001810  
 F-NT2RM4001813//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//7.1e-31:176:84//  
 20 AC005036  
 F-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//  
 4.4e-34:195:95//M37712  
 F-NT2RM4001823//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.3e-51:490:75//U49046  
 F-NT2RM4001828//Human zinc finger containing protein ZNF157 (ZNF157) mRNA, complete cds.//5.6e-74:688:  
 25 72//U28687  
 F-NT2RM4001836//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete se-  
 quence.//1.0:406:60//AC000076  
 F-NT2RM4001841//Mus musculus A kinase anchor protein (AKAP-KL) mRNA, alternatively spliced isoform 2,  
 complete cds.//1.6e-131:831:86//AF033275  
 30 F-NT2RM4001842//HS\_3163\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3163 Col=20 Row=M, genomic survey sequence.//1.5e-05:355:60//AQ168513  
 F-NT2RM4001856//Caenorhabditis elegans cosmid K08F11.//4.0e-23:823:60//U70855  
 F-NT2RM4001858//Notophthalmus viridescens NvTbox1 mRNA, partial cds.//6.4e-11:266:66//U64433  
 F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//6.9e-149:704:98//Y17711  
 35 F-NT2RM4001876//F.nubripes GSS sequence, clone 060E22bA4, genomic survey sequence.//5.7e-48:600:68//  
 Z88651  
 F-NT2RM4001880//CIT-HSP-2348J1.TF CIT-HSP Homo sapiens genomic clone 2348J1, genomic survey se-  
 quence.//0.0025:61:88//AQ060809  
 F-NT2RM4001905//R.norvegicus CYP3A1 gene, 5' flanking region.//2.5e-29:535:67//X98335  
 40 F-NT2RM4001922//HS\_2237\_A1\_C10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//2.2e-73:364:98//AQ033732  
 F-NT2RM4001930//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX10, complete sequence.//  
 4.9e-10:269:63//AB005248  
 F-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//7.6e-152:311:  
 45 100//AC005207  
 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//1.1e-170:808:98//AF098162  
 F-NT2RM4001953//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B13E4;  
 HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.7e-45:310:86//AC004046  
 F-NT2RM4001965//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
 non-small cell lung cancer, segment 11/11.//1.6e-107:622:90//AB020868  
 50 F-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//3.9e-24:221:76//X99330  
 F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.0e-61:527:76//AB018341  
 F-NT2RM4001984//Human DNA sequence from cosmid U151E3, between markers on chromosome X.//5.8e-07:  
 502:60//Z82253  
 55 F-NT2RM4001987//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey se-  
 quence.//2.6e-33:177:99//AQ051701  
 F-NT2RM4002013//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//0.019:65:90//  
 AC005921

F-NT2RM4002018//Human high molecular weight B cell growth factor mRNA sequence.//1.0:527:571/L15344  
 F-NT2RM4002034//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//0.11:322:60//AL008712  
 5 F-NT2RM4002044//Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds.//0.015:513:61//U01882  
 F-NT2RM4002054//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.0e-44:473:76//AC005283  
 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds.//1.0e-171:803:98//AB014540  
 10 F-NT2RM4002062//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0031:298:59//AC005122  
 F-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//1.1e-147:705:98//U82267  
 F-NT2RM4002066//Human mRNA for KIAA0192 gene, partial cds.//3.4e-73:889:69//D83783  
 15 F-NT2RM4002067//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//1.1e-53:295:76//AC005216  
 F-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//7.8e-25:277:75//AF072758  
 F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.0e-23:588:61//AF059569  
 F-NT2RM4002093//Rat PYPB1 mRNA for pyrimidine binding protein 1.//3.1e-68:544:69//X60789  
 20 F-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.0e-121:762:86//D12646  
 F-NT2RM4002128//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312  
 F-NT2RM4002140  
 25 F-NT2RM4002145//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//1.8e-49:736:65//AC004152  
 F-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.5e-70:454:85//AF035940  
 F-NT2RM4002161//Homo sapiens mRNA for LAFPTase, isoform 1, partial.//4.2e-151:763:96//AJ130763  
 F-NT2RM4002174//Helicobacter pylori 26695 section 18 of 134 of the complete genome.//2.1e-16:580:60//AE000540  
 30 F-NT2RM4002189//Homo sapiens DNA sequence from BAC 722E9 on chromosome 22q13.2-13.33. Contains ESTs.//1.0e-07:792:61//AL008636  
 F-NT2RM4002194//Mus musculus semaphorin 11a mRNA, complete cds.//3.2e-132:782:87//AF030430  
 F-NT2RM4002205//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//1.5e-40:292:84//L14684  
 35 F-NT2RM4002213  
 F-NT2RM4002226//Mus musculus p190-B gene, complete cds.//0.099:350:59//U87160  
 F-NT2RM4002251//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//1.0:428:58//AC004448  
 40 F-NT2RM4002256//Mouse genomic DNA, chromosome 17, clone cosmid 49.1, genomic survey sequence.//9.4e-60:294:81//AB005959  
 F-NT2RM4002266//Fugu rubripes GSS sequence, clone 006118aG12, genomic survey sequence.//3.3e-12:217:67//AL024779  
 F-NT2RM4002278//HS\_3089\_A1\_E05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3089 Col=9 Row=L, genomic survey sequence.//1.9e-64:381:92//AQ121653  
 45 F-NT2RM4002281  
 F-NT2RM4002287//CIT-HSP-2327E14.TF CIT-HSP Homo sapiens genomic clone 2327E14, genomic survey sequence.//9.0e-49:336:86//AQ042515  
 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds.//2.1e-48:511:72//D87457  
 50 F-NT2RM4002301//Human NotI linking clone 924A053D, genomic survey sequence.//8.9e-05:62:91//U49881  
 F-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudo-gene similar to GPISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//4.9e-115:729:87//AL032822  
 F-NT2RM4002339//Homo sapiens PAC clone DJ0728D04, complete sequence.//1.1e-97:457:93//AC004865  
 55 F-NT2RM4002344//Caenorhabditis elegans cosmid K04A8.//2.2e-06:190:69//U64489  
 F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//2.8e-149:708:98//AB014549  
 F-NT2RM4002374//Homo sapiens 12q24 PAC P336P3 (Research Park Cancer Institute Human Genome PAC library) complete sequence.//0.00040:312:63//AC002978

F-NT2RM4002383//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//6.8e-29:378:66//AL031284

F-NT2RM4002390

F-NT2RM4002398//CIT-HSP-2288N22. TR CIT-HSP Homo sapiens genomic clone 2288N22, genomic survey sequence.//3.4e-35:184:100//AQ001110

F-NT2RM4002409//Archaeoglobus fulgidus section 15 of 172 of the complete genome.//2.0e-16:468:59//AE001092

F-NT2RM4002438//Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.//1.6e-16:123:91//U89336

F-NT2RM4002446//Human DNA sequence from cosmid 443D9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands.//9.6e-64:467:84//Z92845

F-NT2RM4002452

F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 22, complete sequence.//2.2e-24:201:86//Z85988

F-NT2RM4002460//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//1.3e-45:487:70//AC004690

F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.7e-163:777:98//AF083255

F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//2.3e-93:464:97//AB014591

F-NT2RM4002493

F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-41:442:75//AC005484

F-NT2RM4002504//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//3.8e-31:233:87//AL031577

F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic survey sequence.//7.7e-08:274:62//AL027162

F-NT2RM4002532

F-NT2RM4002534

F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partial cds.//3.8e-53:394:81//AF072759

F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//6.4e-160:902:89//AF022962

F-NT2RM4002567//CITBI-E1-2503J7. TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//8.5e-31:220:88//AQ263402

F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase T5 mRNA, complete cds.//5.2e-05:199:65//AF049344

F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.89:275:61//AC004875

F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//3.7e-44:768:64//AC005454

F-NT2RM4002623//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-34:574:65//AC005122

F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//3.9e-111:582:95//AB013385

F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//1.1e-153:747:96//AJ012449

F-NT2RP1000040//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//1.6e-125:243:88//AP000047

F-NT2RP1000063//Caenorhabditis elegans cosmid F31C3, complete sequence.//9.6e-09:414:59//Z92784

F-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsal2//2.8e-183:548:91//X98834

F-NT2RP1000101//H.sapiens CpG island DNA genomic MseI fragment, clone 28b4, forward read cpq28b4.ft1a.//6.0e-27:163:95//Z60555

F-NT2RP1000111//CIT-HSP-2307O14. TR CIT-HSP Homo sapiens genomic clone 2307O14, genomic survey sequence.//1.2e-11:128:81//AQ016069

F-NT2RP1000112//Human Kinase (TTK) mRNA, complete cds.//1.0e-38:324:81//M86699

F-NT2RP1000124//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.59:476:59//AL034557

F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor.//2.7e-35:535:681//E08546

F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//6.7e-05:77:90//AF011792

F-NT2RP1000170//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//

- 1.9e-20:431.64//AC006030  
 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence.//2.5e-138:679:97//AF070535  
 F-NT2RP1000191  
 5 F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase, partial cds.//5.3e-05:220.61//D89496  
 F-NT2RP1000243//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//4.7e-51:508.69//AC004373  
 F-NT2RP1000259  
 10 F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeats mRNA, complete cds.//7.8e-142:866:88//AF042383  
 F-NT2RP1000324//RPC111-81O21.TJ RPC111 Homo sapiens genomic clone R-81O21, genomic survey sequence.//2.8e-29:182.92//AQ285136  
 F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//4.2e-147:693.98//AF053551  
 15 F-NT2RP1000333//Caenorhabditis elegans cosmid C03D6, complete sequence.//1.4e-08:281.61//Z75525  
 F-NT2RP1000348//H. sapiens CpG island DNA genomic Mse1 fragment, clone 12f1, reverse read cpG12f1.rt1c.//1.7e-09:71:100//Z56610  
 F-NT2RP1000357  
 F-NT2RP1000358 5.7e-16:403.61//AC005456  
 20 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds.//9.8e-125:497:86//AB014538  
 F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds.//1.8e-176:877:96//AF064594  
 F-NT2RP1000409//Homo sapiens repetitive sequences, alphoid DNA, 2482bp.//4.6e-106:700:84//AJ001558  
 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//9.4e-178:710:98//AB011159  
 25 F-NT2RP1000416  
 F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//1.0:198:60//LA0178  
 F-NT2RP1000439//HS\_2182\_A1\_D06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=G, genomic survey sequence.//2.1e-68:441:87//AQ024305  
 F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//3.8e-57:185.88//AP000047  
 30 F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.7e-132:204:99//AC004453  
 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence.//4.9e-80:196.95//AC002985  
 35 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds.//1.9e-55:440:80//U47634  
 F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//2.6e-92:562.88//Z99297  
 40 F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//2.0e-130:622:98//D67686  
 F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN genes, complete cds's.//0.11:360:58//M81648  
 F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.9e-34:209:93//AC004895  
 45 F-NT2RP1000547//Cricetus griseus COP-coated vesicle membrane protein CHOP24 mRNA, partial cds.//1.2e-08:331:63//U26264  
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds.//4.4e-81:295:92//AF017418  
 F-NT2RP1000577//HS\_2228\_B2\_C05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=10 Row=F, genomic survey sequence.//1.9e-31:179:75//AQ185128  
 50 F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partial cds.//4.7e-34:223:90//U31620  
 F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770  
 F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.3e-89:584:84//M62419  
 55 F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 22 Contains EST, complete sequence.//1.0:203:63//Z85989  
 F-NT2RP1000677//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//0.0034:350:61//AC005943

F-NT2RP1000688//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//5.2e-10:120:80//X69907  
F-NT2RP1000695

F-NT2RP1000701//Sequence 1 from patent US 5580968.//2.4e-99:624:86//30536

5 F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-19:188:81//AC004932

F-NT2RP1000730

F-NT2RP1000733//Human chromosome 16p13-1 BAC clone CIT987SK-551G9 complete sequence.//1.3e-30:315:75//U95742

10 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//8.0e-122:604:96//AF101434

F-NT2RP1000746//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//1.5e-83:466:92//AQ186344

F-NT2RP1000767//Homo sapiens full-length insert cDNA clone ZD81B04.//2.8e-21:144:91//AF086442

15 F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840

F-NT2RP1000796//T.thermophilus phosphofructokinase 1 (PFK1) gene, complete cds.//0.76:263:64//M71213

F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.5e-77:163:96//Z93244

20 F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds.//1.3e-147:424:96//AF048837

F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-89:702:79//AF047020

25 F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.7e-169:842:96//AL022398

F-NT2RP1000846//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//3.3e-15:196:76//U96629

30 F-NT2RP1000851//Homo sapiens PAC clone 267D11 from 12, complete sequence.//1.6e-144:724:96//AC004812

F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840

F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//6.7e-106:551:95//AF064094

35 F-NT2RP1000902//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//0.0097:55:100//Z82199

F-NT2RP1000915//H.sapiens genomic DNA fragment (clone J32A032R).//1.3e-30:174:97//Z94761

F-NT2RP1000916

F-NT2RP1000943//Hylcobates lar huntingtin gene, partial exon.//0.19:103:72//L49362

40 F-NT2RP1000944//HS\_2129\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=24 Row=F, genomic survey sequence.//0.032:140:63//AQ065269

F-NT2RP1000947//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//3.7e-53:461:78//U62483

F-NT2RP1000954//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//0.030:89:78//B01950

45 F-NT2RP1000958//Caenorhabditis elegans cosmid K01C8, complete sequence.//3.9e-11:445:61//Z49068

F-NT2RP1000959//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.3e-57:326:92//AC004263

F-NT2RP1000966//Human nucleolin gene, complete cds.//3.4e-64:197:981//M60858

F-NT2RP1000980//CIT-HSP-2314B10.TF CIT-HSP Homo sapiens genomic clone 2314B10, genomic survey sequence.//0.32:137:68//AQ017126

50 F-NT2RP1000988//Human chromosome 3p21.1 gene sequence.//8.0e-72:665:80//L13435

F-NT2RP1001011//Drosophila melanogaster DNA repair protein (mel-41) gene, complete cds, and TH1 gene, partial cds.//1.3e-31:497:65//U34925

F-NT2RP1001013//HS\_3068\_B1\_809\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3068 Col=17 Row=D, genomic survey sequence.//1.0e-24:414:66//AQ127667

55 F-NT2RP1001014//HS\_3252\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//0.00052:83:81//AQ034711

F-NT2RP1001033//Homo sapiens chromosome 17, clone hRPC-1073\_F\_15, complete sequence.//1.3e-134:241:99//AC004686



- F-NT2RP1001073//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//2.5e-59:451:83//AC004993
- F-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//4.5e-93:476:96//U82267
- 5 F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//6.6e-54:217:89//AC004938
- F-NT2RP1001113
- F-NT2RP1001173
- 10 F-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//8.1e-26:373:681//U79139
- F-NT2RP1001185//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-32:388:73//AC006039
- F-NT2RP1001199
- F-NT2RP1001247//Homo sapiens signaling molecule LEFTY-A gene, exon 1.//2.0e-29:166:96//AF081508
- 15 F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//7.3e-50:128:99//AC002036
- F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//4-3e-91:344:93//AF029914
- F-NT2RP1001286//Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's-//0.54:292:63//L44140
- F-NT2RP1001294
- 20 F-NT2RP1001302
- F-NT2RP1001310//Rabbit skeletal muscle mRNA for ryanodine receptor.//1.5e-07:335:64//X15750
- F-NT2RP1001311//RPC111-67O14.TK RPC111 Homo sapiens genomic clone R-67O14, genomic survey sequence.//0.26:80:75//AQ239291
- F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//8.8e-75:304:98//AC004228
- 25 F-NT2RP1001361//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//2.7e-57:412:84//X68847
- F-NT2RP1001385
- F-NT2RP1001395//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.4e-72:535:83//AF071316
- 30 F-NT2RP1001410//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D),TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//5.8e-105:570:94//AL021878
- F-NT2RP1001424
- 35 F-NT2RP1001432
- F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence.//1.7e-84:422:97//AF052149
- F-NT2RP1001457//Xenopus laevis notchless (nle) mRNA, complete cds.//1.3e-47:471:73//AF069737
- F-NT2RP1001466//HS\_3006\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=16 Row=G, genomic survey sequence.//0.56:289:60//AQ154336
- 40 F-NT2RP1001475//H.sapiens genomic DNA fragment (clone NLMA194R).//0.00011:91:79//Z95375
- F-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.1/4-0e-87:563:85//L11316
- F-NT2RP1001494
- F-NT2RP10015431//Drosophila melanogaster DNA sequence (P1 DS01142 (D148)), complete sequence.//1.9e-27:387:67//AC004280
- 45 F-NT2RP1001546//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//8.0e-63:314:98//AF054840
- F-NT2RP1001569//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//1.2e-68:514:81//U17343
- F-NT2RP1001616//Human clone 23665 mRNA sequence.//7.6e-40:496:74//U09013
- 50 F-NT2RP1001665//CIT-HSP-2059N5.TF CIT-HSP Homo sapiens genomic clone 2059N5, genomic survey sequence.//2.4e-45:305:88//B69912
- F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence.//1.5e-135:685:96//AF091081
- F-NT2RP2000006//HS\_3061\_B2\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=6 Row=F, genomic survey sequence.//1.9e-17:394:67//AQ178856
- 55 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds.//3.5e-14:241:68//AB002390
- F-NT2RP2000008//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//1.7e-34:147:99//AL034424
- F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//1.4e-32:345:75//

AC005066

F-NT2RP2000032//F.rubripes GSS sequence, clone 060E22aG10, genomic survey sequence.//5.0e-41:445:72//Z88655

F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//1.9e-76:383:97//AB018290

5 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//2.4e-95:467:97//AF061749

F-NT2RP2000054//CIT-HSP-2328J24.TF CIT-HSP Homo sapiens genomic clone 2328J24, genomic survey sequence.//3.3e-39:236:91//AQ043092

10 F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds.//3.2e-50:311:90//D78610

F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds.//3.0e-55:766:66//AF059485

F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//2.0e-118:597:95//AC005754

F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence.//0.0017:423:60//AC006037

15 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//2.1e-77:278:97//AF050079

F-NT2RP2000079//H.sapiens CpG island DNA genomic MseI fragment, clone 40c2, forward read cpG40c2.f1k.//3.2e-33:197:95//Z55440

F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//2.2e-158:752:98//AB018338

20 F-NT2RP2000091//HS\_2228\_A2\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=4 Row=C, genomic survey sequence.//0.26:55:90//AQ146363

F-NT2RP2000097

F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.5e-05:482:60//AC004961

25 F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-22:274:69//AC003973

F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//4.9e-114:551:97//AB018356

F-NT2RP2000120//HS\_3000\_B1\_E03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=5 Row=J, genomic survey sequence.//1.8e-21:129:97//AQ090365

30 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//4.2e-119:607:96//AF054177

F-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.3e-07:339:63//AC004827

F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.0e-101:638:85//M62419

35 F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.45:377:58//AL034370

F-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.0e-73:317:87//AC005924

40 F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP Homo sapiens genomic clone 2353L5, genomic survey sequence.//3.0e-14:123:90//AQ263431

F-NT2RP2000173

F-NT2RP2000175

F-NT2RP2000183//F.rubripes GSS sequence, clone 168M02aC2, genomic survey sequence.//3.7e-06:152:66//AL007295

45 F-NT2RP2000195//Human DNA sequence from clone 4514 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//7.6e-62:170:99//AL023581

F-NT2RP2000205

F-NT2RP2000208//Homo sapiens chromosome 19, overlapping cosmids R29828 and F25496, complete sequence.//7.2e-80:170:90//AC003030

50 F-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//5.5e-64:400:85//AC004382

F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3) (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island, ESTs and STSs.//2.2e-07:280:66//Z97632

55 F-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//8.8e-30:508:67//U88401

F-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.0e-79:504:

- 87//AC004066  
F-NT2RP2000248  
F-NT2RP2000257//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORK-  
ING DRAFT SEQUENCE.//0.0078:286:60//AL021388
- 5 F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 2349P21, genomic survey se-  
quence.//5.7e-82:416:97//AQ059184  
F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-39315 (BC301323), complete sequence.//4.5e-  
29:310:73//AC006116  
F-NT2RP2000274
- 10 F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//6.3e-20:260:73//X74904  
F-NT2RP2000288  
F-NT2RP2000289  
F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//4.6e-69:744:70//  
M27877
- 15 F-NT2RP2000298//Streptomyces coelicolor cosmid 2E9.//4.4e-05:502:59//AL021530  
F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.1e-13:173:76//AC006082  
F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the  
HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE  
pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs,  
20 complete sequence.//8.3e-144:731:95//AL022398  
F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,  
complete sequence.//1.9e-102:555:90//AL034430  
F-NT2RP2000329//Bovine mitochondrial GTP-AMP phosphotransferase mRNA, complete cds.//6.4e-105:639:87//  
M25757
- 25 F-NT2RP2000337//HS\_2060\_B1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2060 Col=1 Row=J, genomic survey sequence.//0.78:218:60//AQ243333  
F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//3.6e-129:627:  
97//U83981  
F-NT2RP2000369//HS\_2182\_B1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=2182 Col=21 Row=D, genomic survey sequence.//2.5e-87:421:99//AQ024835
- 30 F-NT2RP2000412//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like  
pseudogene, ESTs, STs and GSSs.//0.72:170:65//AL021327  
F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//5.0e-66:375:93//L28010  
F-NT2RP2000420//Homo sapiens full-length insert cDNA YQ86E07.//9.2e-77:423:93//AF075093
- 35 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//2.1e-126:609:  
96//AF102265  
F-NT2RP2000438//CITBI-E1-2519O19.TR CITBI-E1 Homo sapiens genomic clone 2519O19, genomic survey se-  
quence.//0.96:61:78//AQ276878  
F-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.1e-17:341:67//  
AC004691
- 40 F-NT2RP2000459//H.sapiens mRNA for imogen 38.//5.7e-21:158:87//Z68747  
F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//3.2e-11:160:  
73//Z92844  
F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//0.0031:187:66//  
AC005229
- 45 F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066G04aC1, genomic survey sequence.//8.8e-07:179:  
64//AL026277  
F-NT2RP2000516//Mus musculus t complex testis-specific protein (Tctex2) gene, wild type, promoter sequence.//  
0.19:72:81//U21671
- 50 F-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING  
DRAFT SEQUENCE.//5.0e-115:570:96//AL022318  
F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//8.4e-37:196:98//AB005543  
F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.81:354:60//  
AC005321
- 55 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//1.3e-149:732:97//AB014514  
F-NT2RP2000644//HS\_3211\_A1\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
nomic clone Plate=3211 Col=11 Row=K, genomic survey sequence.//3.6e-42:282:86//AQ175486  
F-NT2RP2000656

F-NT2RP2000658//CITBI-E1-2518N15.TF CITBI-E1 Homo sapiens genomic clone 2518N15, genomic survey sequence.//0.57:141.66//AQ278386  
 F-NT2RP2000668  
 5 F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12 unordered pieces.//4.3e-22:433:62//AC004916  
 F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.7e-22:270.75//AC005913  
 F-NT2RP2000710//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-32:574:64//AC005122  
 10 F-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//4.8e-113:546:98//AC004540  
 F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.97:115:70//AC004965  
 15 F-NT2RP2000758//Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds.//9.7e-16:162:77//U62293  
 F-NT2RP2000764//HS\_2254\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=14 Row=H, genomic survey sequence.//0.071:45.95//AQ068887  
 F-NT2RP2000809  
 20 F-NT2RP2000812//Egernia stokesii clone EST3 microsatellite.//0.040:158:64//AF069698  
 F-NT2RP2000814  
 F-NT2RP2000816  
 F-NT2RP2000819  
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds.//1.1e-26:390:70//AB002292  
 F-NT2RP2000842//H. sapiens mRNA for G protein-coupled receptor Edg-2.//1.2e-44:255:93//Y09479  
 25 F-NT2RP2000845  
 F-NT2RP2000863//Human partial cDNA sequence, clone x874.//5.9e-29:173:94//Z47045  
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds.//2.4e-140:732:94//AB018284  
 F-NT2RP2000892  
 F-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//3.4e-129:610:98//AB018266  
 30 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-37:212:84//AC005014  
 F-NT2RP2000938//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.6e-126:682:93//Z69890  
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//5.8e-112:533:98//AB018298  
 35 F-NT2RP2000965  
 F-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//9.2e-101:505:96//AL021393  
 F-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//1.6e-72:498:82//AC005277  
 40 F-NT2RP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//7.4e-12:171:77//AC002394  
 F-NT2RP2001036//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//1.2e-37:390:76//AC004167  
 F-NT2RP2001044//HS\_2253\_B1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence.//0.21:276:61//AQ069224  
 45 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//3.2e-144:696:97//AB007957  
 F-NT2RP2001065  
 F-NT2RP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//4.3e-104:775:81//U91561  
 50 F-NT2RP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds.//3.7e-69:488:82//AF000423  
 F-NT2RP2001094//Human DNA sequence from PAC 410B11 on chromosome X contains STS.//7.4e-11:490:61//Z86063  
 F-NT2RP2001119//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE.//5.1e-30:316:76//AL031596  
 55 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds.//1.1e-31:519:63//D87072  
 F-NT2RP2001137//HS\_2193\_B2\_D12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=H, genomic survey sequence.//1.8e-11:136:78//AQ032187

F-NT2RP2001149//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//6.2e-29:247:78//AC000076

F-NT2RP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.23:207:66//AL009178

F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//2.3e-112:567:96//AB007949

F-NT2RP2001174//RPC111-58L2.TK RPC111 Homo sapiens genomic clone R-58L2, genomic survey sequence.//7.6e-07:196:64//AQ237306

F-NT2RP2001196

F-NT2RP2001218

F-NT2RP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//1.1e-09:320:65//U92893

F-NT2RP2001233//Human ZFP-36 mRNA for a zinc finger protein.//6.1e-71:681:72//X51760

F-NT2RP2001245//HS\_3062\_B1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence.//1.5e-05:268:63//AQ143177

F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//2.5e-106:514:97//AB018353

F-NT2RP2001277//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//0.32:183:64//AE001430

F-NT2RP2001290//M.musculus mRNA for I47 clone.//8.6e-102:641:86//X61455

F-NT2RP2001295//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE.//0.20:171:63//AL022594

F-NT2RP2001312//Bovine synaptophysin mRNA, complete cds.//0.98:253:58//M22967

F-NT2RP2001327//Human B12 protein mRNA, complete cds.//5.8e-29:359:71//M80783

F-NT2RP2001328//CIT-HSP-2335A5.TF CIT-HSP Homo sapiens genomic clone 2335A5, genomic survey sequence.//1.3e-65:366:94//AQ038539

F-NT2RP2001347//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.8e-31:325:77//AJ003147

F-NT2RP2001366//H.sapiens CpG island DNA genomic MseI fragment, clone 4e11, forward read cpG4e11.f1a.//1.7e-12:98:92//Z61305

F-NT2RP2001378//HS\_3054\_B2\_A03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=6 Row=B, genomic survey sequence.//9.8e-17:131:89//AQ100721

F-NT2RP2001381//Arabidopsis thaliana BAC T2L5.//0.080:434:59//AF096371

F-NT2RP2001392//S.pristinaespiralis snbC gene & amp; snbDE gene.//0.019:267:59//Y11548

F-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//1.9e-16:133:78//Z93242

F-NT2RP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds.//1.3e-63:419:84//AF080219

F-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//3.1e-98:747:79//U76759

F-NT2RP2001423//Xenopus laevis ER1 mRNA, complete cds.//3.7e-34:269:85//AF015454

F-NT2RP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//3.2e-13:164:78//AC003065

F-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//3.0e-06:136:71//AF046702

F-NT2RP2001440//cDNA sequence coding for gamma protein.//7.9e-83:553:86//E02350

F-NT2RP2001445//P.falciparum complete gene map of plastid-like DNA (IR-A).//1.5e-09:829:57//Y95275

F-NT2RP2001449//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.3e-136:766:90//X75931

F-NT2RP2001450

F-NT2RP2001467

F-NT2RP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 2374H21, genomic survey sequence.//7.9e-14:151:80//AQ109561

F-NT2RP2001511//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-22:462:64//AF005355

F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//2.0e-136:657:97//Y14494

F-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//1.2e-37:357:64//AC004596

F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//1.6e-103:384:94//AF035586

F-NT2RP2001560

F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//4.4e-123:590:98//

AB007957

F-NT2RP2001576//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.038:580:58//U32943

F-NT2RP2001581//Mus musculus semaphorin VIa mRNA, complete cds.//6.5e-09:222:66//AF030430

F-NT2RP2001597//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//0.0057:361:60//U72648

F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//7.2e-137:647:98//AB018340

F-NT2RP2001613

F-NT2RP2001628//H.sapiens (xs128) mRNA, 380bp.//1.7e-15:279:68//Z36784

F-NT2RP2001634//Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds.//5.4e-123:606:96//AF030233

F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kd subunit brain-specific isoform mRNA, complete cds.//4.2e-144:687:97//AF058718

F-NT2RP2001663//H.sapiens mRNA for 2-phosphopyruvate-hydratase-alpha-enolase.//1.0e-36:372:74//X84907

F-NT2RP2001675//S.pombe chromosome I cosmid c2G11.//0.070:507:59//Z54354

F-NT2RP2001677//Mouse BAC CltbCJ7 219mt, genomic sequence, complete sequence.//2.0e-60:232:96//AC005259

F-NT2RP2001678//HS\_2007\_A2\_A04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=8 Row=A, genomic survey sequence.//7.3e-62:370:91//AQ269699

F-NT2RP2001699//RPC111-57B17.TK RPC111 Homo sapiens genomic clone R-57B17, genomic survey sequence.//0.99:141:63//AQ115592

F-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//9.4e-117:604:95//AC004079

F-NT2RP2001721//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//1.0:273:61//AL030998

F-NT2RP2001740//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c in DGCR Region, complete sequence.//1.0:356:62//AC000090

F-NT2RP2001748//Human mRNA for KIAA0003 gene, complete cds.//3.7e-18:151:86//D14697

F-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.0e-145:715:97//AC004783

F-NT2RP2001813//Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence.//0.38:340:60//AE001378

F-NT2RP2001839//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Library D\_ Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.026:253:60//AQ090347

F-NT2RP2001861//Homo sapiens mRNA for paraplegin.//0.89:146:71//Y16610

F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0.040:174:62//AF027219

F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete cds.//2.8e-44:483:71//AB012309

F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//1.8e-87:496:92//AL031864

F-NT2RP2001898//Human Inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//9.2e-112:633:90//M74161

F-NT2RP2001900//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone R08A5, WORKING DRAFT SEQUENCE.//0.0026:360:62//Z82281

F-NT2RP2001907//H.sapiens CpG island DNA genomic Mse1 fragment, clone 97f11, forward read cp97f11.f1a.//4.2e-26:206:84//Z64125

F-NT2RP2001926//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.5e-06:621:59//AC004688

F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-47D9, genomic survey sequence.//3.1e-50:282:93//B04856

F-NT2RP2001943//Drosophila melanogaster cosmid 25E8.//0.00036:248:60//AL009196

F-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.8e-78:232:99//AC005033

F-NT2RP2001947//Homo sapiens full-length insert cDNA clone ZD81B04.//2.0e-28:172:94//AF086442

F-NT2RP2001969//H.sapiens CpG island DNA genomic Mse1 fragment, clone 152a8, reverse read cp9152a8.rt1a.//1.0e-20:123:99//Z59378

F-NT2RP2001976

F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117  
 F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//3.1e-35:180:80//L22022  
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.8e-61:314:97//AB018299  
 F-NT2RP2002032//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//0.76:189:65//AC005895  
 5 F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.9e-12:160:79//AC004825  
 F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//0.0014:123:73//AC004029  
 F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete  
 10 sequence.//2.2e-86:722:77//AC004552  
 F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.//0.13:350:61//AL033375  
 F-NT2RP2002058//S.cerevisiae chromosome XII reading frame ORF YLR129w.//9.7e-11:480:60//Z73301  
 F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//6.5e-97:610:86//  
 15 U87306  
 F-NT2RP2002070//beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta -ADD=ad-  
 ducin beta subunit 63 kda isoform/membrane skeleton protein (alternatively spliced, exon 10 to 13 region) [human,  
 Genomic, 1851 nt, segment 3 of 3]//0.0059:107:73//S81083  
 F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.0e-127:643:96//AF052183  
 20 F-NT2RP2002078//F12016-T7.1 IGF Arabidopsis thaliana genomic clone F12016, genomic survey sequence.//  
 0.14:191:64//AQ249805  
 F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094:325:60//AC004917  
 F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//9.8e-111:533:97//AJ007509  
 F-NT2RP2002105//H.sapiens CpG island DNA genomic MseI fragment, clone 10h8, forward read cpq10h8.ft1a.//  
 2.4e-29:178:94//Z58857  
 25 F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 2023E9, genomic survey se-  
 quence.//2.5e-32:202:92//B64468  
 F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds.//0.095:319:59//  
 M25874  
 30 F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0:258:63//D85923  
 F-NT2RP2002172//HS\_3020\_B1\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3020 Col=3 Row=P, genomic survey sequence.//1.2e-11:124:82//AQ093169  
 F-NT2RP2002185//RPC111-67B15.TJ RPC111 Homo sapiens genomic clone R-67B15, genomic survey se-  
 quence.//2.8e-18:109:100//AQ201833  
 35 F-NT2RP2002192//Human PM-Scl-75 autoantigen (PM-scl1) mRNA, complete cds.//2.7e-36:363:78//U09215  
 F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//9.5e-  
 82:477:89//AF032872  
 F-NT2RP2002208  
 F-NT2RP2002219//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
 40 DRAFT SEQUENCE.//1.0:378:58//AL034557  
 F-NT2RP2002231//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces.//0.60:560:56//AC005308  
 F-NT2RP2002235//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.59:341:60//J03998  
 F-NT2RP2002252//Mus musculus mSin3A (sin3A) mRNA, complete cds.//3.5e-81:398:87//U22394  
 45 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//6.6e-50:315:89//AF005418  
 F-NT2RP2002259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING  
 DRAFT SEQUENCE.//9.7e-67:340:89//AL033527  
 F-NT2RP2002270//RPC111-77C23.TV RPC111 Homo sapiens genomic clone R-77C23, genomic survey se-  
 quence.//2.9e-18:79:93//AQ268098  
 50 F-NT2RP2002292//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING  
 DRAFT SEQUENCE.//1.0:290:60//AL031033  
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.5e-93:467:96//  
 AF069532  
 F-NT2RP2002316//HS\_2171\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 55 nomic clone Plate=2171 Col=22 Row=H, genomic survey sequence.//7.3e-94:463:97//AQ119673  
 F-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//3.9e-123:640:95//AB015594  
 F-NT2RP2002333  
 F-NT2RP2002373//F.fubripes GSS sequence, clone 026F10aB8, genomic survey sequence.//0.46:234:61//

Z87330

F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//9.4e-138.673:97//AF038958

F-NT2RP2002394//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.79:421:56//X95275

5 F-NT2RP2002408//F.rubripes GSS sequence, clone 080G11aA8, genomic survey sequence.//5.7e-15:220:71//AL015615

F-NT2RP2002426//Sus scrofa SCAMP1 gene, exon 9.//7.1e-71:582:80//AJ223742

F-NT2RP2002439//Caenorhabditis elegans cosmid T07D3.//0.0018:210:67//AF016682

10 F-NT2RP2002442//Caenorhabditis elegans cosmid T03F1.//2.8e-18:295:67//U88169

F-NT2RP2002457//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//1.9e-06:281:66//AC004381

F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds.//0.039:207:63//D42045

F-NT2RP2002475

15 F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//2.4e-123:607:96//AB005289

F-NT2RP2002498//Arabidopsis thaliana BAC F3D13.//0.73:395:57//AF069300

F-NT2RP2002503//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//7.2e-18:134:90//AC006213

F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-157:761:97//AB018334

F-NT2RP2002520

20 F-NT2RP2002537

F-NT2RP2002546//Homo sapiens Chromosome 11q12 pac pDJ741n15, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.83:252:60//AC004127

F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//5.9e-93:186:99//AC005317

25 F-NT2RP2002591//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//4.0e-38:175:78//Z98304

F-NT2RP2002595//Sequence 2 from patent US 5763220.//1.5e-84:430:95//AR012155

F-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//1.9e-43:282:87//U19181

F-NT2RP2002609//Mus musculus defender against death 1 (DAD1) gene, partial cds.//1.5e-11:99:90//AF051310

30 F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1316 bp.//15.6e-27:460:63//Y10806

F-NT2RP2002621

F-NT2RP2002643//Rat calmodulin III gene for calmodulin, promoter region and exon 1.//0.023:322:60//D90397

35 F-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//3.9e-149:794:94//AC005384

F-NT2RP2002701//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//9.2e-10:129:75//AL034380

F-NT2RP2002706//S.griseus secA gene.//1.3e-05:311:63//Y10980

40 F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.5e-40:631:65//AB014572

F-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//4.8e-65:600:73//AF041107

F-NT2RP2002736//S.pombe chromosome II cosmid c887.//0.17:352:58//AL033388

F-NT2RP2002740//Absidia glauca ORF, 3' end; (+) mating type surface protein (PSSP15) gene, complete cds; ORF, 5' end.//0.0073:274:66//M94861

45 F-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//7.5e-29:628:62//D89016

F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//3.6e-31:568:67//AC005296

F-NT2RP2002752//Human BAC clone RG317M02 from 7p15-p21, complete sequence.//1.7e-08:206:63//AC002433

50 F-NT2RP2002753//Human DNA sequence from cosmid B11B7 on chromosome 22 contains ESTs.//2.8e-71:195:89//Z82171

F-NT2RP2002769//Streptomyces fradiae tyactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//0.0016:412:60//U78289

F-NT2RP2002778//CIT-HSP-2059C5.TF CIT-HSP Homo sapiens genomic clone 2059C5, genomic survey sequence.//6.8e-18:186:79//B69837

55 F-NT2RP2002800

F-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.2e-41:134:94//AC006078

F-NT2RP2002857//Rat T-cell receptor active beta-chain V-region (V-beta6-J-beta2.5) mRNA, partial cds, clone



TRB-4.//0.85:93.68//M18845

F-NT2RP2002862//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//5.0e-67:390:91//AQ186344

F-NT2RP2002880

5 F-NT2RP2002891//CIT-HSP-2310O14.TF CIT-HSP Homo sapiens genomic clone 2310O14, genomic survey sequence.//0.11:53:90//AQ019792

F-NT2RP2002925//Pig mRNA for carbonyl reductase, complete cds.//0.66:194:65//D16511

F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//2.3e-135:628:99//AF038392

10 F-NT2RP2002929//F.rubripes GSS sequence, clone 123I23aA1, genomic survey sequence.//3.9e-06:66:83//AL017246

F-NT2RP2002939

F-NT2RP2002954

15 F-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//1.3e-47:411:79//U62483

F-NT2RP2002979//CIT-HSP-2340D12.TF CIT-HSP Homo sapiens genomic clone 2340D12, genomic survey sequence.//4.6e-96:476:97//AQ057233

F-NT2RP2002980//Sequence 20 from Patent EP0705842.//4.0e-13:100:94//A52230

20 F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.4e-09:272:61//AF059569

F-NT2RP2002987//Homo sapiens (subclone 6\_d9 from P1 H21) DNA sequence, complete sequence.//1.0e-22:293:67//AC000958

F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//4.0e-74:502:84//AF025424

25 F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-46:474:76//AC004765

F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//4.2e-23:202:82//AC005703

30 F-NT2RP2003073//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//3.4e-59:330:82//Z83822

F-NT2RP2003099//HS\_3008\_B2\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3008 Col=18 Row=F, genomic survey sequence.//1.4e-71:362:96//AQ089786

F-NT2RP2003108//Sequence 59 from patent US 5773577.//0.95:123:69//AR014362

35 F-NT2RP2003117//HS\_2034\_B2\_D12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=24 Row=H, genomic survey sequence.//1.5e-88:461:96//AQ230797

F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//4.3e-46:470:72//AF079765

F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//5.7e-10:436:61//AC005329

40 F-NT2RP2003129//P.thunbergii cab gene.//0.00044:541:60//X61915

F-NT2RP2003137//CIT-HSP-2300J6.TR CIT-HSP Homo sapiens genomic clone 2300J6, genomic survey sequence.//5.0e-78:393:97//AQ012976

F-NT2RP2003157//Human DNA sequence from cDNA 16pHQG;16 from chromosome 16p13.3.//5.4e-07:137:71//Z84716

45 F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//1.8e-111:581:93//D67025

F-NT2RP2003161//CITBI-E1-2506E20.TR CITBI-E1 Homo sapiens genomic clone 2506E20, genomic survey sequence.//0.0025:156:67//AQ262657

F-NT2RP2003164

50 F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.4e-43:334:79//U91328

F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds.//0.91:346:62//U50040

55 F-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING DRAFT SEQUENCE.//1.7e-108:511:90//AL031597

F-NT2RP2003206

F-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//2.9e-136:726:93//X74794

F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.6e-51:348:

86//AF023657  
 F-NT2RP2003237//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//2.6e-56:415:83//AL031447  
 5 F-NT2RP2003243//RPC11-36J1.TP RPC11-11 Homo sapiens genomic clone RPC11-11-36J1, genomic survey sequence.//2.1e-16:112:93//AQ047107  
 F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//6.0e-114:696:87//L38481  
 F-NT2RP2003272//RPC11-67B15.TJ RPC11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//3.8e-16:110:94//AQ201833  
 10 F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.5e-145:714:96//AB014525  
 F-NT2RP2003280//RPC11-14I2.TVB RPC11-11 Homo sapiens genomic clone RPC11-11-14I2, genomic survey sequence.//6.4e-77:400:95//B85286  
 F-NT2RP2003286//CIT-HSP-2336D3.TF CIT-HSP Homo sapiens genomic clone 2336D3, genomic survey sequence.//5.3e-29:287:73//AQ041024  
 15 F-NT2RP2003293//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.5e-54:508:74//AC003973  
 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//6.1e-85:416:97//AB006572  
 F-NT2RP2003297//S.pombe pho2 gene for specific p-nitrophenylphosphatase.//0.60:309:64//X62722  
 20 F-NT2RP2003307//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//1.0e-45:442:75//AF055666  
 F-NT2RP2003308//D.melanogaster cm mRNA.//1.1e-63:697:70//X58374  
 F-NT2RP2003329//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete sequence.//0.040:145:64//AC005288  
 F-NT2RP2003339  
 25 F-NT2RP2003347//Plasmodium falciparum MAL3P7, complete sequence.//0.12:275:60//AL034559  
 F-NT2RP2003367//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//0.83:225:63//AC005510  
 F-NT2RP2003391  
 F-NT2RP2003393//HS\_3218\_A2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=18 Row=C, genomic survey sequence.//0.021:93:79//AQ204356  
 30 F-NT2RP2003394  
 F-NT2RP2003401  
 F-NT2RP2003433//Rattus rattus sec61 homologue mRNA, complete cds.//4.2e-61:533:75//M96630  
 F-NT2RP2003445//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SE-  
 35 QUENCE.//2.1e-49:301:72//AP000023  
 F-NT2RP2003446  
 F-NT2RP2003456//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.0018:366:60//AJ235272  
 F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//7.5e-16:189:68//AC004770  
 40 F-NT2RP2003480//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-25:197:85//M21977  
 F-NT2RP2003499 2.1e-08:408:61//AB000826  
 F-NT2RP2003506//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-33:192:96//AC005236  
 45 F-NT2RP2003511//Ceratopteris richardii mRNA for CRHB11, partial cds.//1.0:328:60//AB013801  
 F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//7.3e-76:403:93//D87460  
 F-NT2RP2003517//Human osteosarcoma cell line U-2 OS mRNA fragment for PDGF-B chain (PDGF= platelet-derived growth factor).//1.5e-24:151:95//X03702  
 F-NT2RP2003522//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.3e-101:564:91//M21977  
 50 F-NT2RP2003533//Human DNA sequence from cosmid F1121 on chromosome 6.//2.0e-40:315:75//Z80899  
 F-NT2RP2003543  
 F-NT2RP2003559//H.sapiens CpG island DNA genomic MseI fragment, clone 90a5, reverse read cp90a5.r11a.//1.1e-20:122:99//Z56144  
 F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//8.8e-27:664:63//M34551  
 55 F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds.//4.1e-113:541:98//AB007931  
 F-NT2RP2003581  
 F-NT2RP2003596//F.rubripes GSS sequence, clone 036L10aF12, genomic survey sequence.//1.9e-11:210:65//AL012756

- F-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds.//1.9e-123:587:98//AF030233
- F-NT2RP2003629
- 5 F-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//7.8e-88:582:84//AJ006215
- F-NT2RP2003668//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//5.6e-47:335:83//AC005081
- F-NT2RP2003687//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//1.2e-06:133:74//AC003684
- 10 F-NT2RP2003691//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 525L6, WORKING DRAFT SEQUENCE.//1.7e-47:337:81//AL023807
- F-NT2RP2003702//Rattus norvegicus ovarian-specific protein mRNA, complete cds.//1.3e-65:458:82//U44803
- F-NT2RP2003704//H.sapiens CpG island DNA genomic MseI fragment, clone 2a9, reverse read cpq2a9.r1e.//3.8e-17:170:84//Z60615
- 15 F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-108:518:98//AB011097
- F-NT2RP2003713//HS\_2016\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=9 Row=D, genomic survey sequence.//1.3e-11:102:90//AQ226895
- F-NT2RP2003714//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.4e-27:249:78//AC003973
- 20 F-NT2RP2003727//RPC11-77119.TV RPC11 Homo sapiens genomic clone R-77119, genomic survey sequence.//3.4e-26:284:74//AQ268303
- F-NT2RP2003737//Homo sapiens clone DJ1022114, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.6e-74:194:91//AC004951
- F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-911E12, complete sequence.//1.7e-92:165:96//AC003964
- 25 F-NT2RP2003760//B.primigenius mRNA for coat protein gamma-cop.//4.5e-76:696:73//X92987
- F-NT2RP2003764//Homo sapiens gene for MTG16, exon 1b, partial sequence.//1.0:109:69//AB013275
- F-NT2RP2003769
- F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, complete sequence.//3.0e-96:467:98//AC004771
- 30 F-NT2RP2003777
- F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//7.2e-107:731:82//S70011
- F-NT2RP2003793//CIT-HSP-2326L12.TF CIT-HSP Homo sapiens genomic clone 2326L12, genomic survey sequence.//7.0e-20:124:95//AQ038761
- 35 F-NT2RP2003825//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//B.9e-06:151:74//AC004491
- F-NT2RP2003840//Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.//0.018:145:69//AC005167
- 40 F-NT2RP2003857//HS\_3227\_A2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=8 Row=M, genomic survey sequence.//0.96:257:61//AQ030467
- F-NT2RP2003859
- F-NT2RP2003871//Homo sapiens 12q24 PAC RPC11-74B13 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.0e-12:369:65//AC002375
- 45 F-NT2RP2003885//CITBI-E1-2514D6.TF CITBI-E1 Homo sapiens genomic clone 2514D6, genomic survey sequence.//0.13:167:64//AQ265722
- F-NT2RP2003912//hek1=serine/threonine- and tyrosine-specific protein kinase [mice, erythroleukemia cells, mRNA, 4263 nt].//1.3e-136:838:86//S45828
- F-NT2RP2003952
- 50 F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.1e-28:165:96//AB014459
- F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.6e-24:298:74//AL031282
- 55

- F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//9.9e-160:783.96//AB03847  
F-NT2RP2003984
- 5 F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.7e-26:260.77//AC000382  
F-NT2RP2003988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701.70//AL031681  
F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//3.0e-123:693.91//AL023580  
F-NT2RP2004014
- 10 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//5.8e-83:427.87//AC004780  
F-NT2RP2004042  
F-NT2RP2004066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134O19, WORKING DRAFT SEQUENCE.//5.6e-110:528.98//AL034555
- 15 F-NT2RP2004081  
F-NT2RP2004098//HS\_2216\_A1\_B12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, genomic survey sequence.//1.0e-07:86.84//AQ145694  
F-NT2RP2004124//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.0e-25:155.94//AQ136993
- 20 F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence.//1.0:220.62//AB007645  
F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.93:480:56//AC002493
- 25 F-NT2RP2004165//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.051:265.61//AC005140  
F-NT2RP2004170//Homo sapiens distal-less homeobox protein (DLX7) gene, complete cds.//1.0:162.66//AF028235
- 30 F-NT2RP2004172//S.pombe chromosome II cosmid c24E9.//1.7e-06:466.56//AL021816  
F-NT2RP2004187//Homo sapiens full-length insert cDNA YQ86E07.//3.5e-17:354.64//AF075093  
F-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//9.4e-53:397.82//AF003998  
F-NT2RP2004196  
F-NT2RP2004207//Human von Willebrand factor pseudogene corresponding to exons 23 through 34.//0.0023:386.61//M60676
- 35 F-NT2RP2004226//HS\_2186\_A1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2186 Col=5 Row=G, genomic survey sequence.//7.8e-58:370.87//AQ063813  
F-NT2RP2004232//H.sapiens mRNA for protein kinase C mu.//1.2e-34:448.67//X75756  
F-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//5.2e-108:510.99//AB015718  
F-NT2RP2004240//Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).//1.1e-12:489:61//AP000006
- 40 F-NT2RP2004242  
F-NT2RP2004245  
F-NT2RP2004270//Streptomyces coelicolor cosmid 1A9.//7.5e-07:462.62//AL034446  
F-NT2RP2004300//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//3.5e-11:299.64//AC005781
- 45 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//4.5e-150:735.97//AF000416  
F-NT2RP2004321//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//0.98:267.59//AC004423  
F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, complete sequence.//1.6e-40:419:75//AC002519
- 50 F-NT2RP2004347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.2e-72:439.82//AL031650  
F-NT2RP2004364  
F-NT2RP2004365  
F-NT2RP2004366//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//0.92:427.57//AL031864
- 55 F-NT2RP2004373//Homo sapiens cosmids Qc15C1 and 94B6 from Xq28, complete sequence.//2.6e-26:493.65//AF035397

F-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=F, genomic survey sequence.//2.9e-11:83.96//AQ063969

F-NT2RP2004392

5 F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//1.1e-17:1:875.95//AC005164

F-NT2RP2004399//Homo sapiens SYBL1 gene.//1.4e-24:467.64//AJ004799

F-NT2RP2004400//Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence.//0.00074:455.59//AF069441

10 F-NT2RP2004412//H.sapiens CpG island DNA genomic MseI fragment, clone 34g4, reverse read cpq34g4.rt1a.//5.0e-27:154.98//Z65369

F-NT2RP2004425

F-NT2RP2004463//Streptomyces coelicolor cosmid 2E9.//0.0053:196.65//AL021530

F-NT2RP2004476//Drosophila melanogaster cosmid 67A9.//5.2e-15:377.63//AL034388

15 F-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//4.3e-100:497.97//AC005591

F-NT2RP2004512//Plasmodium falciparum MAL3P5, complete sequence.//2.3e-07:815.57//AL034556

F-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//8.5e-138:718.95//AC004890

F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds.//1.4e-137:687.96//AB011163

20 F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP Homo sapiens genomic clone 2387G7, genomic survey sequence.//2.1e-85 :484.91//AQ239555

F-NT2RP2004568//H.vulgar GAA-satellite DNA.//2.0e-07:292.62//Z50100

F-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//4.5e-44:512.72//AL023755

25 F-NT2RP2004587//Candida albicans cytoskeleton assembly control protein (SLA2) gene, partial cds.//1.0:344.56//AF092908

F-NT2RP2004594//nbxb0019H13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019H13r, genomic survey sequence.//0.053:324.60//AQ258020

30 F-NT2RP2004600

F-NT2RP2004602//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//0.12:109.73//AC005176

F-NT2RP2004614

F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//2.6e-102:496.98//AJ006291

F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.6e-153:728.98//AB007929

35 F-NT2RP2004675//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//0.092:239.61//AC005805

F-NT2RP2004681//Human DNA sequence from clone 51J23 on chromosome Xq26.3-27.3. Contains an EST and GSSs, complete sequence.//1.0:236.61//AL031312

F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.3e-59:327.94//AB014525

40 F-NT2RP2004709//HS\_2033\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=8 Row=J, genomic survey sequence.//1.9e-15:187.74//AQ230714

F-NT2RP2004710//HS\_3185\_B2\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=14 Row=H, genomic survey sequence.//9.9e-10:110.84//AQ172885

F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//6.4e-117:582.96//AB007947

45 F-NT2RP2004743//Human DNA sequence from PAC 37M17 chromosome X.//0.14:138.71//Z78022

F-NT2RP2004767//H.sapiens CpG island DNA genomic MseI fragment, clone 65c11, reverse read cpq65c11.rt1a.//1.3e-24:217.81//Z62210

F-NT2RP2004768//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//1.6e-45:54.71//AF024636

50 F-NT2RP2004775//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//5.8e-13:697.59//AE001398

F-NT2RP2004791//Human HeLa mRNA isolated as a false positive in a two-hybrid screen.//5.0e-53:353.84//U56252

F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.5e-116:594.95//AF058953 F-NT2RP2004802

55 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.1e-101:495.97//AF054179

F-NT2RP2004841//Human DNA sequence from cosmid J138O17, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//7.6e-82:531.84//Z72519

F-NT2RP2004861//Fugu rubripes GSS sequence, clone 040017bA3, genomic survey sequence.//0.96:183.64//AL025645

- F-NT2RP2004897//Human Chromosome X clone bWDX187, complete sequence.//4.8e-142:710:96//AC004383  
 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//2.0e-82:418:95//AB007144  
 F-NT2RP2004936  
 5 F-NT2RP2004959//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//3.5e-25:218:83//AQ150183  
 F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//2.5e-59:339:79//U56732  
 F-NT2RP2004962//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//3.6e-19:187:72//U91328  
 10 F-NT2RP2004967//Plasmodium falciparum MAL3P6, complete sequence.//0.0020:297:61//Z98551  
 F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mRNA, complete cds.//0.22:162:69//L29029  
 F-NT2RP2004982//F26D4-Sp6 IGF Arabidopsis thaliana genomic clone F26D4, genomic survey sequence.//0.13:273.61/B12642  
 15 F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds.//1.5e-20:431:65//D63478  
 F-NT2RP2004999  
 F-NT2RP2005000//R.rattus gene for beta-1 subunit of Na,K-ATPase.//0.019:240:63//X63375  
 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//6.0e-159:782:97//AB014515  
 F-NT2RP2005003//H.sapiens Staf50 mRNA.//3.1e-42:430:75//X82200  
 20 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//1.4e-98:501:96//AF100141  
 F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//1.0:209:63//AC004849  
 F-NT2RP2005020  
 F-NT2RP2005022//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-43:98.93//AC000380  
 25 F-NT2RP2005031//HS\_2052\_B2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=20 Row=N, genomic survey sequence.//0.019:363:61//AQ231464  
 F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene.//0.70:174:65//U64454  
 F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//0.20:519:57//AC005696  
 30 F-NT2RP2005108  
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//2.0e-103:495:98//AB014564  
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//2.9e-27:157:98//X98743  
 35 F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5.//0.00024:547.59//AJ223012  
 F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//0.95:191:62//AC004527  
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.6e-89:447:96//AF045583  
 40 F-NT2RP2005147//HS\_3184\_A1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=1 Row=1, genomic survey sequence.//0.10:294:60//AQ252226  
 F-NT2RP2005159//H.sapiens CpG island DNA genomic MseI fragment, clone 132g6, forward read cpg132g6.ft1a.//1.1e-13:93:97//Z59162  
 F-NT2RP2005162//Caenorhabditis elegans cosmid F01F1.//2.6e-20:394:64//U13070  
 45 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.4e-125:633:96//AJ007509  
 F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00016:316:60//U80808  
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.51:52:92//AC005189  
 50 F-NT2RP2005239//S.pombe chromosome II cosmid c21D10.//1.3e-22:356:67//AL031536  
 F-NT2RP2005254  
 F-NT2RP2005270//H.sapiens genomic DNA (chromosome 3; clone NL197R).//0.58:132:65//X87513  
 F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//9.0e-103:656:85//D30666  
 F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//3.4e-37:302:84//L26335  
 55 F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.1e-122:604:96//AF060219  
 F-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//4.0e-140:670:98//AJ007590  
 F-NT2RP2005293//HS\_3245\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=3245 Col=19 Row=J, genomic survey sequence.//8.2e-37:223.92//AQ217454  
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-95:483.96//AB014576  
 F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds.//8.2e-22:166.90//U11701  
 5 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//0.39:353.62//AF032387  
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds.//8.8e-29:456.66//AB011138  
 F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//0.72:431.61//Z92844  
 10 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//4.7e-99:489:96//AF072247  
 F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon.//0.93:105.67//L49358  
 F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds.//2.4e-08:97.83//M77184  
 F-NT2RP2005407  
 15 F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete sequence.//0.014:235:62//AC005346  
 F-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//4.0e-107:532.97//AC055548  
 F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence.//1.0:239:61//B97865  
 20 F-NT2RP2005457//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//4.7e-25:245.79//X68647  
 F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12 Contains EST, CA repeat, STS, GSS, retroviral sequence, complete sequence.//4.6e-111:724.86//AL031679  
 F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-39315 (BC301323), complete sequence.//6.5e-18:152.75//AC008116  
 25 F-NT2RP2005472//Human DNA sequence from clone 1118D24 on chromosome 1p36.11-36.33. Contains part of a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo) gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Binding Protein 2, TBPII, TNF-R2, CD120B, TNFBR). Contains ESTs, STSs, GSSs, genomic marker D1S434 and a ca repeat polymorphism. complete sequence.//4.4e-12:89.97//AL031276  
 30 F-NT2RP2005476//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//4.3e-40:463.73//AC004130  
 F-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.2e-115:228.99//AC006030  
 35 F-NT2RP2005491//HS\_2253\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=20 Row=M, genomic survey sequence.//4.6e-23:234.80//AQ116847  
 F-NT2RP2005495  
 F-NT2RP2005496//HS\_3064\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=15 Row=K, genomic survey sequence.//5.3e-90:436.98//AQ143097  
 40 F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds.//1.4e-63:503.78//M64931  
 F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//0.86:183.63//AC005880  
 F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28.//1.0:160.65//U82695  
 45 F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//3.9e-81:444.92//AF092563  
 F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds.//6.9e-18:112.99//AB018307  
 F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds.//1.1e-06:282.60//M14993  
 F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.9e-153:747.97//AJ012449  
 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.9e-130:618.98//AB007963  
 50 F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence.//3.1e-43:277.89//AF046734  
 F-NT2RP2005555//HS\_2188\_A2\_D04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=8 Row=G, genomic survey sequence.//8.0e-05:195.65//AQ086723  
 F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//2.5e-44:473.71//AF062529  
 55 F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//0.99:213.65//AC005016  
 F-NT2RP2005600//H.sapiens CpG island DNA genomic MseI fragment, clone 172d12, reverse read cpg172d12.r1a.//0.32:134.63//Z57359  
 F-NT2RP2005605

- F-NT2RP2005620//Homo sapiens epsilon 2a mRNA, complete cds.//9.8e-91:447:97//AF062085  
F-NT2RP2005622
- F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//8.6e-17:411:61//U10556  
F-NT2RP2005637//NATI (NAT1\*10)=acetyltransferase 1 {3' region, polyadenylation polymorphism} [human, unrelated Caucasians, mRNA Partial Mutant, 300 nt].//0.22:156:65//S78829
- 5 F-NT2RP2005640//Mouse U6 RNA gene.//5.5e-19:249:76//X06980  
F-NT2RP2005645//HS\_2201\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=14 Row=H, genomic survey sequence.//0.30:159:65//AQ068763  
F-NT2RP2005651//H.sapiens DNA sequence.//0.00037:150:66//Z22493
- 10 F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds.//4.7e-07:351:62//AB006626  
F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds.//8.2e-98:472:98//AF064605  
F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//2.4e-94:462:98//AF089814  
F-NT2RP2005683//HS-1024-B1-H05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=9 Row=P, genomic survey sequence.//0.99:156:64//B34405  
F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//7.7e-10:328:61//M77836  
F-NT2RP2005694  
F-NT2RP2005701//Homo sapiens 12p13.3 BAC RPC111-288K12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.72:160:65//AC005183
- 20 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//1.6e-124:599:97//AB018342  
F-NT2RP2005719//R.norvegicus mRNA for metallothionein-III.//0.86:117:64//X89603  
F-NT2RP2005722//Human zinc finger protein ZNF136.//2.6e-44:415:77//U09367  
F-NT2RP2005723//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//6.9e-15:153:81//AC002528
- 25 F-NT2RP2005726//Homo sapiens clone DJ0577P23, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.1e-41:138:95//AC005627  
F-NT2RP2005732//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//0.61:303:60//Z93017  
F-NT2RP2005741//Homo sapiens PALM gene, exon 1 and joined CDS.//0.52:116:67//Y16270
- 30 F-NT2RP2005748//Human Koz11 mRNA for zinc finger protein, partial.//0.11:136:66//X52342  
F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//7.8e-22:134:96//AF068868  
F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.2e-100:486:98//AF082516
- 35 F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds.//0.00073:425:56//D21853  
F-NT2RP2005767//G.gallus PB1 gene.//2.1e-73:544:80//X90849  
F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//6.2e-15:153:82//M77836  
F-NT2RP2005775//Sus scrofa mRNA for soluble angiotensin-binding protein, complete cds.//1.2e-121:649:88//D11336
- 40 F-NT2RP2005781//Pseudomonas aeruginosa gene for MexX and MexY, complete cds.//0.96:184:60//AB015853  
F-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.9e-63:222:96//AL034423  
F-NT2RP2005804//Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds.//2.6e-07:232:64//AF010579
- 45 F-NT2RP2005812  
F-NT2RP2005815//Streptomyces sp. gene for alkaline serine protease I.//0.031:358:59//X74103  
F-NT2RP2005835//Rattus norvegicus mRNA for p47, complete cds.//2.5e-107:449:91//AB002086  
F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//5.1e-05:144:73//Z68873  
F-NT2RP2005853//RPC111-24D4.TKBF RPC111 Homo sapiens genomic clone RPC111-24D4, genomic survey sequence.//6.4e-13:130:85//AQ013490
- 50 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//1.7e-174:829:98//AF092564  
F-NT2RP2005859//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 914P20, WORKING DRAFT SEQUENCE.//0.25:174:62//AL034553
- 55 F-NT2RP2005868//Fugu rubripes GSS sequence, clone 103124aF4, genomic survey sequence.//7.8e-06:92:79//AL027276  
F-NT2RP2005886//HS\_3187\_A2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3187 Col=16 Row=G, genomic survey sequence.//7.1e-95:494:95//AQ155885



- F-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//7.2e-32:660:66//L11316  
 F-NT2RP2005901//H.sapiens CpG island DNA genomic MseI fragment, clone 15b5, reverse read cpq15b5.rt1a.//0.0026:66:84//Z54729
- 5 F-NT2RP2005908//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.4e-49:481:75//AC004241  
 F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//6.6e-61:657:73//U63840  
 F-NT2RP2005942//H.sapiens PAP mRNA.//1.6e-46:618:67//X76770  
 F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//1.0e-48:533:71//AC005207
- 10 F-NT2RP2006023//HS\_3048\_A1\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=21 Row=A, genomic survey sequence.//2.1e-25:167:91//AQ126553  
 F-NT2RP2006038//CIT-HSP-384K4.TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey sequence.//3.9e-06:102:74//B51912  
 F-NT2RP2006043//Human intercrine-alpha (hiRH) mRNA, complete cds.//1.9e-05:418:59//U19495
- 15 F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55.//0.0035:226:65//AF016861  
 F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5.//3.9e-11:121:85//D17047  
 F-NT2RP2006071  
 F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete sequence.//0.46:264:59//AF027207
- 20 F-NT2RP2006100//Human Chromosome X, complete sequence.//3.2e-94:488:95//AC004073  
 F-NT2RP2006103//HS\_2254\_A2\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=4 Row=G, genomic survey sequence.//5.7e-27:156:96//AQ129602  
 F-NT2RP2006106//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.2e-62:655:71//AC000378
- 25 F-NT2RP2006141//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//1.2e-69:316:98//AL034405  
 F-NT2RP2006166//Homo sapiens chromosome 4 clone B32I8, complete sequence.//3.1e-45:387:81//AC004063  
 F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase Lac4A cell line point mutant mRNA, complete cds.//0.99:111:73//U62587
- 30 F-NT2RP2006186//Homo Sapiens mRNA for KIAA0654 protein, partial cds.//7.8e-113:567:96//AB014554  
 F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence.//2.8e-28:718:62//AC005232  
 F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-83:239:94//AC006057  
 F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.4e-116:618:93//X96484
- 35 F-NT2RP2006237//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence.//2.0e-18:118:97//AQ012480  
 F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//7.6e-102:635:86//U49055  
 F-NT2RP2006258//RPCI11-9N9.TP RPCI11 Homo sapiens genomic clone RPCI11-9N9, genomic survey sequence.//8.6e-05:181:63//B71615
- 40 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//0.44:111:71//X97630  
 F-NT2RP2006275//Pseudorabies virus UL[5,6,7,8,8.5,9,10,11,12,13] genes.//2.0e-05:501:59//X97257  
 F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.7e-138:679:97//AF035262  
 F-NT2RP2006320//P.falciparum pfmdr1 gene.//0.00013:425:60//X56851
- 45 F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.1e-19:545:62//AC003973  
 F-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745I14, WORKING DRAFT SEQUENCE.//8.9e-18:131:90//AL033532  
 F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//6.2e-125:602:98//AC004893
- 50 F-NT2RP2006364//Homo sapiens chromosome 19, cosmid R27139, complete sequence.//2.1e-06:241:65//AC005514  
 F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic survey sequence.//7.8e-06:148:70//AL029590  
 F-NT2RP2006393//Human DNA sequence from clone 80119 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//6.8e-06:167:70//AL022727
- 55 F-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y131F4, WORKING DRAFT SEQUENCE.//4.2e-92:363:84//AL023808

F-NT2RP2006441  
 F-NT2RP2006454//Sequence 8 from Patent WO9517522.//2.9e-06:180.66//A45338  
 F-NT2RP2006456  
 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//3.4e-148:545.98//AJ006266  
 5 F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons encoding ch1-ch4 and secretion domains, partial cds.//0.061:201.66//U50149  
 F-NT2RP2006472  
 F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism,  
 10 complete sequence.//8.8e-10:273.66//Z93929  
 F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene, exon 6.//0.71:174.59//U40965  
 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//6.6e-114:669.90//AF038966  
 15 F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone B2-1.//6.0e-26:503.63//M20855  
 F-NT2RP2006573//Molluscum contagiosum virus subtype 1, complete genome.//0.44:134.71//U60315  
 F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033.//5.0e-16:140.85//U50537  
 F-NT2RP3000002//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//3.8e-32:214.89//U14571  
 F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.8e-136:637.98//  
 20 AJ011972  
 F-NT2RP3000046//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//5.4e-05:57.16//L14320  
 F-NT2RP3000047  
 F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.0e-67:626.74//  
 25 M27877  
 F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence.//3.5e-10:394.64//AC001227  
 F-NT2RP3000068  
 F-NT2RP3000072//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//1.0:301.61//AC004746  
 F-NT2RP3000080//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING  
 30 DRAFT SEQUENCE.//1.9e-44:297.79//AL021391  
 F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds.//4.5e-33:528.65//U12536  
 F-NT2RP3000092//RPC11-22M5.TV RPC1-11 Homo sapiens genomic clone RPC1-11-22M5, genomic survey sequence.//3.3e-27:157.97//B84237  
 35 F-NT2RP3000109//Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds.//0.92:185.64//L29260  
 F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.2e-112:286.89//AC005189  
 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//9.0e-181:849.98//AB011164  
 40 F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPC.264\_B\_14, complete sequence.//4.2e-24:155:94//AC005884  
 F-NT2RP3000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING DRAFT SEQUENCE.//7.2e-43:269.81//AL023583  
 F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9.//0.098:405.57//L39063  
 45 F-NT2RP3000207//Drosophila melanogaster DNA sequence (P1 DS00164 (D269)), complete sequence.//0.9e:608.55//AC004716  
 F-NT2RP3000220  
 F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.0e-18:509.58//AF09569  
 50 F-NT2RP3000235//Mouse Cosmid ma53a016 from 14D1-D2, complete sequence.//3.5e-05:224.65//AC004101  
 F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds.//2.1e-109:691.86//D86972  
 F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence.//0.20:119.68//Z70213  
 F-NT2RP3000252//Homo sapiens cosmid 1F1, complete sequence.//9.8e-78:174.88//AF065393  
 F-NT2RP3000255  
 55 F-NT2RP3000267  
 F-NT2RP3000299//Mus musculus Crk-associated substrate (Cas-b) mRNA, complete cds.//5.9e-48:374.82//U48853  
 F-NT2RP3000312//Fruit fly (D. melanogaster) Glued mRNA, complete cds.//4.9e-22:583.63//J02932

- F-NT2RP3000320//RPC111-36J1.TP RPC1-11 Homo sapiens genomic clone RPC1-11-36J1, genomic survey sequence.//4.4e-06:87.88//AQ407107
- F-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//5.5e-26:283:79//U78090
- 5 F-NT2RP3000333//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 973M2, WORKING DRAFT SEQUENCE.//1.0:309:60//AL033533
- F-NT2RP3000341//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//6.7e-42:465:74//Z97181
- 10 F-NT2RP3000348
- F-NT2RP3000350//Homo sapiens cosmid 1F1, complete sequence.//3.4e-79:174:88//AF065393
- F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//2.2e-127:816:85//M25757
- F-NT2RP3000361//Schizosaccharomyces pombe DNA for pre-mRNA splicing factor, complete cds.//0.0075:288:58//D83743
- 15 F-NT2RP3000366//Mus musculus ras-related protein (rab18) mRNA, complete cds.//7.1e-134:693:94//L04966
- F-NT2RP3000393//Rattus norvegicus mRNA for GABA-B R2 receptor.//0.049:308:60//AJ011318
- F-NT2RP3000397//S.cerevisiae chromosome VII reading frame ORF YGL120c.//0.00012:441:58//Z72642
- F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//5.0e-174:841:97//AF071185
- F-NT2RP3000418//Homo sapiens chromosome 17, clone hRPK.1053\_B\_8, complete sequence.//7.9e-53:817:68//AC006083
- 20 F-NT2RP3000433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//6.1e-31:590:63//AL031681
- F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22aB10, genomic survey sequence.//4.0e-19:169:81//AL026471
- 25 F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//2.4e-41:459:65//Z84488
- F-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.1e-100:365:87//AL031650
- F-NT2RP3000451//HS\_2024\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2024 Col=19 Row=I, genomic survey sequence.//0.011:367:57//AQ229420
- 30 F-NT2RP3000456//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//1.5e-89:458:96//AQ055548
- F-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.043:147:70//Z97353
- 35 F-NT2RP3000487//H.sapiens CpG island DNA genomic MseI fragment, clone 11b11, forward read cpg11b11.ft1a.//1.7e-11:96:92//Z84440
- F-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X16667
- F-NT2RP3000526//Homo sapiens full-length insert cDNA clone YZ38E04.//4.1e-30:283:76//AF086071
- 40 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966
- F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//11.9e-14:220:70//AF081260
- F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//0.00019:361:60//AC002554
- 45 F-NT2RP3000561//Homo sapiens PAC clone DJ094216 from 7q11, complete sequence.//9.0e-171:827:98//AC006012
- F-NT2RP3000562
- F-NT2RP3000578//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271
- F-NT2RP3000582//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//B73597
- 50 F-NT2RP3000584
- F-NT2RP3000590//H.sapiens CpG island DNA genomic MseI fragment, clone 170d7, forward read cpg170d7.ft1a.//3.0e-22:128:100//Z59723
- F-NT2RP3000592//CIT-HSP-228BJ7.TR CIT-HSP Homo sapiens genomic clone 228BJ7, genomic survey sequence.//2.2e-78:382:98//B98868
- 55 F-NT2RP3000596//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00076:143:67//AQ109305
- F-NT2RP3000599//Caenorhabditis elegans cosmid T19B10, complete sequence.//1.2e-13:295:66//Z74043

- F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.37:520:57//L14320
- F-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//8.8e-155:526:97//AC006128
- 5 F-NT2RP3000622//HS\_3213\_A2\_D02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//4.1e-29:238:85//AQ175104
- F-NT2RP3000624//Homo sapiens clone DJ0800G07, complete sequence.//0.47:75:80//AC004890
- F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.078:393:58//AL031313
- 10 F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.4e-96:541:79//U171363
- F-NT2RP3000644//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.2e-46:421:77//AC005089
- F-NT2RP3000661
- 15 F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.//1.7e-11:292:65//AL022237
- 20 F-NT2RP3000685//H.sapiens mRNA for novel protein.//2.4e-80:460:92//X99961
- F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10F6.//1.0:141:65//Z77872
- F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds.//6.1e-20:127:96//D50930
- F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//1.1e-46:622:67//AF015264
- 25 F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//4.7e-37:429:70//U16655
- F-NT2RP3000753
- F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//2.8e-38:519:69//Z99281
- F-NT2RP3000815//HS\_2237\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=2 Row=G, genomic survey sequence.//0.79:151:61//AQ067252
- 30 F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds.//0.36:378:58//L39387
- F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds.//0.0025:291:62//U02513 F-NT2RP3000836//Mouse complement factor H-related protein mRna, complete cds, clone 9C4.//0.69:563:57//M29009
- 35 F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//2.1e-46:666:68//Z86062
- F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequence.//3.4e-92:193:93//AC005581
- 40 F-NT2RP3000847//Human HepG2 3' region cDNA, clone hmd5d02.//3.4e-32:261:81//D16938
- F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.1e-44:358:81//AC005082
- F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome 1q24. Contains the LNHR (SELL) gene coding for Lymph Node Homing Receptor (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte surface antigen Leu-8, TQ1, GP90-MEL, LECAM1 Leukocyte-Endothelial Cell Adhesion Molecule 1, CD62L). Contains the SELE gene coding for E-Selectin precursor (CD62E, ELAM-1 Endothelial Leukocyte Adhesion Molecule 1, LECAM-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknown gene with homology to predicted yeast, plant and worm proteins. Contains ESTs and STSs, complete sequence.//4.4e-123:150:98//AL021940
- 50 F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, genomic survey sequence.//0.016:185:65//B60831
- F-NT2RP3000865
- F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//2.0e-29:766:60//U53445
- 55 F-NT2RP3000869//H.sapiens gene for plectin.//1.1e-12:700:60//Z54367
- F-NT2RP3000875//HS\_2236\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2236 Col=19 Row=N, genomic survey sequence.//0.98:153:68//AQ154007
- F-NT2RP3000901//Human herpesvirus 2 glycoprotein B precursor (UL27) gene, complete cds.//0.44:213:65//

AF021340  
 F-NT2RP3000904//Rat Na<sup>+</sup> channel mRNA, 3' end.//3.6e-106:505.99//M27223  
 F-NT2RP3000917//Mouse mRNA for Dhml protein, complete cds.//3.1e-132:691.93//D38517  
 F-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//  
 3.2e-97:585.88//AF015264  
 F-NT2RP3000968//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//5.8e-70:181:  
 89//U91326  
 F-NT2RP3000980//R. norvegicus CYP3A1 gene, 5' flanking region.//6.1e-26:507.66//X98335  
 F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529  
 F-NT2RP3001004//H.sapiens CpG island DNA genomic MseI fragment, clone 39c1, reverse read cp939c1.rt1a./  
 15.9e-27:150.99//Z60925  
 F-NT2RP3001007//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.11:  
 610.57//AC006039  
 F-NT2RP3001055//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORK-  
 ING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352.67//AC005653  
 F-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//1.4e-49:437.77//X78927  
 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//8.4e-50:534.74//  
 AF060219  
 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds.//1.2e-14:474.60//AB018325  
 F-NT2RP3001096//CIT-HSP-2305P8.TF CIT-HSP Homo sapiens genomic clone 2305P8, genomic survey se-  
 quence.//3.4e-37:222.93//AQ021278  
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712.64//D86969  
 F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma  
 (polg) gene, complete sequence.//2.7e-116:186.99//AC005317  
 F-NT2RP3001111  
 F-NT2RP3001113//Human DNA sequence from cosmid U157D4, between markers DXS366 and DXS87 on chro-  
 some X.//2.4e-05:702.58//Z68871  
 F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.9e-170:821.98//  
 AC005189  
 F-NT2RP3001116//HS\_3075\_A1\_F01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3075 Col=1 Row=K, genomic survey sequence.//7.3e-49:290.92//AQ120581  
 F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from  
 gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island,  
 complete sequence.//1.4e-121:588.97//AL031864  
 F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687.75//U09367  
 F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39, UL40 and UL41.//6.8e-05:344:  
 64//Z49078  
 F-NT2RP3001133//Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds.//0.00021:529:60//  
 AF027735  
 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.6e-179:851.96//AB018305  
 F-NT2RP3001147//RPC11-3M16.TP RPC1-11 Homo sapiens genomic clone RPC1-11-3M16, genomic survey se-  
 quence.//2.1e-15:106.96//B48859  
 F-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
 DRAFT SEQUENCE.//2.0e-159:418.95//AL034379  
 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:891.98//AJ006266  
 F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.1-41 Contains GSS, com-  
 plete sequence.//1.1e-69:207.97//AL034351  
 F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//0.16:475.58//AC005507  
 F-NT2RP3001216//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-  
 05:561.56//AC004845  
 F-NT2RP3001221  
 F-NT2RP3001232//Mouse mRNA for serine protease PC6, complete cds.//1.0e-11:120.87//D12619  
 F-NT2RP3001236  
 F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule-associated protein.//3.9e-19:501.61//X51396  
 F-NT2RP3001245//CITBI-E1-2505C1.TF1 CITBI-E1 Homo sapiens genomic clone 2505C1, genomic survey se-  
 quence.//8.5e-70:337.100//AQ242007

F-NT2RP3001253//CITBI-E1-2505N14.TR CITBI-E1 Homo sapiens genomic clone 2505N14, genomic survey sequence.//0.83:235.60//AQ260430

F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds.//3.8e-47:761:64//AB018269

F-NT2RP3001268//Homo sapiens zinc finger protein (HZF6) mRNA, 5' UTR and partial cds.//2.3e-64:618:72//AF027513

5 F-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//2.6e-99:669:83//Y18101

F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//0.99:400:58//U07561

10 F-NT2RP3001281//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//5.9e-39:304:70//AC005837

F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds.//7.6e-47:544:69//D87457

F-NT2RP3001307//Ambystoma tigrinum RPE65 protein mRNA, complete cds.//2.4e-27:547:63//AF047465

15 F-NT2RP3001318//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00022:624:60//AC004709

F-NT2RP3001325//Caenorhabditis elegans cosmid F36H12.//0.25:523:59//AF078790

F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds.//5.1e-29:345:73//D86966

F-NT2RP3001339//Rattus norvegicus myotonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds.//1.2e-151:821:91//AF021935

20 F-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//5.3e-27:247:81//AF083105

F-NT2RP3001355//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-16:130:76//AC000052

F-NT2RP3001356

F-NT2RP3001374

25 F-NT2RP3001383//Homo sapiens DNA sequence from PAC 140C12 on chromosome 6q26-q27.//0.00082:365:61//AL008628

F-NT2RP3001384//Homo sapiens HRIHFB2018 mRNA, partial cds.//6.4e-157:743:98//AB015332

F-NT2RP3001392//Human DNA sequence from PAC 302D9 on chromosome 22q11.2-qter. Contains STS, complete sequence.//0.045:359:61//Z82198

30 F-NT2RP3001396//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.3e-16:336:65//AC004296

F-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.1e-100:711:82//U49046

F-NT2RP3001399//Homo sapiens PAC clone DJ1106E03 from 7q31.3-q3, complete sequence.//5.4e-20:245:73//AC005521

35 F-NT2RP3001407//RPCI11-41A20.TP RPCI11 Homo sapiens genomic clone RPCI11-41A20, genomic survey sequence.//0.051:306:59//AQ029031

F-NT2RP3001420//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.90:170:65//AL021327

F-NT2RP3001426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//2.9e-89:138:98//AL031447

40 F-NT2RP3001427//CIT-HSP-2302H24.TF CIT-HSP Homo sapiens genomic clone 2302H24, genomic survey sequence.//8.1e-36:212:94//AQ020997

F-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tp) mRNA, complete cds.//8.5e-73:431:91//U69668

45 F-NT2RP3001432//HS\_3032\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=B, genomic survey sequence.//0.00024:111:76//AQ096619

F-NT2RP3001447

F-NT2RP3001449//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.1e-105:223:99//AL031282

55 F-NT2RP3001453//Ralstonia sp. E2 positive phenol-degradative gene regulator (poxR), phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds.//0.75:349:59//AF026065

F-NT2RP3001457  
 F-NT2RP3001459  
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds.//1.3e-08:168:70//  
 AF072836  
 5 F-NT2RP3001490  
 F-NT2RP3001495//Human oxidoreductase (HHcMA56) mRNA, complete cds.//1.0e-26:191:90//U13395  
 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//  
 8.5e-171:804:98//AF064801  
 10 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete, cds.//8.9e-140:743:  
 91//U36499  
 F-NT2RP3001529//Streptomyces griseus DNA for ribosomal protein L21, ribosomal protein L27, Obg, complete  
 cds.//2.1e-14:517:59//D87916  
 F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic survey sequence.//4.7e-05:217:  
 63//AF078176  
 15 F-NT2RP3001554//Rattus norvegicus microtubule-associated protein 1A MAP1A (Mtap-1) mRNA, complete cds.//  
 4.3e-17:332:67//M83196  
 F-NT2RP3001580//RPC11-91E19.TV RPC11 Homo sapiens genomic clone R-91E19, genomic survey se-  
 quence.//4.2e-15:110:91//AQ281332  
 F-NT2RP3001587//S.pombe chromosome II cosmid c16H5.//6.6e-28:491:64//AL022104  
 20 F-NT2RP3001589//RPC11-68M15.TK RPC11 Homo sapiens genomic clone R-68M15, genomic survey se-  
 quence.//8.7e-108:517:98//AQ237629  
 F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete  
 sequence.//1.0e-09:257:65//AC004674  
 25 F-NT2RP3001608//Methylococcus capsulatus methane monooxygenase component A alpha chain, methane mo-  
 noxygenase A beta chain and methane monooxygenase component C genes, complete cds.//0.59:450:57//  
 M90050  
 F-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger  
 protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST,  
 STS, GSS, complete sequence.//1.8e-42:278:79//AL021608  
 30 F-NT2RP3001629  
 F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein.//1.5e-63:276:97//AJ130978  
 F-NT2RP3001642//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.018:127:66//Z68117  
 F-NT2RP3001646  
 F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.4e-171:816:98//AJ012449  
 35 F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protein (Scm) mRNA, complete cds.//1.6e-  
 38:542:66//U49793  
 F-NT2RP3001676//HS\_3090\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3090 Col=7 Row=D, genomic survey sequence.//3.1e-07:333:64//AQ123250  
 F-NT2RP3001678//Drosophila melanogaster; Chromosome 3L; Region 63C5-63D3; P1 clone DS01859, WORK-  
 40 ING DRAFT SEQUENCE, 6 unordered pieces.//1.0:539:57//AC004358  
 F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and  
 non-small cell lung cancer, segment 3/11.//2.8e-130:355:96//AB020860  
 F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//  
 2.1e-37:512:70//AF059273  
 45 F-NT2RP3001690//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey se-  
 quence.//2.8e-19:123:95//AQ012480  
 F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds.//9.4e-11:167:74//D31962  
 F-NT2RP3001708//H.sapiens CpG island DNA genomic Mse1 fragment, clone 4g7, reverse read cpq4g7.rt1d.//  
 1.3e-17:113:97//Z61312  
 50 F-NT2RP3001712//M.musculus mRNA for HP1-BP74 protein.//2.2e-95:601:88//X99642  
 F-NT2RP3001716  
 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.4e-159:  
 565:97//AF054177  
 F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2)-mRNA, partial cds.//1.7e-132:786:  
 88//AF008554  
 55 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds.//3.9e-104:811:78//D50918  
 F-NT2RP3001739//Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete se-  
 quence.//6.5e-07:178:69//AC000097

- F-NT2RP3001752//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//5.2e-31:311:77//AL031311
- F-NT2RP3001753//Sequence 29 from patent US 5658882.//0.11:513:58//162381
- 5 F-NT2RP3001764//Sequence 6 from Patent WO9706245.//6.4e-47:673:66//A59888
- F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10.//0.078:290:63//U39644
- F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//2.8e-151:710:98//AB007928
- F-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.2e-26:213:85//U13262
- 10 F-NT2RP3001799//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//8.4e-51:168:95//AL031284
- F-NT2RP3001819//S. glaucosens genes strU, strX, strV and strW for 5'-hydroxystreptomycin production and transport polypeptides.//0.084:526:58//X89010
- F-NT2RP3001844//HS\_3110\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=19 Row=J, genomic survey sequence.//1.5e-40:232:82//AQ140433
- 15 F-NT2RP3001854//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.14:452:58//AC005505
- F-NT2RP3001855//Mus musculus homeobox protein PKNOX1 (Pknox1) mRNA, complete cds.//2.7e-39:575:67//AF061270
- 20 F-NT2RP3001857//M. musculus tex292 mRNA (5'region).//8.7e-07:106:81//X80434
- F-NT2RP3001896
- F-NT2RP3001898//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 163G9, WORKING DRAFT SEQUENCE.//0.094:456:60//AL008733
- F-NT2RP3001915//Caenorhabditis elegans cosmid C12D8, complete sequence.//0.58:482:56//Z73969
- 25 F-NT2RP3001926//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.42:401:58//AL034557
- F-NT2RP3001929//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//3.1e-28:263:77//AC004651
- F-NT2RP3001931
- F-NT2RP3001938//CIT-HSP-2165E8.TR CIT-HSP Homo sapiens genomic clone 2165E8, genomic survey sequence.//3.6e-24:182:91//B95475
- 30 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//1.8e-165:815:96//AB014575
- F-NT2RP3001944
- F-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//4.8e-62:304:89//AC005844
- 35 F-NT2RP3001989//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//8.2e-10:564:60//AF030694
- F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//2.5e-57:361:80//Z83822
- 40 F-NT2RP3002004//Sequence 3 from patent US 5798245.//1.6e-26:104:100//AR025386
- F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.0053:633:58//AC004137
- F-NT2RP3002014//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//1.3e-32:334:68//AC004640
- 45 F-NT2RP3002033//H. sapiens DNA sequence.//0.012:214:63//Z22493
- F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin.//8.7e-116:713:86//X53773
- F-NT2RP3002054//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.6e-12:613:60//AL021841
- 50 F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X.//0.17:566:59//Z77249
- F-NT2RP3002057//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//3.3e-24:167:82//AC005682
- F-NT2RP3002062
- F-NT2RP3002063//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.24:508:58//AJ235272
- 55 F-NT2RP3002081//HS\_2001\_B1\_E06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//9.7e-22:155:90//AQ218494
- F-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-



- plete sequence.//9.6e-66:562:77//AC006210  
 F-NT2RP3002102//CIT-HSP-2307B10.TR CIT-HSP Homo sapiens genomic clone 2307B10, genomic survey sequence.//5.9e-16:214:74//AQ018040  
 F-NT2RP3002108  
 5 F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.6e-29:414:68//AC004020  
 F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (pIIB) and polyketide synthase type I (pIIC) genes, complete cds.//0.96:434:60//AF003370  
 F-NT2RP3002147//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329F2, WORKING DRAFT SEQUENCE.//1.3e-63:380:91//AL031710  
 10 F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//9.9e-60:315:80//U95742  
 F-NT2RP3002163  
 F-NT2RP3002165//M.musculus HCNGP mRNA.//1.4e-142:867:87//X68061  
 15 F-NT2RP3002166//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//0.090:394:59//AC006121  
 F-NT2RP3002173//HS\_3062\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=9 Row=N, genomic survey sequence.//3.3e-101:509:96//AQ193219  
 F-NT2RP3002181//Human DNA sequence from clone 24c18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//4.5e-106:432:84//AL021808  
 20 F-NT2RP3002244//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.63:353:60//AC005321  
 F-NT2RP3002248//HS\_3029\_A1\_D10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=19 Row=G, genomic survey sequence.//3.5e-10:125:79//AQ094880  
 F-NT2RP3002255//Bovine herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5' end.//5.6e-09:629:59//L14321  
 25 F-NT2RP3002273//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//4.9e-35:366:74//B03004  
 F-NT2RP3002276//B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex.//0.023:326:60//X64898  
 30 F-NT2RP3002303//Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome.//3.8e-12:643:57//AE000810  
 F-NT2RP3002304//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-09:490:60//AC005504  
 35 F-NT2RP3002330//Human DNA sequence from cosmid L58b6, Huntington's Disease Region, chromosome 4p16.3, containing STS matches.//1.9e-93:572:88//Z49862  
 F-NT2RP3002343//HS\_3010\_A2\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=16 Row=C, genomic survey sequence.//9.0e-75:373:97//AQ119068  
 40 F-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.9e-64:588:75//X16396  
 F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene, alternatively spliced form.//1.3e-164:770:98//Y16355  
 F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds.//1.4e-190:911:98//AB018331  
 45 F-NT2RP3002399  
 F-NT2RP3002402//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//7.2e-25:249:79//D89340  
 F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//1.2e-138:649:99//AB014578  
 F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP Homo sapiens genomic clone 367N3, genomic survey sequence.//5.0e-18:115:96//B78927  
 50 F-NT2RP3002501//Caenorhabditis elegans cosmid K01C8, complete sequence.//0.00020:170:65//Z49068  
 F-NT2RP3002512//Homo sapiens clone 664 unknown mRNA, partial sequence.//1.6e-59:308:97//AF091088  
 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds.//1.4e-144:763:93//U35246  
 F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.8e-178:833:98//AB018272  
 55 F-NT2RP3002549//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-26:123:72//AC004821  
 F-NT2RP3002566//Streptomyces viridifaciens sigma factor (hrdD) gene, complete cds.//0.76:459:59//U60418  
 F-NT2RP3002587//Homo sapiens chromosome Y, clone 264\_M.20, complete sequence.//4.6e-13:199:76//

AC004617

F-NT2RP3002590//Porphyra purpurea chloroplast, complete genome.//0.88:284:60//U38804

F-NT2RP3002602//CIT978SK-A-441H11-2.TPB CIT978SK Homo sapiens genomic clone A-441H11, genomic survey sequence.//2.0e-22:140:95//B68331

F-NT2RP3002603

F-NT2RP3002628//C.acetobutylicum dnaJ and orfB genes.//2.0e-05:333:60//X69050

F-NT2RP3002631

F-NT2RP3002650//Mus musculus mRNA for cartilage-associated protein (CASP).//1.5e-20:641:62//AJ006469

F-NT2RP3002659//Bovine herpesvirus type 1 UL22-35 genes.//5.2e-05:621:59//Z78205

F-NT2RP3002660//Homo sapiens PAC clone DJ1006K12 from Tq31.2-q31, complete sequence.//0.98:453:57//AC004946

F-NT2RP3002663//Homo sapiens chromosome 19, cosmid F6697, complete sequence.//3.3e-22:407:67//AC006129

F-NT2RP3002671//S.pombe chromosome III cosmid c553.//1.0e-12:336:66//AL023704

F-NT2RP3002682//Caenorhabditis elegans cosmid F17C11, complete sequence.//1.3e-21:448:64//Z72507

F-NT2RP3002687//CIT978SK-A-789B1.TP CIT978SK Homo sapiens genomic clone A-789B1, genomic survey sequence.//2.5e-25:173:91//B51656

F-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.2e-73:728:74//D17577

F-NT2RP3002701//CITBI-E1-2507L14.TF CITBI-E1 Homo sapiens genomic clone 2507L14, genomic survey sequence.//0.0012:55:92//AQ263530

F-NT2RP3002713

F-NT2RP3002763//Caenorhabditis elegans cosmid T20F10, complete sequence.//0.98:209:63//Z81594

F-NT2RP3002770

F-NT2RP3002785//Homo sapiens laminin beta-4 chain precursor (LAMB4) mRNA, alternatively spliced short variant, partial cds.//0.78:515:57//AF029325

F-NT2RP3002799//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//1.9e-21:167:79//AL022718

F-NT2RP3002810//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence.//0.32:187:66//AC005549

F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds.//6.9e-54:615:70//AF004715

F-NT2RP3002861//Caenorhabditis elegans cosmid M03F4.//4.2e-05:226:65//U64601

F-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.0e-93:638:83//AF030430

F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds.//8.5e-89:557:88//AB001895

F-NT2RP3002877//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//7.9e-12:160:78//AC006087

F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//5.7e-180:853:98//AB018314

F-NT2RP3002911//RPCI11-24N15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-24N15, genomic survey sequence.//2.3e-13:442:61//B88815

F-NT2RP3002948//, complete sequence.//2.2e-110:637:91//AC005500

F-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.7e-166:793:98//AC005754

F-NT2RP3002955//Human HepG2 partial cDNA, clone hmd3c02m5.//0.00011:61:95//D17024

F-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.2e-128:808:85//D30666

F-NT2RP3002972//H.sapiens (xs168) mRNA, 381bp.//1.5e-43:312:85//Z36820

F-NT2RP3002978//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00044:527:57//AC005505

F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence.//0.92:341:60//AC001644

F-NT2RP3002988//HS\_3015\_A1\_B07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=13 Row=C, genomic survey sequence.//4.4e-05:379:58//AQ091708

F-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.4e-72:197:79//AF109905

F-NT2RP3003032//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-80, complete sequence.//1.6e-08:809:58//AL010153

F-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//4.1e-111:804:81//U78090

- F-NT2RP3003061//Human mRNA for ankyrin (variant 2.1).//1.4e-12:633:59//X16609  
 F-NT2RP3003068//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//0.034:282:60//AC002410  
 F-NT2RP3003071//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read  
 cpg13d12.r1tc.//6.8e-15:95:100//Z64565
- 5 F-NT2RP3003078  
 F-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//8.1e-72:732:71//D88315  
 F-NT2RP3003121  
 F-NT2RP3003133//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.5e-12:168:76//  
 AC004510
- 10 F-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//4.0e-148:908:87//  
 D12646  
 F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//2.0e-31:658:63//  
 U17995  
 F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds.//3.5e-22:430:63//AF017639
- 15 F-NT2RP3003150  
 F-NT2RP3003157//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.9e-92:493:94//AQ155489  
 F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete  
 cds.//8.6e-06:228:65//AF064868
- 20 F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein.//7.4e-73:737:71//X78933  
 F-NT2RP3003197  
 F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//  
 4.1e-48:640:67//AF015264  
 F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence.//0.0033:69:81//U31059
- 25 F-NT2RP3003210//Homo sapiens SYBL1 gene.//1.1e-34:430:70//AJ004799  
 F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//6.3e-75:  
 776:74//U20286  
 F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein.//1.8e-62:575:74//AJ006064  
 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//3.7e-128:617:98//AF055460
- 30 F-NT2RP3003251//H.sapiens Stat50 mRNA.//3.5e-67:651:76//X82200  
 F-NT2RP3003264//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING  
 DRAFT SEQUENCE, 8 unordered pieces.//0.015:473:58//AC004153  
 F-NT2RP3003278//H.sapiens CpG island DNA genomic MseI fragment, clone 28b4, forward read cpg28b4.ft1a.//  
 4.0e-27:174:93//Z60555
- 35 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//1.3e-131:694:93//L36983  
 F-NT2RP3003290//Homo sapiens nickel-specific induction protein (Cap43) mRNA, complete cds.//1.7e-64:662:  
 71//AF004162  
 F-NT2RP3003301//Spinacia oleracea mRNA for ATP-dependent protease Lon, complete cds.//4.9e-37:682:64//  
 D85610
- 40 F-NT2RP3003302//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.6e-95:680:82//AC006213  
 F-NT2RP3003311//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete se-  
 quence.//1.0:191:62//AC004527  
 F-NT2RP3003313//Streptomyces coelicolor cosmid 5A7.//0.0084:403:61//AL031107  
 F-NT2RP3003327//H.sapiens Stat50 mRNA.//2.5e-29:253:67//X82200
- 45 F-NT2RP3003330  
 F-NT2RP3003344  
 F-NT2RP3003346//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//9.0e-41:296:  
 84//AC005284  
 F-NT2RP3003353//Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a  
 BAC end-sequence (GSS).//0.047:404:60//AL021069
- 50 F-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//  
 8.3e-122:632:96//AC005519  
 F-NT2RP3003384//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unor-  
 dered pieces.//0.0036:127:74//AC000360  
 F-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//2.0e-110:843:79//U09874
- 55 F-NT2RP3003403//Human Chromosome X, complete sequence.//7.5e-21:647:61//AC002407  
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//1.0e-20:430:  
 63//U09063

- F-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COP57b) mRNA, complete cds.//4.2e-139:524:90//AF071317
- F-NT2RP3003427//HS-1051-A1-D03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=5 Row=G, genomic survey sequence.//8.8e-18:111:97//B40173
- 5 F-NT2RP3003433//HS\_2219\_B2\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=22 Row=B, genomic survey sequence.//1.2e-57:410:83//AQ145866
- F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.2e-181:853:98//AF004828
- 10 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.6e-173:826:98//AB018268
- F-NT2RP3003491//CIT-HSP-2344O1.TR CIT-HSP Homo sapiens genomic clone 2344O1, genomic survey sequence.//1.2e-39:213:97//AQ057124
- F-NT2RP3003500//HS\_3000\_B1\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.025:253:60//AQ090347
- 15 F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (LANL), complete sequence.//0.95:279:60//AC004234
- F-NT2RP3003552//Homo sapiens clone UWGC:y54c222 from 6p21, complete sequence.//1.8e-88:166:84//AC006049
- F-NT2RP3003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//8.9e-17:245:72//AL031985
- 20 F-NT2RP3003564//HS\_3141\_B1\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3141 Col=19 Row=N, genomic survey sequence.//2.7e-79:442:93//AQ187798
- F-NT2RP3003572
- F-NT2RP3003576//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.8e-55:275:84//AC005632
- 25 F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein.//1.1e-94:488:95//X56387
- F-NT2RP3003621//Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.//6.0e-88:463:84//AC004235
- F-NT2RP3003625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING DRAFT SEQUENCE.//0.98:307:60//AL031600
- 30 F-NT2RP3003656
- F-NT2RP3003659//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271
- F-NT2RP3003665//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//0.011:279:65//AC002096
- 35 F-NT2RP3003672
- F-NT2RP3003680//Drosophila melanogaster; Chromosome 2R; Region 39B1-39B3; P1 clone DS05527, WORKING DRAFT SEQUENCE, 9 unordered pieces.//3.4e-16:425:64//AC005811
- F-NT2RP3003686//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-27:153:98//AQ136993
- 40 F-NT2RP3003701
- F-NT2RP3003716//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.6e-107:788:82//U42975
- F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//2.3e-148:700:98//AB018300
- 45 F-NT2RP3003746//CIT-HSP-2306A10.TF CIT-HSP Homo sapiens genomic clone 2306A10, genomic survey sequence.//0.39:212:61//AQ015785
- F-NT2RP3003795//Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B and 1C (SYNGR1A, SYBGR1B, SYNGR1C), both genes downstream of a putative CpG island. Contains ESTs, an STS, GSSs, genomic marker D22S1155 and a ca repeat polymorphism, complete sequence.//4.2e-21:445:66//AL022326
- 50 F-NT2RP3003799//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//1.0:257:63//AF038458
- F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosine-specific protein kinase, complete cds.//1.2e-63:484:81//M17031
- 55 F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//AC005321
- F-NT2RP3003809//Bovine herpesvirus 1 complete genome.//7.2e-12:615:60//AJ004801
- F-NT2RP3003819

- F-NT2RP3003825  
F-NT2RP3003828//Human rRNA primary transcript internal transcribed spacer 2 (ITS2).//6.2e-16:543.62//X17626  
F-NT2RP3003831//RPC11-50N15.TJ RPC11 Homo sapiens genomic clone R-50N15, genomic survey sequence.//1.1e-21:174.85//AQ082633
- 5 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//8.0e-47:242.98//AF070611  
F-NT2RP3003842//RPC11-44E5.TJ RPC11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//9.7e-25:143.97//AQ195884  
F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds.//4.2e-36:335.68//AB018268  
F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//4.1e-174:805.99//AB018343
- 10 F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//2.7e-109:709.84//U19181  
F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds.//8.9e-11:193.70//U20554  
F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//2.6e-47:404.77//AF057358
- 15 F-NT2RP3003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.68:597.55//AC005504  
F-NT2RP3003989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404H4, WORKING DRAFT SEQUENCE.//0.37:548.56//AL031661  
F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNCG2) mRNA, complete cds.//0.021:433:58//U58837
- 20 F-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//1.4e-164:838.94//X84692  
F-NT2RP3004016//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018K9, WORKING DRAFT SEQUENCE.//0.0042:356.62//AL031726  
F-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 809F4, WORKING DRAFT SEQUENCE.//6.8e-112:627.82//AL022400
- 25 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds.//2.2e-61:774.67//AB002317  
F-NT2RP3004070//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//7.9e-17:484.62//AL021939
- 30 F-NT2RP3004078//M.musculus (BALB/c) MRF2 mRNA.//1.9e-102:684.83//X76089  
F-NT2RP3004093//F24P17-Sp6 IGF Arabidopsis thaliana genomic clone F24P17, genomic survey sequence.//0.021:207.63//B09433  
F-NT2RP3004095//Homo sapiens clone NH0486122, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.5e-25:272.77//AC005038
- 35 F-NT2RP3004110//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.6e-28:223.73//AC003973  
F-NT2RP3004125//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds.//2.2e-28:637.63//AF000560  
F-NT2RP3004145  
F-NT2RP3004148
- 40 F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds.//6.5e-120:578.98//AF032900  
F-NT2RP3004189//M.musculus tex292 mRNA (5'region).//1.1e-06:102.82//X80434  
F-NT2RP3004206//D.melanogaster cm mRNA.//7.3e-69:715.71//X58374  
F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//4.8e-42:650.66//D64009
- 45 F-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//8.4e-55:184.84//D42052  
F-NT2RP3004215//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//0.22:458:60//AC006084  
F-NT2RP3004242//Caenorhabditis elegans cosmid ZK632, complete sequence.//1.6e-29:409:69//Z22181  
F-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//3.6e-117:242.100//AC005385
- 50 F-NT2RP3004253//H.sapiens 28S rRNA V8 region (LAN5-6).//2.6e-12:589.59//X69353  
F-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//1.2e-88:489.91//AF013967  
F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//3.1e-153:733.98//AF088982  
F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//1.3e-24:597.61//AF007871
- 55 F-NT2RP3004332  
F-NT2RP3004334//L.esculentum gene for fruit ripening polygalacturonase.//0.23:501.57//X80908  
F-NT2RP3004341//Human DNA sequence from clone 503G16 on chromosome 6p23 Contains EST, CpG island, complete sequence.//0.0014:198.66//Z93020

- F-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877
- F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-49:480:75//AC004025
- 5 F-NT2RP3004378//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE.//1.8e-23 :352:67//AC005653
- F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1.//7.2e-140:804:90//X97249
- F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678
- F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206
- 10 F-NT2RP3004451//RPC11-51J15.TK RPC11 Homo sapiens genomic clone R-51J15, genomic survey sequence.//8.8e-19:180:82//AQ052326
- F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917
- F-NT2RP3004466//HS\_3038\_B2\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458
- 15 F-NT2RP3004470//H.sapiens CpG island DNA genomic MseI fragment, clone 81a11, reverse read cpg81a11.rt1a.//7.0e-25:148:96//Z56029
- F-NT2RP3004472//RPC11-42M5.TJ RPC11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//1.6e-20:143:92//AQ052792
- F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925
- 20 F-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.0e-119:679:90//U47024
- F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//7.1e-155:752:97//AB012851
- F-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//4.0e-67:265:84//AC006023
- 25 F-NT2RP3004503//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//1.2e-55:415:78//AC004673
- F-NT2RP3004504//M.musculus mRNA for CPBE protein.//2.0e-110:618:91//Y08260
- F-NT2RP3004507//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.3e-46:433:76//AC005328
- F-NT2RP3004527//Homo sapiens mRNA; transcriptional unit N144, 5' end.//1.1e-100:508:97//AJ002574
- 30 F-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.0e-93:442:84//L11316
- F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//8.5e-145:679:98//AB014532
- F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//2.8e-169:793:98//AB011126
- F-NT2RP3004566//Mus musculus kruppel-related zinc finger protein (Emzf1) mRNA, complete cds.//6.9e-18:433:64//AF031955
- 35 F-NT2RP3004569//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//5.3e-15:138:84//AQ280780
- F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//1.0e-179:860:97//AF026445
- 40 F-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//4.2e-150:711:98//AB007946
- F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//1.1e-158:796:95//AJ006266
- F-NT2RP3004617//Homo sapiens clone DJ1152C17, WORKING DRAFT SEQUENCE, 1 unordered pieces.//9.3e-14:360:65//AC004977
- F-NT2RP3004618//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.9e-52:539:73//AF005355
- 45 F-NT2RP3004669//Bm-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells. Genomic, 2160 nt].//0.046:437:57//S69350
- F-NT2RP3004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.9e-05:625:59//Z98882
- 50 F-NT2RP4000008//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//1.5e-155:844:92//AC006121
- F-NT2RP4000023//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.//0.012:417:59//AB012242
- F-NT2RP4000035//Homo sapiens BAC clone NH0353P23 from 2, complete sequence.//8.0e-18:242:74//AC005035
- 55 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds.//2.1e-81:556:85//AF029761
- F-NT2RP4000051//Mus musculus mRNA for cartilage-associated protein (CASP).//1.6e-19:654:63//AJ006469
- F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.5e-149:720:97//AJ012449
- F-NT2RP4000102//Plasmodium falciparum MAL3P2, complete sequence.//0.28:336:57//AL034558

- F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//4.4e-166:774:99//AB011538  
 F-NT2RP4000111//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.6e-137:678:91//X75931  
 F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//3.3e-114:548:98//AB007952  
 F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.2e-104:677:85//U35776  
 5 F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//7.2e-54:327:74//L20681  
 F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA, partial sequence.//2.2e-62:360:92//AF091088  
 F-NT2RP4000159//RPC11-75N16.TJ RPC11 Homo sapiens genomic clone R-75N16, genomic survey sequence.//2.6e-19:119:98//AQ267551  
 10 F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//3.3e-49:683:67//AC006210  
 F-NT2RP4000185//Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.//1.1e-99:543:93//U92989  
 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.9e-174:825:98//AB014600  
 F-NT2RP4000212//, complete sequence.//4.0e-131:233:94//AC005300  
 15 F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.8e-161:751:99//AC005261  
 F-NT2RP4000218//RPC11-69B7.TJ RPC11 Homo sapiens genomic clone R-69B7, genomic survey sequence.//1.7e-84:413:98//AQ268504  
 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470  
 20 F-NT2RP4000246//Mus musculus neural variant mena+++ protein (Mena) mRNA, complete cds.//2.1e-120:707:87//U72523  
 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//2.8e-128:604:99//AF091092  
 F-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.27:124:69//AQ043515  
 25 F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-32:619:63//Z71408  
 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds.//4.7e-41:685:63//D63481  
 F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//6.9e-05:756:59//U59322  
 F-NT2RP4000323  
 30 F-NT2RP4000355  
 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.0e-140:654:99//AB018281  
 F-NT2RP4000367//Homo sapiens ikappaB kinase complex associated protein (IKAP) mRNA, complete cds.//2.6e-135:649:97//AF044195  
 F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//2.0e-23:524:62//AJ235272  
 35 F-NT2RP4000376//Sequence 1 from patent US 5580968.//1.6e-115:716:87//I30536  
 F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//4.3e-05:450:58//D63850  
 F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-39315 (BC301323), complete sequence.//9.2e-37:336:69//AC006116  
 40 F-NT2RP4000415//Caenorhabditis elegans cosmid C42D8.//0.30:222:60//U56966  
 F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4.//1.8e-48:580:69//AL021086  
 F-NT2RP4000424//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.6e-42:265:81//AC003101  
 45 F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 2370F8, genomic survey sequence.//2.0e-56:287:98//AQ110194  
 F-NT2RP4000449//CIT-HSP-2366N18.TR CIT-HSP Homo sapiens genomic clone 2366N18, genomic survey sequence.//2.4e-42:236:95//AQ076183  
 F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0.17:158:67//AC003982  
 50 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.00034:532:57//Z72499  
 F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds.//0.0094:616:58//U10483  
 F-NT2RP4000481  
 F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150.//5.7e-24:633:60//Z38125  
 55 F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//2.4e-62:667:73//X74904  
 F-NT2RP4000515  
 F-NT2RP4000517//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//1.6e-179:851:98//AC006238

F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//6.7e-33:203.93//AJ010840  
 F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk2/tyr3) gene, alternative 5' coding  
 exon 2C.//0.26:162.61//U23720  
 5 F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds.//1.2e-139:809:89//U32498  
 F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12.//1.0e-06:404:59//AF003386  
 F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 DS02109 (D53)), complete sequence.//1.3e-05:  
 498.58//AC002443  
 F-NT2RP4000556//Sequence 1 from Patent EP 0285405.//1.2e-18:586:61//05465  
 10 F-NT2RP4000560//Murine genomic DNA; partially digested Sau3a fragment, cloned into cosmid vector  
 pEMBLcos2, complete sequence.//2.5e-53:183:82//AF059580  
 F-NT2RP4000588//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 414D7, WORKING  
 DRAFT SEQUENCE.//0.00062:253:65//AL033543  
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//3.2e-138:666:98//  
 AF067730  
 15 F-NT2RP4000638//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.0e-06:78:89//AQ099333  
 F-NT2RP4000648//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associ-  
 ated zinc finger protein, complete cds.//1.9e-11:104:85//AB017335  
 F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.//0.34:350:62//AF100904  
 20 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856.//3.3e-167:785:  
 99//AB004852  
 F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cds.//3.7e-07:261:65//U61149  
 F-NT2RP4000724//Human endogenous retrovirus env mRNA.//9.2e-136:474:89//X82272  
 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds.//3.1e-41:350:71//AB011178  
 25 F-NT2RP4000737//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//1.0:504:58//  
 L19301  
 F-NT2RP4000739//CIT-HSP-2010022.TR CIT-HSP Homo sapiens genomic clone 2010022, genomic survey se-  
 quence.//1.1e-24:161:93//B57903  
 F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence.//0.052:493:58//AC004917  
 30 F-NT2RP4000787//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mR-  
 NA, complete cds.//9.6e-18:259:68//U22818  
 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//1.5e-174:816:98//AB007939  
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.97:52:92//  
 AC005189  
 35 F-NT2RP4000837//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING  
 DRAFT SEQUENCE.//2.1e-128:644:97//AL034420  
 F-NT2RP4000839//RPC11-6D8.TP RPC1-11 Homo sapiens genomic clone RPC1-11-6D8, genomic survey se-  
 quence.//1.5e-44:281:91//B48216  
 F-NT2RP4000855//Rattus norvegicus mRNA for aminopeptidase-B, complete cds.//9.5e-43:722:64//D87515  
 40 F-NT2RP4000865//Human zinc finger protein ZNF136.//6.8e-95:415:78//U09367  
 F-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//7.0e-87:646:80//  
 AJ001616  
 F-NT2RP4000879//N.tabacum mRNA for ubiquitin activating enzyme E1.//9.0e-17:806:58//Y10804  
 45 F-NT2RP4000907//Mouse NLR-1 mRNA for leucine-rich-repeat protein, complete cds.//6.8e-153:934:86//  
 D45913  
 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein.//9.4e-79:584:78//AJ224901  
 F-NT2RP4000918//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//2.0e-  
 08:609:58//AC004290  
 F-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//3.5e-64:415:  
 87//U42975  
 50 F-NT2RP4000927//H.sapiens genomic DNA (chromosome 3; clone NRL062R).//0.75:175:62//X87547  
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//3.5e-163:781:97//  
 AF069532  
 F-NT2RP4000929//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence WORKING  
 DRAFT SEQUENCE, 4 unordered pieces.//0.94:763:56//AC004688  
 55 F-NT2RP4000955//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//  
 1.0e-128:673:96//AC005519  
 F-NT2RP4000973//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.6e-15:255:69//AL032657



- F-NT2RP4000975//CIT-HSP-230716.TF CIT-HSP Homo sapiens genomic clone 230716, genomic survey sequence.//6.5e-31.317:79//AQ015742
- F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end.//0.88:54:90//M22942
- F-NT2RP4000984//Rhodobacter sphaeroides mRNA.//0.76:214:64//M83823
- 5 F-NT2RP4000989//F.rubripes GSS sequence, clone 011A11aE12, genomic survey sequence.//1.0:149:65//AL010911
- F-NT2RP4000996//Penaeus setiferus microsatellite Pse017 repeat region.//3.3e-08:139:74//AF047358
- F-NT2RP4000997//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//3.6e-126:824:84//AF025424
- 10 F-NT2RP4001004
- F-NT2RP4001006//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//1.4e-110:861:78//U83176
- F-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//2.0e-135:789:89//U67140
- 15 F-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.7e-120:718:88//U20086
- F-NT2RP4001041//Schizosaccharomyces pombe mRNA, partial cds, clone: SY 0717.//4.1e-22:452:64//D89170
- F-NT2RP4001057
- F-NT2RP4001064//Mus musculus mRNA for cartilage-associated protein (CASP).//1.2e-20:639:62//AJ006469
- 20 F-NT2RP4001078//Streptomyces coelicolor cosmid 1C2.//0.0025:474:59//AL031124
- F-NT2RP4001079//Rat alternatively spliced mRNA.//1.4e-141:832:88//M93018
- F-NT2RP4001080//H.sapiens PTB-4 gene for polypirimidine tract binding protein.//9.0e-64:628:70//X65372
- F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//4.7e-84:604:86//AB011164
- F-NT2RP4001095
- 25 F-NT2RP4001100//CITBI-E1-2503J7. TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//9.4e-17:185:79//AQ263402
- F-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//1.0e-143:760:87//M96629
- F-NT2RP4001122
- F-NT2RP4001126//Homo sapiens shox gene, alternatively spliced products, complete cds.//4.2e-17:636:61//U82668
- 30 F-NT2RP4001138//Homo sapiens PAC clone DJ1121E10 from 7q21.1-q2, complete sequence.//2.5e-23:408:60//AC004969
- F-NT2RP4001143//Sequence 5 from patent US 5753432.//1.8e-39:276:86//AR008079
- F-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.7e-116:684:89//AC005095
- 35 F-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//3.0e-48:581:66//D67067
- F-NT2RP4001150//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.4e-25:193:67//AC004952
- 40 F-NT2RP4001159//Human FMR1 gene, 5' end.//0.28:130:66//L19476
- F-NT2RP4001174//FMR1 (CGG repeats) [human, Fragile X syndrome patient, Genomic, 429 nt].//0.0014:187:67//S74494
- F-NT2RP4001206//Dictyostellium discoideum random slug cDNA19 protein (rscd9) mRNA, partial cds.//0.032:453:58//U82511
- 45 F-NT2RP4001207//HS\_2248\_A1\_C03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=5 Row=E, genomic survey sequence.//0.00018:58:94//AQ192358
- F-NT2RP4001210//Homo sapiens chromosome 10 clone CIT987SK-1019O18 map 10p11.2-10p12.1, complete sequence.//0.93:515:58//AC005877
- 50 F-NT2RP4001213//Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant, complete cds.//3.6e-44:187:74//U37251
- F-NT2RP4001219//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.3e-15:288:67//AL032657
- F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.2e-26:855:60//AF059569
- F-NT2RP4001235//RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI11-18E11, genomic survey sequence.//2.7e-15:101:98//B88081
- 55 F-NT2RP4001256//Amycolatopsis mediterranei 3-amino-5-hydroxy benzoic acid synthase (rifD) gene, complete cds.//1.0:459:59//U33061
- F-NT2RP4001260//Sequence 2 from Patent WO9601901.//0.0018:246:63//A48324

F-NT2RP4001274//Homo sapiens, complete sequence.//2.5e-05:201.67//AC005854  
 F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15, genomic survey sequence.//3.5e-18:138.92//AQ043228  
 5 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.4e-30:535.65//AF043250  
 F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//3.5e-145:795.91//AJ001119  
 F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109.94//B89870  
 10 F-NT2RP4001339//HS\_3205\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=15 Row=J, genomic survey sequence.//7.1e-24:305.73//AQ183725  
 F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete sequence.//1.9e-17:106.91//AC004918  
 F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase.//7.6e-40:631.66//X91011  
 15 F-NT2RP4001351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING DRAFT SEQUENCE.//2.7e-30:608.64//AL031428  
 F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7.//0.23:540.57//AL031107  
 F-NT2RP4001372//RPC111 Homo sapiens genomic clone R-49L11, genomic survey sequence.//8.5e-23:129.100//AQ051701  
 F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1.//0.15:213.61//X78609  
 20 F-NT2RP4001375  
 F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311\_F\_12, complete sequence.//7.3e-28:153.88//AC005722  
 F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.2e-47:518.73//AC004691  
 25 F-NT2RP4001407//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.00079:686.57//UJ3998  
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds.//2.0e-76:818.71//D86957  
 F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein.//3.5e-87:839.73//X78933  
 F-NT2RP4001442  
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds.//0.21:218.63//AB018326  
 30 F-NT2RP4001474//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109.90//U49884  
 F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds.//2.5e-59:480.75//D10523  
 F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//9.7e-39:392.72//AF049612  
 F-NT2RP4001502//H.sapiens (D8S135) DNA segment containing GT repeat.//2.7e-24:147.96//X61693  
 35 F-NT2RP4001507//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.93:394.58//AC005308  
 F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.1e-143:820.89//U20086  
 40 F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNR048w.//2.2e-05:319.61//Z71663  
 F-NT2RP4001551//S.pombe chromosome II p1 p8B7.//0.64:335.60//AL032684  
 F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPC111-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.0:309.58//AC004806  
 45 F-NT2RP4001567//HS\_2166\_B1\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=13 Row=F, genomic survey sequence.//0.99:188.59//AQ086290  
 F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds.//7.0e-53:566.72//D79989  
 F-NT2RP4001571//RPC111-21F20.TP RPC111 Homo sapiens genomic clone RPC11-21F20, genomic survey sequence.//2.8e-19:119.97//B85885  
 50 F-NT2RP4001574//B.primitivus mRNA for coat protein gamma-cop.//5.8e-129:813.85//X92987  
 F-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//3.4e-131:795.86//AJ223830  
 F-NT2RP4001592//S.aureus gene for isoleucyl-tRNA synthetase.//1.3e-14:663.59//X74219  
 F-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//6.4e-10:135.73//AC002364  
 55 F-NT2RP4001614//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.4e-06:78.89//AQ099333  
 F-NT2RP4001634  
 F-NT2RP4001638//cSRL-161F1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic

- clone cSRL-161FI, genomic survey sequence.//4.9e-12:144:76/B02870  
 F-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//3.8e-69:437:86//Y11092  
 F-NT2RP4001656//HS\_2013\_A1\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2013 Col=1 Row=G, genomic survey sequence.//2.0e-30:207:89//AQ224793  
 5 F-NT2RP4001677//Hylobates lar huntingtin gene, partial exon.//0.23:105:71//L49362  
 F-NT2RP4001679//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462023, WORKING  
 DRAFT SEQUENCE.//2.7e-45:351:84//AL031431  
 F-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.8e-30:163:88//  
 U96629  
 10 F-NT2RP4001725//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.1e-  
 13:402:63//AC004296  
 F-NT2RP4001730//RPC11-37M21.TK RPC1-11 Homo sapiens genomic clone RPC1-11-37M21, genomic survey  
 sequence.//0.88:177:67//AQ029840  
 F-NT2RP4001739  
 15 F-NT2RP4001753//H.sapiens telomeric DNA sequence, clone 12QTEL023, read 12QTELOO023.seq.//4.9e-36:  
 192:98//Z96232  
 F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//2.3e-140:866:86//L11316  
 F-NT2RP4001790//Homo sapiens clone NH0569124, complete sequence.//1.4e-29:327:74//AC005678  
 F-NT2RP4001803  
 20 F-NT2RP4001822//Homo sapiens tetraspan TM4SF (TSPAN-4) mRNA, complete cds.//1.0e-16:576:60//  
 AF054841  
 F-NT2RP4001823//Human DNA sequence from clone 181C9 on chromosome 22q13.2-13.33. Contains a PHAPI2  
 Leucine Rich Acidic Nuclear Protein pseudogene, part of a putative novel gene, ESTs, STSs and GSSs, complete  
 sequence.//2.1e-08:801:59//Z98743  
 25 F-NT2RP4001828  
 F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds.//2.2e-53:555:73//D31888  
 F-NT2RP4001841  
 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds.//1.7e-55:813:65//AB014572  
 F-NT2RP4001861//Human simple repeat polymorphism.//0.0014:145:66//M87691  
 30 F-NT2RP4001889//HS\_2052\_B1\_H06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2052 Col=11 Row=P, genomic survey sequence.//1.0e-23:187:86//AQ270425  
 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//7.3e-76:178:95//  
 AC005014  
 F-NT2RP4001896//T3B4TFC TAMU Arabidopsis thaliana genomic clone T3B4, genomic survey sequence.//0.99:  
 354:61//B26193  
 35 F-NT2RP4001901//Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.//  
 0.031:409:60//AB011413  
 F-NT2RP4001927//HS\_2216\_B1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2216 Col=5 Row=H, genomic survey sequence.//4.9e-32:216:89//AQ184677  
 40 F-NT2RP4001938//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.2e-83:709:79//U49046  
 F-NT2RP4001946//HS\_3021\_B2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3021 Col=20 Row=P, genomic survey sequence.//7.6e-09:120:76//AQ133185  
 F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alterna-  
 tively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin,  
 subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs,  
 45 complete sequence.//2.1e-18:421:65//AL022577  
 F-NT2RP4001953//CIT-HSP-2294D14.TR CIT-HSP Homo sapiens genomic clone 2294D14, genomic survey se-  
 quence.//0.030:358:61//AQ005028  
 F-NT2RP4001966//Mus musculus DOC4 (Doc4) mRNA, complete cds.//2.5e-68:812:68//AF059485  
 50 F-NT2RP4001975//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//1.9e-57:555:75//  
 AC003976  
 F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic  
 clone cSRL-143G4, genomic survey sequence.//8.9e-21:123:98//B01950 F-NT2RP4002047//Saccharomyces  
 cerevisiae chromosome XII cosmid 8003.//1.6e-29:520:64//U17243  
 55 F-NT2RP4002052//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey se-  
 quence.//2.8e-22:137:96//B80243  
 F-NT2RP4002058//T20L11-T7 TAMU Arabidopsis thaliana genomic clone T20L11, genomic survey sequence.//  
 0.019:141:65//AQ248640

- F-NT2RP4002071//CIT-HSP-2314J9.TF CIT-HSP Homo sapiens genomic clone 2314J9, genomic survey sequence.//0.99:163.63//AQ027223
- F-NT2RP4002075//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.15:506:59//Z92841
- 5 F-NT2RP4002078//RPC11-73M20.TJ RPC11 Homo sapiens genomic clone R-73M20, genomic survey sequence.//4.8e-21:130:96//AQ269030
- F-NT2RP4002081//F.rubripes GSS sequence, clone 190Q22bB9, genomic survey sequence.//0.0024:350:60//Z92062
- F-NT2RP4002083//M.musculus tex27 mRNA.//8.2e-77:456:89//X80437
- 10 F-NT2RP4002408//Caenorhabditis elegans serine/threonine kinase LET-502 (let-502) mRNA, complete cds.//3.7e-18:541:62//U85515
- F-NT2RP4002791
- F-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//4.7e-39:385:75//AC002383
- 15 F-NT2RP4002905//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//6.5e-91:672:83//AC004662
- F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds.//2.9e-37:193:99//M33197
- F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs.//7.9e-51:300:80//Z82901
- 20 F-NT2RP5003477//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.7e-77:150:100//AC000380
- F-NT2RP5003492
- F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSs and CpG island.//1.7e-111:623:93//Z81365
- 25 F-NT2RP5003506//H.sapiens CpG island DNA genomic Mse1 fragment, clone 71h2, reverse read cpq71h2.r1a.//1.4e-49:283:93//Z62703
- F-NT2RP5003512//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312
- F-NT2RP5003522//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.8e-101:211:96//AC005236
- 30 F-NT2RP5003524//Homo sapiens beta-spectrin (HSPTB1) gene, exon 14 and partial cds.//0.00056:650:57//AF013178
- F-NT2RP5003534//H.sapiens CpG island DNA genomic Mse1 fragment, clone 14c10, forward read cpq14c10.ft1b.//0.00013:70:91//Z54631
- 35 F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.2e-67:373:94//AB007934
- F-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//5.8e-93:518:81//AC005510
- F-OVARC1000006//Gallus gallus histone H2A (H2A-VIII) gene, complete cds.//9.1e-56:392:84//U38933
- F-OVARC1000013
- 40 F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//5.6e-170:815:98//AF058922
- F-OVARC1000017//Streptomyces glaucescens tcm operon.//0.37:347:60//M80674
- F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds.//6.8e-36:238:89//AF064603
- F-OVARC1000058
- F-OVARC1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cds.//2.5e-36:192:98//U85625
- 45 F-OVARC1000068//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING DRAFT SEQUENCE.//0.14:554:57//AL023883
- F-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 596C15, WORKING DRAFT SEQUENCE.//5.3e-104:197:100//AL031387
- F-OVARC1000085//Human DNA sequence from clone 191N21 on chromosome 6q27 Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA factor (TFIID), proteasome subunit HC5, EST, STS, GSS, complete sequence.//1.6e-116:588:96//AL031259
- 50 F-OVARC1000087//HS\_2004\_B2\_E11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence.//7.1e-11:94:94//AQ221037
- F-OVARC1000091//hnbxb0020P17r CUGI Rice BAC Library Oryza sativa genomic clone hnbxb0020P17r, genomic survey sequence.//5.2e-05:238:64//AQ258489
- 55 F-OVARC1000092//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.1e-10:720:58//AC004617
- F-OVARC1000106//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

omic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//9.9e-05:141:73//AQ175369

F-OVARC1000109

F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.6e-133:663:96//AF069250

5 F-OVARC1000114//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//2.3e-51:547:70//AL022574

F-OVARC1000133//Homo sapiens clone GS512121, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.62:349:61//AC005027

F-OVARC1000139//Caenorhabditis elegans cosmid F09D1.//2.5e-18:314:64//AF040640

10 F-OVARC1000145//HS\_2257\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=22 Row=H, genomic survey sequence.//5.8e-30:203:90//AQ304854

F-OVARC1000148//CIT-HSP-2345A22.TR CIT-HSP Homo sapiens genomic clone 2345A22, genomic survey sequence.//1.1e-26:146:100//AQ056703

F-OVARC1000151//Sequence 1 from patent US 5665588.//2.6e-61:677:70//I64695

15 F-OVARC1000168//Homo sapiens chromosome 19, cosmid R31343, complete sequence.//4.9e-19:381:63//AC005764

F-OVARC1000191//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//1.3e-06:745:57//AL034557

F-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//6.4e-161:781:97//AC004604

20 F-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//9.2e-33:511:65//AF068332

F-OVARC1000212//F.nubripes GSS sequence, clone 185L11aC1, genomic survey sequence.//1.1e-13:139:79//AL019910

25 F-OVARC1000240//Sequence 1 from patent US 5710024.//1.4e-129:623:98//812226

F-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-112:697:87//AF060194

F-OVARC1000288 2.2e-22:181:83//J00345

F-OVARC1000302//A-192A9.TIP CIT978SK Homo sapiens genomic clone A-192A9, genomic survey sequence.//4.8e-18:110:99//B18003

30 F-OVARC1000304//Mouse mRNA from Mov10 locus.//5.5e-100:631:85//X52574

F-OVARC1000309

F-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.1e-122:325:95//AC005236

35 F-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.0e-46:339:84//U19614

F-OVARC1000335//Caenorhabditis elegans cosmid F15B10.//0.020:545:57//AF036696

F-OVARC1000347//Homo sapiens clone GS051M12, complete sequence.//0.71:252:59//AC005007

F-OVARC1000384//Homo sapiens expanded SCAT CAG repeat.//2.2e-09:276:64//AF020275

40 F-OVARC1000408//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KVLQT1 gene, complete sequence.//0.61:343:59//AC003693

F-OVARC1000411//S. cerevisiae chromosome XI reading frame ORF YKL202w.//0.075:242:60//Z28201

F-OVARC1000414//Homo sapiens PAC clone DJ0905M06 from 7q31, complete sequence.//0.00088:285:62//AC005166

45 F-OVARC1000420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 371H6, WORKING DRAFT SEQUENCE.//0.14:487:60//AL031718

F-OVARC1000427//Homo sapiens clone UWGC:rg041a03 from 7p14-15, complete sequence.//4.9e-30:195:84//AC005826

F-OVARC1000431//Plasmodium falciparum MAL3P2, complete sequence.//1.3e-05:651:59//AL034558

50 F-OVARC1000437//Chicken tensin mRNA, complete cds.//9.6e-54:296:78//M74165

F-OVARC1000440//Human PINCH protein mRNA, complete cds.//2.7e-19:116:99//U09284

F-OVARC1000442//Human DNA sequence from clone 816K17 on chromosome 20p12.2-13 Contains TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANS-GLUTAMINASE 3), and another member of the Transglutaminase family, complete sequence.//1.0e-21:202:79//AL031678

55 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.0e-138:566:99//AB014583

F-OVARC1000461

F-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//4.7e-

124:850:93//AF023451  
 F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//1.0e-15:510:59//AC004221  
 F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomic survey sequence.//2.5e-06:272:62//AJ227191  
 F-OVARC1000479//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.1e-117:652:90//E12829  
 F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//1.7e-13:709:60//Z99297  
 F-OVARC1000496//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//6.0e-23:316:72//AL031733  
 F-OVARC1000520//Homo sapiens supravillin mRNA, complete cds.//2.1e-113:539:99//AF051850  
 F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.0e-149:716:98//AC005024  
 F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//5.8e-137:545:97//AC004510  
 F-OVARC1000543//HS\_3055\_A2\_F10\_MF CIT Approved Human Genomic\_Sperm Library D Homo sapiens genomic clone Plate=3055 Col=20 Row=K, genomic survey sequence.//0.19:104:71//AQ102820  
 F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//4.4e-136:670:97//AL022069  
 F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence.//1.3e-15:262:69//AC002965  
 F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence.//1.9e-41:476:70//AF046733  
 F-OVARC1000573//HS\_3241\_B1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=5 Row=P, genomic survey sequence.//2.2e-101:530:95//AQ211942  
 F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.7e-97:445:90//AC002414  
 F-OVARC1000578//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//9.1e-27:354:72//AC003973  
 F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//0.97:276:62//AL023775  
 F-OVARC1000605  
 F-OVARC1000622//Homo sapiens (subclone 2\_d8 from P1 H42) DNA sequence, complete sequence.//7.2e-60:457:82//L81648  
 F-OVARC1000640//Human BAC clone RG326K09 from 7q21, complete sequence.//6.2e-58:499:80//AC002069  
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//5.1e-77:424:93//D43772  
 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//4.8e-99:536:94//AB011162  
 F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-29c7, genomic survey sequence.//2.5e-57:336:91//B04244  
 F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.6e-81:291:84//AJ001713  
 F-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//8.2e-158:782:96//AL034424  
 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.5e-151:549:99//AF027156  
 F-OVARC1000689//nbxb0003aG01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003M01f, genomic survey sequence.//0.17:499:60//AQ050003  
 F-OVARC1000700  
 F-OVARC1000703//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//3.5e-26:425:65//U34925  
 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//3.7e-109:451:91//AF038661  
 F-OVARC1000730  
 F-OVARC1000746  
 F-OVARC1000769//HS\_2056\_B2\_G06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=12 Row=N, genomic survey sequence.//8.8e-19:147:86//AQ245905

- F-ovarC1000771//M.musculus mRNA for GTP-binding protein.//2.2e-62:305:78//X95403  
 F-ovarC1000781//Sequence 5 from Patent WO9722695.//1.9e-89:705:78//A63552  
 F-ovarC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.0e-131:631:98//AC004542
- 5 F-ovarC1000800//Human Chromosome 11q23 PAC clone pDJ254e13, complete sequence.//1.7e-32:295:80//AC003691  
 F-ovarC1000802//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//3.2e-55:356:88//AC004469  
 F-ovarC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//9.5e-27:163:94//Y17711
- 10 F-ovarC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds.//6.0e-150:432:100//AB014543  
 F-ovarC1000850//Homo sapiens PB39 mRNA, complete cds.//1.0e-135:632:99//AF045584  
 F-ovarC1000862//M.musculus mRNA for FT1.//2.6e-109:769:83//Z67963  
 F-ovarC1000876//S.cerevisiae chromosome IX cosmid 9150.//7.4e-21:541:61//Z38125
- 15 F-ovarC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.2e-08:98:88//U20086  
 F-ovarC1000885//B.subtilis 25 kb genomic DNA segment (from sspE to katA).//0.25:231:61//Z82044  
 F-ovarC1000886//CIT-HSP-2171H6.TR CIT-HSP Homo sapiens genomic clone 2171H6, genomic survey sequence.//0.00035:139:69//B89721  
 F-ovarC1000890  
 F-ovarC1000891
- 20 F-ovarC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12.1-12.3. Contains part of a Homeobox domain containing gene and GSSs, complete sequence.//1.4e-18:473:64//AL024494  
 F-ovarC1000912//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.9e-08:378:63//L14320  
 F-ovarC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds.//7.7e-85:440:95//AB011172
- 25 F-ovarC1000924//HS\_2022\_A1\_C01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2022 Col=1 Row=E, genomic survey sequence.//5.7e-21:122:99//AQ269493  
 F-ovarC1000936//Human PAC clone DJ0093103 from Xq23, complete sequence.//1.2e-113:476:91//AC003983  
 F-ovarC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//0.00066:436:61//AL031848
- 30 F-ovarC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//5.0e-89:556:86//AB005549  
 F-ovarC1000948//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:160:64//X95276  
 F-ovarC1000959//CIT-HSP-2348O16.TR CIT-HSP Homo sapiens genomic clone 2348O16, genomic survey sequence.//0.99:270:59//AQ062850
- 35 F-ovarC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.9e-41:577:72//AL009181  
 F-ovarC1000964//P.falciparum malaria antigen (M26-32-2) gene, partial cds.//0.19:83:73//M63270  
 F-ovarC1000971//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.013:670:57//Z92841
- 40 F-ovarC1000984//Leishmania major chromosome 1, complete sequence.//0.80:345:58//AE001274  
 F-ovarC1000996//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.6e-55:403:82//S51858  
 F-ovarC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene, complete cds.//0.33:105:69//AF042785
- 45 F-ovarC1001000//HS\_2247\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=O, genomic survey sequence.//3.1e-60:315:96//AQ153910  
 F-ovarC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//3.1e-124:595:98//AC004190  
 F-ovarC1001010//CIT-HSP-2034M3.TF CIT-HSP Homo sapiens genomic clone 2034M3, genomic survey sequence.//1.0:151:60//B74290
- 50 F-ovarC1001011//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//3.0e-08:149:79//Z78021  
 F-ovarC1001032//Yeast (S.cerevisiae) mitochondrial Tyr-tRNA gene.//3.2e-13:667:60//M12451  
 F-ovarC1001034//Mus musculus Fn54 mRNA, partial cds.//2.5e-119:737:86//AF001533  
 F-ovarC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//2.7e-150:733:97//AF099149
- 55 F-ovarC1001040//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.8e-29:277:76//AC005081  
 F-ovarC1001044//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 36411, WORKING DRAFT SEQUENCE.//0.0017:387:6:1//AL031319

F-OVARC1001051//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.//0.012:112.74//AF053768

F-OVARC1001055//Sequence 1 from patent US 5580754.//3.3e-45:381.81//I30292

5 F-OVARC1001062//hnbx0026H08r CUGI Rice BAC Library Oryza sativa genomic clone hnbx0026H08r, genomic survey sequence.//0.018:344.59//AQ271878

F-OVARC1001065//S. pombe chromosome I cosmid c29E6.//0.86:338.59//Z66525

F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.0e-130:620.98//AF082657

10 F-OVARC1001072//Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions.//9.3e-24:285.65//AF003529

F-OVARC1001074//Human DNA sequence from clone Z3K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//2.0e-07:652.59//AL022153

F-OVARC1001085//Homo sapiens c-syn protooncogene mRNA, complete cds.//5.0e-35:187.99//M14333

15 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.0e-74:289.95//AJ005897

F-OVARC1001107//Homo sapiens SKB1He mRNA, complete cds.//3.6e-72:351.86//AF015913

F-OVARC1001113//Homo sapiens diaphanous 1 (HDI1) mRNA, complete cds.//6.4e-150:710.98//AF051782

F-OVARC1001117//Homo sapiens chromosome 5, P1 clone 328E3 (LBNL H53), complete sequence.//0.99:148.67//AC005178

20 F-OVARC1001118//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.6e-35:302.74//AC000382

F-OVARC1001129//CIT-HSP-647P20.TP CIT-HSP Homo sapiens genomic clone 647P20, genomic survey sequence.//0.94:106.66//B79052

F-OVARC1001154//R. norvegicus mRNA for epithelin 1 and 2.//1.8e-95:462.79//G62322

25 F-OVARC1001161//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.9e-90:496.84//AC004069

F-OVARC1001162

F-OVARC1001167//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00090:219.64//AC004961

30 F-OVARC1001169//Borrelia burgdorferi (section 27 of 70) of the complete genome.//1.0:265.59//AE001141

F-OVARC1001170//H. sapiens (xs170) mRNA, 350bp.//4.6e-58:355.90//Z36823

F-OVARC1001171//CIT-HSP-2285E22.TF CIT-HSP Homo sapiens genomic clone 2285E22, genomic survey sequence.//1.5e-25:152.83//AQ002315

35 F-OVARC1001173//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//0.0024:94.80//AL022323

F-OVARC1001176//Streptomyces plicatus B-N-acetylhexosaminidase (hex) gene, complete cds.//1.0:356.60//AF063001

F-OVARC1001180//G. gallus DNA for polyubiquitin gene Ub II.//0.0062:275.60//X58195

40 F-OVARC1001188//Homo sapiens full-length insert cDNA clone ZD93F03.//1.8e-32:180.97//AF086486

F-OVARC1001200

F-OVARC1001232//Caenorhabditis elegans cosmid F10B5, complete sequence.//0.013:128.67//Z48334

F-OVARC1001240//Human Chromosome 11 pac pDJ360p17, WORKING DRAFT SEQUENCE, 44 unordered pieces.//3.7e-131:811.87//AC001235

45 F-OVARC1001243//Human BAC clone GS117O10 from 7q21-q22, complete sequence.//0.044:457.59//AC003078

F-OVARC1001244//Human homolog of Drosophila female sterile homeotic mRNA, complete cds.//8.4e-118:95//M80613

F-OVARC1001261//Mus musculus putative membrane-associated guanylate kinase 1 (Magi-1) mRNA, alternatively spliced c form, partial cds.//1.4e-95 :649:84//AF027505

50 F-OVARC1001268//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//0.00051:72.83//U35776

F-OVARC1001270

F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds.//2.1e-142:644.96//AB014543

F-OVARC1001282//RPC111-60K8.TK RPC111 Homo sapiens genomic clone R-60K8, genomic survey sequence.//0.0089:285.58//AQ195857

55 F-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//3.0e-20:263.73//U97018

F-OVARC1001306//hnbx0002M13r CUGI Rice BAC Library Oryza sativa genomic clone hnbx0002M13r, genomic survey sequence.//0.98:170.66//AQ156061



- F-ovarC1001329//Homo sapiens BAC clone RG370M10 from 7p15, complete sequence.//1.3e-05:432:61//AC003986
- F-ovarC1001330//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.027:444:59//AC005504
- 5 F-ovarC1001339//Homo sapiens chromosome 17, clone hCIT.124\_H\_2, complete sequence.//0.76:89:74//AC006071
- F-ovarC1001341//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//0.99:45:86//AQ263402
- F-ovarC1001342
- 10 F-ovarC1001344//HS-1059-A2-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=4 Row=O, genomic survey sequence.//1.5e-07:254:67//B44456
- F-ovarC1001357//Homo sapiens Xp22-149 BAC RPC11-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.83:376:61//AC005297
- F-ovarC1001360
- 15 F-ovarC1001369//Homo sapiens clone 162B15, complete sequence.//0.0066:99:76//AC004811
- F-ovarC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.7e-142:683:98//AF034801
- F-ovarC1001376//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//1.9e-52:382:73//AL031680
- F-ovarC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//1.2e-147:683:99//AJ224819
- 20 F-ovarC1001391//S.coelicolor whiB gene.//0.018:454:59//X62287
- F-ovarC1001399//CIT-HSP-229118.TR CIT-HSP Homo sapiens genomic clone 229118, genomic survey sequence.//1.7e-11:104:87//AQ007611
- F-ovarC1001417//Homo sapiens EXLM1 mRNA, complete cds.//3.9e-149:707:98//AB006651
- 25 F-ovarC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.9e-48:586:69//U52426
- F-ovarC1001425//Human DNA sequence from clone 1048E9 on chromosome 22q11.2-12.2 Contains pseudo-gene similar to ribosomal protein S3A and part of a gene similar to C.elegans protein CE02118, ESTs, STS, GSS, complete sequence.//0.0019:96:78//Z97114
- F-ovarC1001436//Caenorhabditis elegans mitotic chromosome and X-chromosome associated MIX-1 protein (mix-1) mRNA, complete cds.//0.77:519:59//U96387
- 30 F-ovarC1001442//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//1.0:167:64//AL031687
- F-ovarC1001453//Human DNA sequence from PAC 453D15 on chromosome 6 contains STS.//4.4e-64:376:79//Z84482
- 35 F-ovarC1001476//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y24F12, WORKING DRAFT SEQUENCE.//0.20:107:71//AL022277
- F-ovarC1001480
- F-ovarC1001489//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.20:281:63//AC005140
- 40 F-ovarC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//8.1e-85:479:92//AF016507
- F-ovarC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence, complete sequence.//1.2e-98:503:83//AC002039
- F-ovarC1001525//Human beta-hexosaminidase alpha chain (HEXA) gene, exon 1.//1.7e-13:87:100//M16411
- 45 F-ovarC1001542//H.sapiens polymorphic repeat associated with glutamate dehydrogenase pseudogene 5.//0.43:190:68//X69219
- F-ovarC1001547//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.017:533:56//AC005140
- F-ovarC1001555//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.4e-159:416:99//AC005037
- 50 F-ovarC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//2.4e-115:540:99//AF031165
- F-ovarC1001600//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//5.5e-13:529:62//AF043945
- F-ovarC1001610//, complete sequence.//1.4e-12:152:77//AC005409
- 55 F-ovarC1001611
- F-ovarC1001615//Human DNA sequence from clone 873P14 on chromosome 20p12 Contains STS, GSS, complete sequence.//0.022:146:70//AL031682
- F-ovarC1001668//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.5e-109:358:96//AB005543

F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds.//1.8e-47:393.81//AB006867  
 F-OVARC1001703//CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 2164L6, genomic survey sequence.//0.94:85.69//B92840  
 F-OVARC1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317C6, WORKING DRAFT SEQUENCE.//1.9e-06:489:61//Z97651  
 5 F-OVARC1001713//Rattus norvegicus neuroligin 2 mRNA, complete cds.//1.0:262.59//U41662  
 F-OVARC1001726//Human telomere associated repeat sequence, complete sequence.//7.5e-08:283.65//M57752  
 F-OVARC1001731//Mus musculus gene for beta-tropomyosin.//2.6e-83:606.81//X12650  
 10 F-OVARC1001745//HS\_3007\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=18 Row=N, genomic survey sequence.//0.00020:269:60//AQ164522  
 F-OVARC1001762//S.pombe chromosome III cosmid c338.//3.0e-17:624:61//AL023781  
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//4.2e-149:708.98//U97670  
 15 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//3.0e-115:580.96//AB014575  
 F-OVARC1001768  
 F-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//5.7e-64:477:78//AC005066  
 F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4q25, complete sequence.//6.5e-11:171:76//AC004704  
 20 F-OVARC1001802//CITBI-E1-2502A17.TR CITBI-E1 Homo sapiens genomic clone 2502A17, genomic survey sequence.//0.98:214.61//AQ264481  
 F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//9.5e-151:712.99//AL023694  
 25 F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.7e-56:522:75//AF068748  
 F-OVARC1001812//Homo sapiens chromosome 17, clone HCIT104N19, complete sequence.//1.7e-63:526.81//AC003662  
 F-OVARC1001813//Human DNA sequence from cosmid U144A10, between markers DXS366 and DXS87 on chromosome X contains STS.//0.17:214.65//Z70224  
 30 F-OVARC1001820//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 445N2, WORKING DRAFT SEQUENCE.//3.2e-55:379:82//AL031779  
 F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//2.8e-17:509:62//AC005609  
 35 F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DXS366 and DXS87 on chromosome X.//0.35:403.58//Z73361  
 F-OVARC1001861//CIT-HSP-2165M3.TR CIT-HSP Homo sapiens genomic clone 2165M3, genomic survey sequence.//2.4e-25:148:96//B94622  
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.2e-18:122.95//AF070611  
 40 F-OVARC1001879//HS\_3026\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=17 Row=L, genomic survey sequence.//4.9e-29:204:87//AQ207748  
 F-OVARC1001880//Human interferon regulatory factor 5 (Hmif5) mRNA, complete cds.//3.5e-05:489:60//U51127  
 F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-29:350:74//AC005020  
 45 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//8.6e-56:300:96//AF061749  
 F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.3e-10:253:66//AL031904  
 50 F-OVARC1001911//HS\_2196\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=22 Row=P, genomic survey sequence.//3.4e-09:123:78//AQ294069  
 F-OVARC1001916//HS\_3054\_B1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=F, genomic survey sequence.//1.2e-31:126:97//AQ099979  
 F-OVARC1001928  
 55 F-OVARC1001942//H.sapiens CpG Island DNA genomic MseI fragment, clone 21d7, forward read cpq21d7.ft1a.//7.2e-12:83.98//Z60390  
 F-OVARC1001943//Aplysia californica potassium channel modulatory factor mRNA, complete cds.//3.5e-50:535:69//AF059179

- F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds.//1.7e-16:294.67//U37263
- F-OVARC1001950//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.5e-20:261.68//AJ011929
- 5 F-OVARC1001987//D.melanogaster G6PD gene, exons 2-4.//0.99:447:57//Z19021
- F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//2.9e-19:178:83//AC005995
- F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence.//0.17:232:62//AL034559
- F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//2.1e-158:739:98//AB007934
- 10 F-OVARC1002068//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//3.0e-17:781:59//AP000011
- F-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.4e-136:683:96//AC006015
- F-OVARC1002107//Homo sapiens BAC clone RG276003 from 7q22-q31.1, complete sequence.//1.0:220:61//AC004668
- 15 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//6.1e-115:557:98//AF041483
- F-OVARC1002127//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//0.013:461:57//AC006241
- F-OVARC1002138//Caenorhabditis elegans cosmid F32D1.//1.0e-29:545:64//AF016427
- 20 F-OVARC1002143//CIT-HSP-2343H20.TR CIT-HSP Homo sapiens genomic clone 2343H20, genomic survey sequence.//2.3e-11:258:67//AQ055576
- F-OVARC1002156
- F-OVARC1002158//F17O7-T7 IGF Arabidopsis thaliana genomic clone F17O7, genomic survey sequence.//1.8e-16:383:66//B11616
- 25 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosinephosphatase.//0.0041:300:64//X79568
- F-OVARC1002182//F.rubripes GSS sequence, clone 123123aA7, genomic survey sequence.//1.4e-10:240:66//AL017241
- F-PLACE1000004//CIT-HSP-2294H13.TF CIT-HSP Homo sapiens genomic clone 2294H13, genomic survey sequence.//8.2e-10:158:75//AQ003859
- 30 F-PLACE1000005//Mouse alpha-1 antitrypsin gene, segment 1.//4.8e-15:89:93//M12585
- F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//3.8e-51:550:72//AF022789
- F-PLACE1000014
- F-PLACE1000031//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.91:333:61//AC004821
- 35 F-PLACE1000040//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//2.6e-20:279:67//Z93023
- F-PLACE1000048//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.6e-63:488:82//AC005177
- 40 F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508
- F-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//1.9e-30:190:94//L22154
- F-PLACE1000066//Homo sapiens PAC clone DJ1106E03 from 7q31.3-q3, complete sequence.//6.0e-63:597:74//AC005521
- 45 F-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.2e-09:143:73//AC005848
- F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete sequence.//0.52:390:60//AC002389
- F-PLACE1000094
- 50 F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//4.4e-129:731:92//AL023580
- F-PLACE1000142//H.sapiens AUH mRNA.//6.4e-09:328:62//X79888
- F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//7.7e-150:737:97//AF058291
- 55 F-PLACE1000185//Sequence 15 from patent US 5691147.//5.7e-106:558:94//I76211 F-PLACE1000213
- F-PLACE1000214//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-06:644:57//AC005504
- F-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695O20, WORKING DRAFT SEQUENCE.//2.6e-39:191:83//AL032818

F-PLACE1000246//HS\_2008\_A2\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=8 Row=G, genomic survey sequence.//0.96:153:61//AQ269813

F-PLACE1000292//Drosophila melanogaster Oregon-R mitochondrial A+T region.//5.1e-12:571:60//U11584

F-PLACE1000308//F.teissieri mitochondrial DNA for tRNA-met, tRNA-Ile, tRNA-Gln & amp; tRNA-Val.//0.00013:369:59//X54011

F-PLACE1000332//HS\_2016\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=H, genomic survey sequence.//7.5e-83:424:96//AQ232106

F-PLACE1000347//CIT-HSP-2326A16.TV CIT-HSP Homo sapiens genomic clone 2326A16, genomic survey sequence.//0.13:46:100//AQ047350

F-PLACE1000374//Mus musculus putative CCAAT binding factor 1 (mCBF) mRNA, alternatively spliced transcript mCBF1, complete cds.//0.00048:84:83//U19891

F-PLACE1000380//F.rupestris GSS sequence, clone 047P21aA10, genomic survey sequence.//0.43:198:62//Z88163

F-PLACE1000383//Homo sapiens myotubularin related protein 1 (MTMR1) mRNA, partial cds.//8.7e-149:740:96//U58032

F-PLACE1000401//Pinctada fucata mRNA for insoluble protein, complete cds.//0.22:484:56//D86074

F-PLACE1000406//Human nuclear matrix protein 55 (nmt55) mRNA, complete cds.//3.3e-19:372:65//U89867

F-PLACE1000420//Homo sapiens chromosome 17, clone hRPK.227\_G\_15, complete sequence.//1.6e-85:421:87//AC005899

F-PLACE1000421//Human GT334 protein (GT334) gene, exons 16 and 17.//0.88:145:68//U61515

F-PLACE1000424//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.076:196:66//AC005189

F-PLACE1000435//HS\_3217\_A2\_A12\_MR CIT Approved Human Genomic-Sperm Library D Homo sapiens genomic clone Plate=3217 Col=24 Row=A, genomic survey sequence.//2.2e-47:438:76//AQ181698

F-PLACE1000444//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-61:616:71//AC004382

F-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//5.8e-18:314:69//AF059580

F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Cosmid Clone 94a In DGCR Region, complete sequence.//1.1e-33:349:76//AC002491

F-PLACE1000492//Rat vacuolar protein sorting homolog v-rps33b mRNA, complete cds.//1.1e-34:256:83//U35245

F-PLACE1000540//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.099:336:58//X95276

F-PLACE1000547//Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds.//5.4e-11:279:63//AF076484

F-PLACE1000562//, complete sequence.//1.7e-97:559:88//AC005409

F-PLACE1000564

F-PLACE1000583//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//3.3e-46:631:68//M27877

F-PLACE1000588//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//7.3e-84:503:88//M55542

F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.8e-164:798:97//AJ012449

F-PLACE1000599//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.018:295:61//X95276

F-PLACE1000610//HS\_2056\_A1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=19 Row=G, genomic survey sequence.//5.3e-24:188:87//AQ235967

F-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.4e-47:687:66//AF044201

F-PLACE1000636

F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.5e-152:747:96//AF102265

F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//2.3e-156:775:97//AJ005896

F-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//8.0e-60:675:70//S78219

F-PLACE1000712

F-PLACE1800716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 779 Col=5 Row=A, genomic survey sequence.//2.7e-42:266:82//B43026

F-PLACE1000748//CIT-HSP-2372J8.TR CIT-HSP Homo sapiens genomic clone 2372J8, genomic survey sequence.//0.023:157:68//AQ113109

- F-PLACE1000749//Plasmodium falciparum MAL3P7, complete sequence.//0.099:664:57//AL034559
- F-PLACE1000755//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00068:206:62//X76589
- F-PLACE1000769//RPC11-3J18.TPB RPC1-11 Homo sapiens genomic clone RPC11-11-3J18, genomic survey sequence.//6.5e-08:93:89//B63806
- 5 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//3.5e-138:663:98//AB014548
- F-PLACE1000786//Drosophila melanogaster cosmid 80H7.//1.4e-43:589:68//AL031027
- F-PLACE1000793//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpq13d12.r11c.//4.6e-09:71:100//Z64565
- 10 F-PLACE1000798//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//5.0e-14:235:72//AC002310
- F-PLACE1000841//Homo sapiens clone NH0441G08, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.013:404:60//AC006158
- F-PLACE1000849//H.sapiens CpG island DNA genomic MseI fragment, clone 72a10, reverse read cpq72a10.r11a.//3.3e-09:82:92//Z62712
- 15 F-PLACE1000856//Hydra vulgaris HT4 mRNA for collagen-like protein, partial cds.//1.0:317:59//AB008935
- F-PLACE1000863//H.sapiens CpG island DNA genomic MseI fragment, clone 53d2, forward read cpq53d2.r11b.//7.3e-37:199:98//Z55621
- F-PLACE1000909//H.sapiens CpG island DNA genomic MseI fragment, clone 173f8, reverse read cpq173f8.r11a.//1.5e-17:128:92//Z57391
- 20 F-PLACE1000931//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//8.1e-55:647:72//AL009181
- F-PLACE1000948
- F-PLACE1000972//RPC11-61B1.TJ RPC11 Homo sapiens genomic clone R-61B1, genomic survey sequence.//1.0e-26:148:99//AQ194348
- 25 F-PLACE1000977//Homo sapiens mRNA for KIAA0672 protein, complete cds.//6.1e-08:413:61//AB014572
- F-PLACE1000979//H.sapiens CpG island DNA genomic MseI fragment, clone 76e8, reverse read cpq76e8.r11a.//2.7e-10:84:94//Z55963
- F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds.//8.0e-140:694:96//AB018267
- 30 F-PLACE1001000//Herpomonas muscarum muscarum kinetoplast 12S rRNA gene.//0.0056:443:58//U01011
- F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sapiens genomic clone 2013L15, genomic survey sequence.//0.99:277:58//B58681
- F-PLACE1001010//Human cosmid g1572c101, complete sequence.//3.6e-55:294:88//AC000357
- F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 from 7p21, complete sequence.//7.2e-33:333:73//AC004741
- 35 F-PLACE1001024
- F-PLACE1001036//CIT-HSP-2373110.TF CIT-HSP Homo sapiens genomic clone 2373110, genomic survey sequence.//1.1e-80:393:98//AQ108662
- F-PLACE1001054//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence.//8.8e-40:483:66//AB013390
- 40 F-PLACE1001062//Mus musculus mRNA encoding lysine-ketoglutarate reductase/saccharopine dehydrogenase.//1.2e-23:224:80//AJ224761
- F-PLACE1001076//HS\_2195\_B1\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=9 Row=H, genomic survey sequence.//0.0014:168:66//AQ066659
- F-PLACE1001088
- 45 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//3.1e-95:489:96//AF065485
- F-PLACE1001104//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.0073:253:62//U01400
- F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds.//2.5e-64:676:71//AF022158
- 50 F-PLACE1001136//Human amphiregulin (AR) gene, exon 5, clones lambda-ARH(6,12).//3.8e-26:174:93//M30702
- F-PLACE1001168
- F-PLACE1001171//Homo sapiens subtelomeric cosmid 11b-1, complete sequence.//7.6e-23:245:68//AC005603
- F-PLACE1001185//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker-CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.010:102:70//AL031177
- 55 F-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//9.3e-82:684:

77//D14336

F-PLACE1001241

F-PLACE1001257//Caenorhabditis elegans cosmid R12E2.//1.1e-16:480:60//AF067219

F-PLACE1001272//H.sapiens subunit of coatomer complex.//0.31:50:96//X70476

5 F-PLACE1001279//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.054:352:60//AC005507

F-PLACE1001280//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//1.0e-10:620:61//L14320

F-PLACE1001294//M.musculus GEG-154 mRNA.//5.0e-107:826:80//X71642

10 F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger protein ZFP-35.//1.2e-67:510:77//X17617

F-PLACE1001311//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-47:491:73//AC005282

F-PLACE1001323//HS-1007-A2-B10-MF.abl CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 328 Col=20 Row=C, genomic survey sequence.//9.6e-26:142:100//B31181

15 F-PLACE1001351

F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds.//8.6e-25:155:95//AB018342

F-PLACE1001377//H.sapiens MADM gene (exon 1).//1.6e-43:393:79//Z48614

F-PLACE1001383//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.5e-119:705:91//AL022324

20 F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//5.7e-08:117:84//AJ001319

F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58//I57340

F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC genes for beta and beta-prime subunits of RNA polymerase (EC 2.7.7.6).//7.2e-11:620:60//X52177

25 F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.0e-145:700:98//AC005412

F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//2.0e-69:365:96//AF091087

F-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202\_h\_3, complete sequence.//8.2e-121:608:97//AC006241

30 F-PLACE1001440//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.3e-06:437:61//AC000384

F-PLACE1001456//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//0.98:348:60//AC003106

F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148

35 F-PLACE1001484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL031660

F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3) gene, exon L.//0.00015:333:59//L78720

F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//0.00016:161:66//AC004373

40 F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//3.7e-22:260:76//AL021786

F-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031667

45 F-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165\_I\_16, complete sequence.//2.7e-139:482:96//AC005669

F-PLACE1001551//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.9e-116:681:89//AC005261

F-PLACE1001570//HS\_3105\_A1\_F06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, genomic survey sequence.//1.2e-10:137:79//AQ139817

50 F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3//1.1e-102:217:99//AB020860

F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//3.7e-104:501:98//AF069984

55 F-PLACE1001608//HS\_2189\_A1\_G07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2189 Col=13 Row=M, genomic survey sequence.//2.9e-60:429:84//AQ0221959

F-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.4e-114:552:98//AC005037

- F-PLACE1001611//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 penicillin binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//0.93:131:71//AL031587
- 5 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.1e-74:702:75//AB018341
- F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds.//1.2e-18:114:100//U17032
- F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//7.7e-159:788:97//AC005971
- F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//7.8e-36:365:73//AL022165
- 10 F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294\_U\_22, complete sequence.//9.1e-149:760:96//AC005921
- 15 F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//2.9e-57:643:71//M16200
- F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958\_E\_11, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.9e-18:284:71//AC005883
- F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds.//6.6e-68:369:73//D83776
- 20 F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3 In IGLC Region, complete sequence.//1.0:274:59//AC000051
- F-PLACE1001729//Streptomyces coelicolor cosmid 1C2.//0.22:433:57//AL031124
- F-PLACE1001739//Caenorhabditis elegans cosmid C18H7.//0.049:341:61//AF067607
- 25 F-PLACE1001740//Homo sapiens chromosome 5, P1 clone 1108H7 (LBNL H81), complete sequence.//4.8e-26:372:68//AC005221
- F-PLACE1001745
- F-PLACE1001746//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MALP1, WORKING DRAFT SEQUENCE.//0.018:472:57//AL031744
- F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//8.8e-159:773:97//AF061243
- 30 F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPCI11-303E5, WORKING DRAFT SEQUENCE, 65 unordered pieces.//1.9e-54:274:81//AC005842
- F-PLACE1001761//HS\_3027\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, genomic survey sequence.//0.095:49:93//AQ130972
- 35 F-PLACE1001771//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//1.0e-146:709:97//AF080394
- F-PLACE1001781 1.3e-08:238:65//AC005637
- F-PLACE1001799//HS\_3075\_B1\_H03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, genomic survey sequence.//1.7e-09:166:69//AQ138474
- 40 F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence.//0.00035:196:66//AF020749
- F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.1e-108:546:96//AF058953
- F-PLACE1001821//RPCI11-35D17.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35D17, genomic survey sequence.//2.1e-55:300:97//AQ045286
- 45 F-PLACE1001844//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//2.8e-67:443:86//AC005177
- F-PLACE1001845//Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence.//0.34:219:64//AC005850
- 50 F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rbtK) and ribitol transporter (rbtT) genes, complete cds.//7.1e-11:505:57//AF045244
- F-PLACE1001897//RPCI11-46D15.TJ RPCI11 Homo sapiens genomic clone R-46D15, genomic survey sequence.//9.3e-08:383:63//AQ194408
- F-PLACE1001912
- F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//7.3e-156:753:98//AF099935
- 55 F-PLACE1001928//HS\_2220\_B2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=8 Row=N, genomic survey sequence.//2.8e-43:233:97//AQ152361
- F-PLACE1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE.//1.6e-07:396:62//AL031596

- F-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.0e-109:602:93//AL023755
- F-PLACE1002004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317E23, WORKING DRAFT SEQUENCE.//1.0e-69:475:87//AL020996
- 5 F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds.//7.2e-97:623:85//U58337
- F-PLACE1002052//HS\_2178\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=H, genomic survey sequence.//4.8e-22:140:95//AQ307908
- F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.0063:371:60//U72284
- 10 F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A.//0.97:248:60//AF043195
- F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds.//1.3e-37:635:64//AB011178
- F-PLACE1002090//Homo sapiens full-length insert cDNA clone ZA85C09.//7.0e-122:583:98//AF086131
- F-PLACE1002115//nbxb0038A20r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0038A20r, genomic survey sequence.//0.039:210:69//AQ291086
- 15 F-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds.//7.1e-61:540:77//AF079527
- F-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCLRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCLRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-125:491:98//AL022162
- 20 F-PLACE1002150//Plasmodium falciparum MAL3P5, complete sequence.//0.12:408:61//AL034556
- F-PLACE1002157//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.1e-44:515:71//AC005539
- F-PLACE1002163//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.98:210:65//AE000662
- 25 F-PLACE1002170//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human BAC Library) complete sequence.//1.2e-06:283:60//AC004805
- F-PLACE1002171//Mus musculus interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds.//1.0e-24:313:71//U06244
- F-PLACE1002205//Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SEQUENCE. 4 unordered pieces.//1.6e-05:428:60//AC005720
- 30 F-PLACE1002213//HS\_3238\_B1\_G03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence.//2.2e-74:371:98//AQ206965
- F-PLACE1002227//HS-1056-B1-C01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence.//2.1e-07:174:71//B42800
- 35 F-PLACE1002256//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-72, complete sequence.//0.022:458:59//AL010142
- F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//3.5e-91:637:84//AL022324
- 40 F-PLACE1002319
- F-PLACE1002342//Caenorhabditis elegans cosmid M03A1.//0.47:403:58//U49956
- F-PLACE1002395//Homo sapiens chromosome 19, cosmid R28991, complete sequence.//1.9e-127:487:93//AC004623
- 45 F-PLACE1002399//Homo sapiens chromosome 17, clone hRKC.235\_1\_10, complete sequence.//5.6e-05:474:59//AC005922
- F-PLACE1002433//Drosophila melanogaster fidipidine gene, exons 1-7.//1.7e-11:613:58//AJ011928
- F-PLACE1002437//M.musculus abc1 mRNA.//5.6e-62:452:85//X75926
- F-PLACE1002438//Dictyostelium discoideum developmental protein DG1098 (DG1098) gene, partial cds.//0.013:372:59//AF081801
- 50 F-PLACE1002450//HS\_3233\_A1\_G01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=1 Row=M, genomic survey sequence.//3.1e-07:449:59//AQ204769
- F-PLACE1002465
- F-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.5e-110:720:85//U69262
- F-PLACE1002477//Homo sapiens Xp22-171-173 BAC GSHB-31214 (Genome Systems Human BAC Library) complete sequence.//3.9e-05:195:71//AC005926
- 55 F-PLACE1002493//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.020:301:60//AC006060
- F-PLACE1002499



- F-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.1e-58:465:80//U50927  
 F-PLACE1002514//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING  
 DRAFT SEQUENCE.//3.7e-08:139:76//Z93930  
 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//9.0e-143:583:95//AB018256  
 5 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//0.00019:193:  
 65//AC004774  
 F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a  
 novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor  
 Type 1 (IL1-R-1). Contains GSSs, complete sequence.//4.7e-25:198:84//AL031575  
 10 F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA, complete cds.//2.0e-13:400:60//L25314  
 F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//3.5e-11:167:72//  
 AC002523  
 F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds.//4.2e-09:370:61//U31443  
 F-PLACE1002591//H. sapiens mRNA for coronin.//7.2e-26:279:74//X89109  
 15 F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
 0.0013:375:64//AC005537  
 F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence.//4.7e-05:556:59//D31785  
 F-PLACE1002625  
 F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.6e-128:229:  
 20 92//AC005281  
 F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//3.6e-107:706:84//  
 AF079765  
 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-  
 186:804:97//AF068180  
 25 F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:  
 64//AF051726  
 F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//I73723  
 F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs  
 and a GSS, complete sequence.//0.0076:161:70//AL031273  
 30 F-PLACE1002772//HS\_3058\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3058 Col=3 Row=C, genomic survey sequence.//0.0046:192:64//AQ134567  
 F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//  
 AF084259  
 F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927  
 35 F-PLACE1002794//CIT-HSP-2368A17.TR CIT-HSP Homo sapiens genomic clone 2368A17, genomic survey se-  
 quence.//1.3e-71:368:96//AQ075879  
 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994  
 F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR005295  
 F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//1.3e-68:687:73//AF039691  
 40 F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//3e-41:240:93//  
 M27877  
 F-PLACE1002839//Human BAC clone RG205G13 from 7q31, complete sequence.//0.00087:213:63//AC003045  
 F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING  
 DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:66//AC005140  
 45 F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete tran-  
 scribed region and flanks.//0.032:275:62//M10126  
 F-PLACE1002881//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING  
 DRAFT SEQUENCE.//4.7e-38:355:76//Z98200  
 F-PLACE1002908//Gallus gallus beta-1,4-galactosyltransferase (Kil) mRNA, complete cds.//0.00012:200:64//  
 50 U19889  
 F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:24:71//AC000120  
 F-PLACE1002962  
 F-PLACE1002968//Plasmodium falciparum MAL3P2, complete sequence.//0.21:410:59//AL034558  
 F-PLACE1002991//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING  
 DRAFT SEQUENCE.//6.8e-121:605:93//AL023755  
 55 F-PLACE1002993//CIT-HSP-233816.TF CIT-HSP Homo sapiens genomic clone 233816, genomic survey se-  
 quence.//1.9e-13:100:95//AQ054760  
 F-PLACE1002996//Mouse U6 RNA gene.//2.0e-13:113:90//X06980

F-PLACE1003025//Plasmodium falciparum MAL3P6, complete sequence.//0.84:374:58//Z98551  
 F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds.//6.1e-130:632:97//AB011088  
 F-PLACE1003044//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829  
 5 F-PLACE1003045//H.sapiens CpG island DNA genomic MseI fragment, clone 47g6, forward read cpq47g6.ft1a.//0.0064:52:96//Z61200  
 F-PLACE1003092//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0031:249:63//B60158  
 10 F-PLACE1003100//Human Hep27 protein mRNA, complete cds.//8.9e-65:650:73//U31875  
 F-PLACE1003108  
 F-PLACE1003136//Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.//6.3e-46:606:68//AC004219  
 F-PLACE1003145  
 15 F-PLACE1003153//RPCI11-13P16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13P16, genomic survey sequence.//2.7e-63:478:82//B76206  
 F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495  
 F-PLACE1003176//HS\_2255\_A2\_B01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey sequence.//6.3e-09:137:76//AQ131934  
 20 F-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-138:791:901//AC005095  
 F-PLACE1003200//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.7e-06:728:57//X95276  
 F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence.//7.5e-05:249:63//AC002466  
 F-PLACE1003238//HS\_3239\_A2\_G02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey sequence.//0.36:64:87//AQ209954  
 25 F-PLACE1003249  
 F-PLACE1003256  
 F-PLACE1003258//HS\_3223\_A1\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey sequence.//1.4e-07:227:65//AQ190317  
 30 F-PLACE1003296//CIT-HSP-2337F11.TF CIT-HSP Homo sapiens genomic clone 2337F11, genomic survey sequence.//1.1e-13:97:95//AQ057429  
 F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//2.3e-92:485:95//M27877  
 F-PLACE1003334  
 35 F-PLACE1003342  
 F-PLACE1003343//Homo sapiens clone DJ1022114, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.0e-20:179:84//AC004951  
 F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//8.0e-143:773:92//U92715  
 40 F-PLACE1003361//Human Cosmid g1248a143 from 7q31.3, complete sequence.//1.9e-30:402:70//AC004095  
 F-PLACE1003366  
 F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence.//7.6e-07:378:60//AL034558  
 F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//6.0e-18:471:61//AC005247  
 45 F-PLACE1003375  
 F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithenium cancer, segment 10.10.//2.3e-157:779:96//AB020878  
 F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.//1.2e-104:596:91//M83680  
 50 F-PLACE1003401//RPCI11-71J5.TJ RPCI11 Homo sapiens genomic clone R-71J5, genomic survey sequence.//0.85:140:85//AQ268588  
 F-PLACE1003420//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0015:286:60//AL021388  
 F-PLACE1003454//Plasmodium falciparum microsatellite pe63 sequence.//0.0084:219:61//AF015470  
 55 F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) gene, complete cds.//1.3e-11:746:60//AF039401  
 F-PLACE1003493  
 F-PLACE1003516//Homo sapiens chromosome 17, clone HRPCC987K16, complete sequence.//8.2e-41:379:78//AC002994

- F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.2e-21:247:76//AF064859
- F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Contains two unknown genes and ESTs, STSs and a GSS.//4.4e-68:502:79//AL008729
- 5 F-PLACE1003528//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//1.0:323:58//AL022336
- F-PLACE1003537//Homo sapiens multispanning membrane protein mRNA, complete cds.//0.0054:322:59//U94831
- 10 F-PLACE1003553//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-78:267:88//AL031297
- F-PLACE1003566//Plasmodium falciparum MAL3P3, complete sequence.//0.00026:514:58//Z98547
- F-PLACE1003575//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.079:755:54//AC004688
- 15 F-PLACE1003583//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.1e-41:212:74//AL022324
- F-PLACE1003584//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-56, complete sequence.//0.0038:465:57//AL010230
- 20 F-PLACE1003592//Homo sapiens chromosome 17, clone 296K1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.72:111:71//AC002557
- F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.096:162:66//AC002476
- F-PLACE1003596//Mus musculus integral membrane protein 1 (Itm1) mRNA, complete cds.//1.4e-54:685:68//L34260
- 25 F-PLACE1003602//Homo sapiens mRNA expressed in placenta.//1.1e-138:679:97//D83200
- F-PLACE1003605//Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.//0.0074:265:63//AC005356
- F-PLACE1003611//HS\_2198\_B1\_D02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence.//2.1e-23:137:97//AQ184475
- 30 F-PLACE1003618//Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence.//3.0e-122:725:89//AC006226
- F-PLACE1003625//HS\_2238\_B2\_D11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=22 Row=H, genomic survey sequence.//4.8e-12:92:94//AQ065662
- F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence.//0.043:264:63//AB011478
- 35 F-PLACE1003669
- F-PLACE1003704//RPC111-23H21.TKBF RPC1-11 Homo sapiens genomic clone RPC1-11-23H21, genomic survey sequence.//7.1e-31:199:91//AQ013830
- F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//4.3e-132:669:95//AF053305
- 40 F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (elF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//1.5e-31:166:99//AL021920
- F-PLACE1003723//HS\_2231\_A2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey sequence.//1.2e-12:114:90//AQ235672
- 45 F-PLACE1003738//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//5.9e-33:592:67//M58297
- F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//3.6e-11:92:93//AF054840
- F-PLACE1003762
- 50 F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE.//4.8e-77:737:76//AP000014
- F-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//2.1e-164:793:98//AC004160
- F-PLACE1003783//HS\_2190\_A2\_C02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence.//1.1e-26:147:100//AQ218757
- 55 F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//4.5e-57:706:68//AC006210
- F-PLACE1003795//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyl-

transferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene.//0.015:296:60//U52112

F-PLACE1003833/Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22. Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339

F-PLACE1003850/P.falciapum histidine-rich protein genes.//0.39:330:60//M17028

F-PLACE1003858/Human DNA sequence from PAC 332O11 on chromosome 1q24-1q25. Contains ESTs and STSs.//4.8e-07:461:59//Z98043

F-PLACE1003864/Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.026:538:56//AC005139

F-PLACE1003870/Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304

F-PLACE1003885/Mus musculus poly(A) polymerase VI mRNA, complete cds.//9.4e-75:754:72//U58134

F-PLACE1003886/Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.7e-20:432:64//AC006030

F-PLACE1003888/Human mRNA for phospholipase C, complete cds.//2.6e-53:702:67//ID42108

F-PLACE1003892/RPC11-24P17.TV RPC1-11 Homo sapiens genomic clone RPC1-11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759

F-PLACE1003900/Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240

F-PLACE1003903/Mus musculus CTP synthetase homolog (CTPsh) mRNA, complete cds.//2.7e-86:533:87//U49385

F-PLACE1003915/Mus musculus clone OST1963, genomic survey sequence.//6.4e-29:251:80//AF046591

F-PLACE1003923/Homo sapiens full-length insert cDNA clone ZD40A05.//2.8e-25:316:70//AF086251

F-PLACE1003932/Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//AC005505

F-PLACE1003936/CIT-HSP Homo sapiens genomic clone 2387C11, genomic survey sequence.//1.0:223:62//AQ239494

F-PLACE1003968/Rattus norvegicus 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413

F-PLACE1004103/Homo sapiens chromosome 19, cosmid R28784, complete sequence.//6.7e-29:241:84//AC005954

F-PLACE1004104/Rattus norvegicus rsec5 mRNA, complete cds.//3.0e-115:719:86//AF032666

F-PLACE1004114/Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000052

F-PLACE1004118/Pseudorabies virus with upstream and downstream sequences.//0.87:209:64//M34651

F-PLACE1004128/M. musculus G protein beta-subunit mRNA, complete cds.//2.5e-62:437:84//M63658

F-PLACE1004149/Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//1.4e-16:342:65//AF005355

F-PLACE1004156/Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p12.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, complete sequence.//1.2e-26:299:74//AL022099

F-PLACE1004161

F-PLACE1004183/Homo sapiens for TOM1-like protein.//1.2e-146:731:96//AJ010071

F-PLACE1004197

F-PLACE1004203/Homo sapiens GPI-anchored membrane protein CDW108 precursor, mRNA, complete cds.//4.0e-144:695:98//AF069493

F-PLACE1004242/Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.3e-151:772:95//AL021326

F-PLACE1004256/HS\_2010\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=B Row=N, genomic survey sequence.//1.5e-44:372:79//AQ252434

F-PLACE1004257/Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//0.00011:349:63//AC005034

F-PLACE1004258/Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806

F-PLACE1004270/Human IgA C alpha 1 switch region (Sa1).//1.7e-08:622:61//L19121

F-PLACE1004274/H.sapiens CpG island DNA genomic MseI fragment, clone 189g, forward read cp189g.ft1b.//8.6e-37:196:98//Z57691

F-PLACE1004277/Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//6.0e-156:756:

97//AF084830

F-PLACE1004284//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence.//  
0.0060:635:57//AB011480

F-PLACE1004289//HS\_3023\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=7 Row=J, genomic survey sequence.//2.4e-12:86:98//AQ094451

F-PLACE1004302//Streptomyces coelicolor cosmid 7H1.//0.26:297:64//AL021411

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//2.9e-150:797:94//Y11588

F-PLACE1004336//Drosophila melanogaster DNA sequence (P1 DS07968 (D117)), complete sequence.//0.87:206:59//AC004267

F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//5.9e-139:688:97//AF100153

F-PLACE1004376//Mus musculus clone OST20307, genomic survey sequence.//4.1e-81:498:89//AF046631

F-PLACE1004384//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1121J18, WORKING DRAFT SEQUENCE.//3.6e-41:482:73//AL031653

F-PLACE1004388//Caenorhabditis elegans cosmid K08F11.//8.6e-26:615:62//U070855

F-PLACE1004405//Homo sapiens clone GS512121, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.2e-150:749:96//AC005027

F-PLACE1004425//Homo sapiens PAC clone DJ0733809 from 7p14-p13, complete sequence.//2.4e-08:129:76//AC005532

F-PLACE1004428//R.norvegicus mRNA for Pristanoyl-CoA Oxidase.//7.0e-17:549:61//X95188

F-PLACE1004437//Human NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//3.1e-129:536:99//U49283

F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 1-24, Interferon Induced 56Kd pseudogene and ESTs.//4.8e-23:231:71//Z74739

F-PLACE1004460//Homo sapiens PAC clone DJ1064B22 from 7q21, complete sequence.//0.96:454:56//AC004954

F-PLACE1004467//HS\_2058\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=F, genomic survey sequence.//2.4e-87:433:98//AQ242700

F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-74:665:70//M27877

F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15; genomic survey sequence.//3.3e-20:140:92//B80243

F-PLACE1004491//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.9e-05:794:57//AC004709

F-PLACE1004506//Human Gx-alpha gene.//1.0e-05:231:63//D90150

F-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAF1150) mRNA, complete cds.//3.2e-146:699:98//AF040701

F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST.//1.4e-33:367:71//Z86001

F-PLACE1004518

F-PLACE1004548//Dictyostelium discoideum MigA (migA) gene, complete cds.//2.6e-05:318:62//U86962

F-PLACE1004550//Human FMR1 gene, 5' end.//0.0018:142:66//L19476

F-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.7e-114:513:85//X75931

F-PLACE1004629//Anolis carolinensis Brain-1 gene, complete cds.//0.00013:188:67//AB001868

F-PLACE1004645//Mycobacterium tuberculosis H3R7v complete genome; segment 138/162.//0.66:337:60//Z95120

F-PLACE1004646//Rattus norvegicus retinal pigment epithelium-specific protein (Rpe65) mRNA, complete cds.//1.1e-19:326:63//AF035673

F-PLACE1004658//H.sapiens CpG Island DNA genomic Mse1 fragment, clone 55h1, forward read cp955h1.ft1a.//12.4e-34:188:98//Z61632

F-PLACE1004664//Caenorhabditis elegans cosmid W10G6, complete sequence.//1.0:148:65//Z81140

F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//1.9e-101:182:95//U07561

F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//4.3e-109:625:91//AF035606

F-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.9e-152:759:96//AB020860

F-PLACE1004686//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the

SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//1.2e-34:320:71//Z95152

F-PLACE1004691//HS\_3044\_A1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey sequence.//0.018:191:63//AQ098323

F-PLACE1004693//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.28:573:57//AL022577

F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence.//0.00081:428:59//Z98551

F-PLACE1004722//HS\_3052\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey sequence.//2.3e-05:104:75//AQ134959

F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498

F-PLACE1004740//RPC111-58A7.TJ RPC111 Homo sapiens genomic clone R-58A7, genomic survey sequence.//8.6e-26:522:65//AQ195766

F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//1.1e-112:711:86//AF061555

F-PLACE1004751

F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//5.4e-171:828:97//AF084367

F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//4.2e-134:763:90//AJ001713

F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34), hypothetical protein EST, STS, GSS, complete sequence.//9.3e-132:759:90//AL022157

F-PLACE1004804

F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.5e-06:403:58//AC004710

F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//9.8e-39:207:99//AC005921

F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete sequence.//8.1e-15:203:73//AC004613

F-PLACE1004824//G.gallus PB1 gene.//1.1e-103:759:80//X90849

F-PLACE1004827//HS\_2230\_A2\_A05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey sequence.//4.1e-38:330:81//AQ299313

F-PLACE1004836//H.sapiens nidogen gene (exon 8).//0.97:116:68//X84825

F-PLACE1004838//HS\_3241\_A2\_A04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence.//1.8e-87:425:98//AQ206740

F-PLACE1004840//Sequence 2 from patent US 5728819.//6.7e-47:285:91//92819

F-PLACE1004868

F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 9.//0.10:14:465:59//Z97344

F-PLACE1004900

F-PLACE1004902//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//3.6e-06:56:100//AQ261184

F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.6e-151:770:91//AC005058

F-PLACE1004918//Mus musculus signaling molecule (ATTP) mRNA, complete cds.//2.6e-68:459:84//U97571

F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//4.4e-106:545:95//AF070671

F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//3.5e-45:226:84//AL020989

F-PLACE1004937

F-PLACE1004969

F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.//0.012:316:61//AC004843

F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.7e-39:394:77//AL031073

F-PLACE1004982//Caenorhabditis elegans cosmid B0507.//0.16:167:65//U64833

- F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.8e-14:590.61//AE001373
- F-PLACE1005026
- F-PLACE1005027
- 5 F-PLACE1005046
- F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.1e-135:675.97//AC005867
- F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//1.9e-159:761.98//AB011148
- 10 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.2e-10:757.56//AF059569
- F-PLACE1005077
- F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//6.9e-29:253.77//AC004673
- 15 F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence.//6.5e-52:446.78//AC002316
- F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.0e-146:734.96//AC005225
- F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//9.8e-83:254.95//AC004476
- 20 F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence.//0.46:179.64//AC003081
- F-PLACE1005111
- F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.00051:287.63//L14320
- 25 F-PLACE1005146//HS\_3071\_A1\_E03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=5 Row=1, genomic survey sequence.//7.4e-38:299.82//AQ103361
- F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence.//2.6e-44:346.82//AC002451
- F-PLACE1005176
- F-PLACE1005181//CIT-HSP-2340O5.TR CIT-HSP Homo sapiens genomic clone 2340O5, genomic survey sequence.//0.99:211.63//AQ054651
- 30 F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 2358N6, genomic survey sequence.//2.7e-07:80.90//AQ074445
- F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence.//0.98:216.61//AC000061
- 35 F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.70:245.63//AC004965
- F-PLACE1005243
- F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence.//0.00041:254.61//Z47812
- F-PLACE1005266//H.sapiens mRNA (fetal brain cDNA a4\_2g).//9.6e-33:177.98//Z70695
- 40 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.6e-148:706.98//AB011182
- F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cds.//2.8e-15:737.60//M69183
- F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//3.8e-111:728.84//M25757
- F-PLACE1005308//Ctetrionomys glareolus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Vole Cg14.//1.0:128.67//AJ233621
- 45 F-PLACE1005313//Caenorhabditis elegans cosmid D2092.//8.8e-11:342.62//U88167
- F-PLACE1005327//HS\_3080\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=24 Row=B, genomic survey sequence.//4.1e-25:147.96//AQ139116
- F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//1.4e-132:399.94//AC004794
- 50 F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-114:237.92//AC000380
- F-PLACE1005373
- F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete sequence.//0.20:305.58//AF017104
- 55 F-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//2.5e-148:760.95//AC003991
- F-PLACE1005453//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y48A6, WORKING DRAFT SEQUENCE.//0.00069:582.59//Z92854
- F-PLACE1005467//Rat mRNA.//0.0014:131.70//M59859

- F-PLACE1005471//Human DNA sequence from clone 4514 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//3.0e-23:530:67//AL023581
- F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQUENCE.//3.3e-131:814:88//Z82191
- 5 F-PLACE1005480//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D),TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//7.0e-34:246:73//AL021878
- F-PLACE1005481//RPC11-74L17.TJ RPC11 Homo sapiens genomic clone R-74L17, genomic survey sequence.//0.37:403:57//AQ266885
- 10 F-PLACE1005494//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//2.1e-67:325:99//AF080394
- F-PLACE1005502//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//0.015:403:61//AC005589
- 15 F-PLACE1005526//H.sapiens CpG island DNA genomic MseI fragment, clone 9f1, reverse read cp9f1.rt1a.//3.6e-27:159:96//Z66485
- F-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.6e-28:449:67//AP000038
- F-PLACE1005530//Homo sapiens clone DJ0691L07, complete sequence.//6.5e-18:234:72//AC004860
- F-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH3, genomic survey sequence.//1.2e-14:123:75//AL025925
- 20 F-PLACE1005554//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//0.43:209:66//X02354
- F-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//9.3e-113:536:97//AC004707
- F-PLACE1005574//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:514:59//AC005504
- 25 F-PLACE1005584//Homo sapiens mRNA for KIAA0617 protein, complete cds.//0.00056:289:63//AB014517
- F-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//1.2e-111:262:89//AC004126
- F-PLACE1005603
- 30 F-PLACE1005611//F16O5TFC IGF Arabidopsis thaliana genomic clone F16O5, genomic survey sequence.//2.0e-10:209:66//B98589
- F-PLACE1005623
- F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.2e-93:230:98//AC005840
- 35 F-PLACE1005639//HS\_3095\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=5 Row=B, genomic survey sequence.//1.2e-05:220:63//AQ123022
- F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//6.4e-150:721:98//AF083255
- F-PLACE1005656//H.sapiens RR2 mRNA for small subunit ribonucleotide reductase.//1.3e-51:480:74//X59618
- 40 F-PLACE1005666//RPC11-78O15.TV RPC11 Homo sapiens genomic clone R-78O15, genomic survey sequence.//8.7e-05:243:62//AQ284667
- F-PLACE1005698//Human membrane-associated lectin type-C mRNA.//1.9e-63:374:85//M98457
- F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.69:633:57//AE001422
- 45 F-PLACE1005730//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//2.0e-24:286:74//AQ231147
- F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.8e-55:621:71//U15635
- F-PLACE1005755//HS\_2213\_A2\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=22 Row=O, genomic survey sequence.//1.4e-25:290:75//AQ136844
- 50 F-PLACE1005763//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//4.5e-40:297:70//M16200
- F-PLACE1005799//H.norvegicus mRNA for mitochondrial isoform of cytochrome b5.//0.91:287:63//Y12517
- F-PLACE1005802//Homo sapiens PAC clone DJ04L15 from Xq23, complete sequence.//5.0e-109:530:98//AC004827
- 55 F-PLACE1005803//HS\_3092\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=19 Row=B, genomic survey sequence.//2.4e-08:76:96//AQ103695
- F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.4e-126:636:96//AF027156
- F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//2.6e-154:739:98//AF065482



- F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-37:355:77//AC004150
- F-PLACE1005834//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-105, complete sequence.//0.00080:663:58//AL010283
- 5 F-PLACE1005845//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00015:340:58//AC004153
- F-PLACE1005850//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs and CpG islands, complete sequence.//1.8e-46:278:85//AL031432
- F-PLACE1005851
- 10 F-PLACE1005876//B. taurus mRNA for cleavage and polyadenylation specificity factor.//5.0e-120:701:89//X75931
- F-PLACE1005884//CIT-HSP-2333O12.TR CIT-HSP Homo sapiens genomic clone 2333O12, genomic survey sequence.//4.6e-78:385:98//AQ039226
- F-PLACE1005890//Schizosaccharomyces pombe bem1/bud5 suppressor (Bem46+) mRNA, partial cds.//9.3e-16:638:57//U29892
- 15 F-PLACE1005898//Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds.//1.0:178:65//U67136
- F-PLACE1005921//M. musculus mRNA for immunity associated protein 38.//6.6e-17:614:59//Y08026
- F-PLACE1005923//RPC111-33G19.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-33G19, genomic survey sequence.//4.0e-10:535:57//AQ046151
- 20 F-PLACE1005925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//0.17:159:65//AL034405
- F-PLACE1005932
- F-PLACE1005934//H.sapiens CpG island DNA genomic MseI fragment, clone 165g2, forward read cpq165g2.f1a.//8.3e-43:247:93//Z57153
- 25 F-PLACE1005936//P.furubipes GSS sequence, clone 069K22aG2, genomic survey sequence.//0.91:116:68//AL014719
- F-PLACE1005951//Rhodospirillum rubrum DMSO/TMAO-sensor kinase (dorS), DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds.//0.0022:495:59//AF016236
- 30 F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.9e-05:442:61//AC004081
- F-PLACE1005955//Caenorhabditis elegans cosmid F01F1.//4.3e-20:409:64//U13070
- F-PLACE1005966//P.falciparum aarp3 gene, exon.//0.0083:270:64//Y08925
- F-PLACE1005968
- 35 F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPC11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//1.0e-100:513:96//AC005866
- F-PLACE1006002//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//2.5e-54:444:77//Z86090
- F-PLACE1006003//HS-1059-A2-G01-MFabi CIT Human Genomic Sperm Library C Homo sapiens genomic clone PlateCT 781 Col=2 Row=M, genomic survey sequence.//3.4e-05:214:64//B44442
- 40 F-PLACE1006011//Mus musculus poly-(ADPribose)-transferase homolog PARP mRNA, complete cds.//4.3e-71:580:79//AF072521
- F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6-complete genomic sequence, complete sequence.//8.6e-32:177:83//AC002299
- 45 F-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//1.8e-34:269:83//U01139
- F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//3.4e-147:719:97//X99906
- F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs), complete sequence.//0.37:332:62//Z97200
- 50 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.3e-145:679:99//AF039023
- F-PLACE1006129
- F-PLACE1006139//Saccharomyces cerevisiae chromosome VI cosmid 9965.//4.8e-27:693:60//D44597
- F-PLACE1006143//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//4.7e-46:435:77//Z93015
- 55 F-PLACE1006157//Sagulinus oedipus mRNA for membrane cofactor protein CD46, complete cds, clone:B2.//0.048:290:60//D85750
- F-PLACE1006159//Homo sapiens chromosome 10 clone CIT987SK-1054O2 map 10q25, complete sequence.//3.2e-129:466:98//AC005661

- F-PLACE1006164//HS\_3003\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=K, genomic survey sequence.//1.4e-70:388.93//AQ118200  
F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//4.3e-78:385.86//AC005239
- 5 F-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.5e-91:630.84//X14972  
F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//3.9e-149:694.99//AF091433  
F-PLACE1006195//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//2.5e-16:283.70//AC003658
- 10 F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//2.2e-94:648.84//L25125  
F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence.//0.15:533.58//U75931  
F-PLACE1006223//F24L20-T7 IGF Arabidopsis thaliana genomic clone F24L20, genomic survey sequence.//0.0068:175.64//B19803
- 15 F-PLACE1006225//CIT-HSP-2335I23.TF CIT-HSP Homo sapiens genomic clone 2335I23, genomic survey sequence.//2.1e-19:149.90//AQ039880  
F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.//0.051:290.58//U91327  
F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//7.4e-158:452.96//AC004142
- 20 F-PLACE1006246//RPC11-36I23.TK RPC1-11 Homo sapiens genomic clone RPC1-11-36I23, genomic survey sequence.//2.6e-31:176.97//AQ045400  
F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.3e-166:791.98//AB014548  
F-PLACE1006262//342E3.TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence.//1.0:228.63//B16447
- 25 F-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20N2, WORKING DRAFT SEQUENCE.//6.6e-172:809.99//AL031320  
F-PLACE1006318  
F-PLACE1006325//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.079:396.59//AC004454
- 30 F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VHSB32-D-JH2 region.//1.0:90.67//M55721  
F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.16:445.56//AC005504  
F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence.//6.1e-05:625.57//AL034559
- 35 F-PLACE1006368//X. laevis mRNA for KLP2 protein.//3.0e-25:376.68//X94082  
F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//2.0e-146:711.97//AC004232  
F-PLACE1006382
- 40 F-PLACE1006385//Homo sapiens epsilon 2a mRNA, complete cds.//5.1e-110:539.97//AF062085  
F-PLACE1006412//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.3e-23:463.68//AC005029  
F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds.//1.3e-109:525.98//AF069735
- 45 F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds.//6.9e-23:531.65//AB011129  
F-PLACE1006445//HS\_3071\_A1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence.//4.7e-74:392.95//AQ 103347  
F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome.//1.1e-40:686.65//AF010496  
F-PLACE1006470//T.brucei kinetoplast maxicircle variable region DNA.//0.99:250.59//Z15118
- 50 F-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//4.3e-120:328.98//AL021977  
F-PLACE1006488//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//6.5e-86:478.91//X53744  
F-PLACE1006492  
F-PLACE1006506
- 55 F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//0.0010:547.58//AC005083  
F-PLACE1006531//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-84:625.80//AF005355

- F-PLACE1006534//Caenorhabditis elegans cosmid Y40H7A, complete sequence.//0.00031:671:58//AL033510  
F-PLACE1006540  
F-PLACE1006552//P.falcapurum glutamic acid-rich protein gnen, complete cds.//6.0e-10:636:59//J03998  
F-PLACE1006598//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//9.8e-25:170:77//AC006044  
F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//6.7e-167:781:99//U97670  
F-PLACE1006617//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//0.98:514:59//AC004470  
F-PLACE1006626//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00079:206:62//X76589  
F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.0012:576:57//AC004015  
F-PLACE1006640//P.falcapurum complete gene map of plastid-like DNA (IR-B).//0.0018:588:59//X95276  
F-PLACE1006673//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0028:469:58//AC004688  
F-PLACE1006678//Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase-I (b3GT1) gene, complete cds.//0.00011:184:64//AF029790  
F-PLACE1006704//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.0013:380:62//U67916  
F-PLACE1006731//Human DNA sequence from PAC 408N23 on chromosome 22q13. Contains HIP, HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN), ESTs and STS.//1.5e-78:520:86//Z98048  
F-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.9e-135:378:99//AC005626  
F-PLACE1006760//CIT-HSP-2336O13.TR CIT-HSP Homo sapiens genomic clone 2336O13, genomic survey sequence.//0.018:147:66//AQ039246  
F-PLACE1006779//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//2.6e-08:823:58//AE001426  
F-PLACE1006782//Homo sapiens clone NH0005N18, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.043:252:65//AC005487  
F-PLACE1006792//HS\_3165\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3165 Col=1 Row=P, genomic survey sequence.//1.4e-11:249:67//AQ149559  
F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.//1.3e-12:155:80//M68513  
F-PLACE1006800//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-92, complete sequence.//6.7e-05:391:62//AL010272  
F-PLACE1006805//paramecium species 1,168 mt dna dimer: replication init. region.//9.1e-09:369:62//K00915  
F-PLACE1006815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING DRAFT SEQUENCE.//0.89:465:58//AL031033  
F-PLACE1006819//Homo sapiens clone DJ1163L11, complete sequence.//1.5e-121:618:91//AC005230  
F-PLACE1006829//Bm-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.011:145:68//S69350  
F-PLACE1006860//Plasmodium falciparum MAL3P7, complete sequence.//2.2e-07:691:58//AL034559  
F-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING DRAFT SEQUENCE.//1.5e-132:643:98//AL033378  
F-PLACE1006878  
F-PLACE1006883//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.//1.0:236:62//Z95120  
F-PLACE1006901//Mus musculus t complex testis-specific protein (Tctex2) gene, t haplotype, promoter sequence.//2.7e-19:171:81//U21672  
F-PLACE1006904  
F-PLACE1006917//H.sapiens CpG island DNA genomic MseI fragment, clone 79g10, forward read cpq79g10.f1a.//1.3e-21:131:98//Z63175  
F-PLACE1006932//Mus musculus FKBP65 binding protein mRNA, complete cds.//0.99:248:61//L07063  
F-PLACE1006935//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//0.85:161:63//AF029308  
F-PLACE1006956//Hylobates lar involucrin gene, complete cds.//0.077:355:61//M35447  
F-PLACE1006958//Mus musculus osmotic stress protein 94 (Osp94) mRNA, complete cds.//2.9e-89:483:86//

U23921

F-PLACE1006961//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//1.6e-06:651:58//AJ223323

F-PLACE1006962//H.sapiens ir1B mRNA.//7.1e-15:202:71//X63417

F-PLACE1006966//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594

F-PLACE1006989//cSRL-172A4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-172A4, genomic survey sequence.//1.0:97:87//B03188

F-PLACE1007014//Rattus norvegicus equilibrative nitrobenzylthioinosine-insensitive nucleoside transporter mRNA, complete cds.//4.2e-07:592:58//AF015305

F-PLACE1007021//Homo sapiens chromosome 19, cosmid F16403; complete sequence.//5.1e-17:285:70//AC005777

F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat.//6.2e-131:775:89//Z82899

F-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.7e-143:675:99//AC004895

F-PLACE1007068//Homo sapiens chromosome 17, clone hRPK.214\_O\_1, complete sequence.//1.3e-131:652:97//AC005224

F-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glycerinaldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//8.3e-158:768:97//AL021368

F-PLACE1007105//Mus musculus muskulin mRNA, complete cds.//4.1e-124:687:91//U72194

F-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:586:56//AC005139

F-PLACE1007112//HS\_2234\_B2\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=20 Row=N, genomic survey sequence.//0.26:200:62//AQ087801

F-PLACE1007132//CIT978SK-A-211C6.TVB CIT978SK Homo sapiens genomic clone A-211C6, genomic survey sequence.//1.3e-40:255:92//B72112

F-PLACE1007140//QN1 orf [Coturnix coturnix, japonica, K2 neuroretinal cells, mRNA Partial, 3884 nt].//4.9e-15:386:62//S68151

F-PLACE1007178//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.011:329:61//AC005140

F-PLACE1007228//Human lipocortin (LIP) 2 gene, upstream region.//0.0036:180:63//M62899

F-PLACE1007238//FMR1 [CGG repeats] [human, Fragile X syndrome patient, Genomic, 429 nt].//2.8e-08:269:63//S74494

F-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.3e-57:405:87//D50495

F-PLACE1007242//HS\_3006\_A1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=21 Row=C, genomic survey sequence.//0.088:191:59//AQ069443

F-PLACE1007243//Human transporter protein (g17) mRNA, complete cds.//7.9e-12:245:66//U49082

F-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//5.2e-144:677:98//Y15908

F-PLACE1007274//HS\_3003\_A1\_D08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=G, genomic survey sequence.//7.4e-49:345:85//AQ294154

F-PLACE1007276//Fugu rubripes GSS sequence, clone 014010aG11, genomic survey sequence.//0.0052:228:62//AL024982

F-PLACE1007282//F.rubripes GSS sequence, clone 019007aB3, genomic survey sequence.//0.024:289:58//AL011743

F-PLACE1007286//Human Chromosome 16 BAC clone CIT987SK-A-256A9, complete sequence.//0.0048:185:69//AC002492

F-PLACE1007301//Dictyostelium discoideum gene for TRFA, complete cds.//0.069:761:57//AB009080

F-PLACE1007317

F-PLACE1007342

F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//5.4e-120:567:98//AF096870

F-PLACE1007367//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-59:613:75//AC005077

F-PLACE1007375//Caenorhabditis elegans cosmid D2092.//1.8e-12:193.70//U88167  
 F-PLACE1007386  
 F-PLACE1007402//HS\_2170\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2170 Col=24 Row=G, genomic survey sequence.//5.6e-06:162.67//AQ125590  
 5 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 2 mRNA, complete sequence.//1.6e-25:165:93//AF093772  
 F-PLACE1007416  
 F-PLACE1007450//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.9e-34:764.62//AC003973  
 10 F-PLACE1007452//Mus musculus bet3 (Bet3) mRNA, complete cds.//4.1e-17:374.64//AF041433  
 F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment.//8.1e-52:317:93//L40391  
 F-PLACE1007460//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//0.0019:280.64//AL031117  
 15 F-PLACE1007478//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 -complete genomic sequence, complete sequence.//2.5e-24:362.71//AC002302  
 F-PLACE1007484  
 F-PLACE1007488//Danio rerio faciogenital dysplasia protein (fgd) mRNA, complete cds.//3.8e-14:293.63//AF017370  
 F-PLACE1007507//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//4.6e-10:152.75//AL031311  
 20 F-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//3.6e-139:477:98//AC004231  
 F-PLACE1007524//Plasmodium falciparum microsatellite 14C sequence.//0.0055:395.59//AF015461  
 F-PLACE1007525//Trypanoplasma borelli mitochondrion cytochrome oxidase subunit 1 (cox1), cytochrome oxidase subunit 2 (cox2), and apocytochrome b (cytb) genes, complete cds, and complete 9S rRNA gene and partial 12S rRNA gene.//0.0013:550:58//U11682 F-PLACE1007537//H. sapiens CpG island DNA genomic MseI fragment, clone 198g6, reverse read cpg198g6.rt1a.//0.98:121:67//Z60280  
 25 F-PLACE1007544//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141.75//U31508  
 30 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds.//3.1e-69:733.71//AB014561  
 F-PLACE1007557//Drosophila yakuba mitochondrial DNA molecule.//0.022:393.61//X03240  
 F-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 545L17, WORKING DRAFT SEQUENCE.//3.6e-114:565.97//AL031665  
 F-PLACE1007598//CIT-HSP-2371G14.TF CIT-HSP Homo sapiens genomic clone 2371G14, genomic survey sequence.//2.0e-22:304.70//AQ111183  
 35 F-PLACE1007618//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//1.0:386.59//AC005245  
 F-PLACE1007621  
 F-PLACE1007632//Homo sapiens 12p13.3 PAC RPC15-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-88:276.96//AC006064  
 40 F-PLACE1007645//Bovine elastin mRNA, partial cds.//2.1e-07:110.79//M26132  
 F-PLACE1007649  
 F-PLACE1007677//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.2e-21:567.64//AL023755  
 45 F-PLACE1007688//Pseudorabies virus immediate-early gene.//2.2e-05:287.66//X15120  
 F-PLACE1007690//Caenorhabditis elegans cosmid R07G3.//0.40:122.70//U23452  
 F-PLACE1007697//Mus musculus LIM/homeobox (Lhx3) gene fragment.//0.85:117.71//L40483  
 F-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//0.0035:75.88//AL031662  
 50 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-147:709.97//AF061243  
 F-PLACE1007725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence.//1.0:510.58//AB005231  
 F-PLACE1007729//Human endogenous retrovirus HML6 proviral clone HML6p, putative leader region, gag, pro and pol pseudogenes.//4.8e-136:516.89//U86698  
 55 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//7.9e-155:728.98//AB014585  
 F-PLACE1007737//Homo sapiens clone DJ0847 O08, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.8e-22:806.60//AC005484  
 F-PLACE1007743//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING

DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504

F-PLACE1007746//HS\_2268\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=19 Row=N, genomic survey sequence.//0.10:171:63//AQ124780

F-PLACE1007791//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P6, WORKING DRAFT SEQUENCE.//0.63:241:58//AL031749

F-PLACE1007807//Homo sapiens chromosome 17, clone hRPK.879\_D\_6, complete sequence.//1.0e-120:743:87//AC005273

F-PLACE1007810//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.0e-113:739:86//AC003658

F-PLACE1007829//CIT-HSP-2383J22.TR CIT-HSP Homo sapiens genomic clone 2383J22, genomic survey sequence.//1.0e-47:254:97//AQ196438

F-PLACE1007843//F.rubripes GSS sequence, clone 162K02bC12, genomic survey sequence.//1.6e-10:148:72//AL006903

F-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//3.4e-177:844:98//AP000010

F-PLACE1007852//Mouse perlecan mRNA, complete cds.//8.5e-39:243:90//M77174

F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//3.9e-189:894:98//AB018309

F-PLACE1007866//CIT-HSP-2353D11.TF.1 CIT-HSP Homo sapiens genomic clone 2353D11, genomic survey sequence.//0.015:279:61//AQ263271

F-PLACE1007877

F-PLACE1007897

F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//2.3e-154:755:97//AB007956

F-PLACE1007946//Human chromosome Y cosmid 56B5 genomic sequence, WORKING DRAFT SEQUENCE.//1.1e-59:310:81//AC003097

F-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//2.1e-61:522:79//AC006157

F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//2.7e-171:813:98//AF084530

F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.5e-153:730:98//AF079529

F-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//3.4e-32:383:74//U13262

F-PLACE1007990//H.sapiens genomic DNA fragment (clone J31A212R).//6.6e-35:198:96//Z94758

F-PLACE1008000//Mus musculus vcll 3 mRNA, complete cds.//1.5e-118:708:88//AF087695

F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.4e-163:786:98//AC005628

F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//1.2e-95:625:84//L31840

F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequence.//0.016:165:65//Z35719

F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome 4p16.3.//4.0e-07:251:64//Z68883

F-PLACE1008095//RPCI11-21F19.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F19, genomic survey sequence.//1.5e-30:166:99//B85883

F-PLACE1008111//Aphidius picipes NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//7.5e-06:414:60//AF069163

F-PLACE1008122//S.cerevisiae chromosome XV reading frame ORF YOL125w.//0.046:477:59//Z74867

F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase Iix genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0068:446:57//AC004586

F-PLACE1008132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//3.6e-20:111:93//Z82199

F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.5e-88:866:73//D14849

F-PLACE1008181//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.//0.0033:727:56//AL034397

F-PLACE1008198//HS\_3073\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=11 Row=E, genomic survey sequence.//2.3e-12:94:92//AQ171450

F-PLACE1008201//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.5e-

- 162:791:97//AC005069  
F-PLACE1008209
- F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds.//0.65:174:66//M26332
- F-PLACE1008244//CIT-HSP-2337B4.TR CIT-HSP Homo sapiens genomic clone 2337B4, genomic survey sequence.//6.7e-28:165:95//AQ039317
- F-PLACE1008273//B.primigenius mRNA for coat protein gamma-cop.//2.8e-71:709:71//X92987
- F-PLACE1008275//D.discoideum actin A-13 gene, 5' flank.//0.12:131:64//M29123
- F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//0.011:96:73//AC005913
- F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//8.2e-86:672:77//AF078779
- F-PLACE1008329//HS\_2027\_A1\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=11 Row=E, genomic survey sequence.//8.7e-09:116:81//AQ244432
- F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//2.2e-141:670:98//AC005176
- F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-27:157:78//AC005000
- F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//1.1e-137:659:98//AB014579
- F-PLACE1008368//CIT-HSP-2311C9.TR CIT-HSP Homo sapiens genomic clone 2311C9, genomic survey sequence.//7.1e-08:398:60//AQ016352
- F-PLACE1008369//HS\_2251\_B1\_A02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=3 Row=B, genomic survey sequence.//2.1e-35:217:93//AQ066512
- F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//1.4e-11:403:64//AC005856
- F-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//3.7e-144:681:99//AL034417
- F-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07, HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//2.8e-45:257:98//AC004604
- F-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//4.3e-148:711:98//D86326
- F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.089:672:56//AC004688
- F-PLACE1008424
- F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//1.0e-88:331:84//AB020864
- F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//0.55:530:58//U62317
- F-PLACE1008437//CIT-HSP-2376H4.TR CIT-HSP Homo sapiens genomic clone 2376H4, genomic survey sequence.//3.3e-78:349:94//AQ112479
- F-PLACE1008455//HS\_2064\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=17 Row=J, genomic survey sequence.//4.7e-59:471:81//AQ246589
- F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//8.9e-43:307:73//AC004526
- F-PLACE1008465//CIT-HSP-2163F24.TR CIT-HSP Homo sapiens genomic clone 2163F24, genomic survey sequence.//8.9e-41:210:99//B90014
- F-PLACE1008488//Mus musculus mRNA for testis-specific protein kinase 1, complete cds.//0.00013:516:58//AB003494
- F-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//1.3e-161:778:98//AL031778
- F-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//1.1e-78:191:100//AF045555
- F-PLACE1008532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//3.8e-24:257:70//Z93097
- F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//1.0e-13:215:71//AC004997
- F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//0.66:263:64//Z99571
- F-PLACE1008584//Homo sapiens cosmid clone U39B3 from Xp22.1-22.2, complete sequence.//1.1e-19:315:68//U73023
- F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-173:812:98//AB018334

- F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.9e-09:198:71//AC005077
- F-PLACE1008625//Homo sapiens chromosome 5, PAC clone 45L14 (LBNL H91), complete sequence.//0.68:568:59//AC005373
- 5 F-PLACE1008626//HS\_3221\_A2\_F03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=K, genomic survey sequence.//1.7e-13:147:82//AQ180967
- F-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//9.7e-98:586:88//Y12836
- F-PLACE1008629//CIT-HSP-201214.TR CIT-HSP Homo sapiens genomic clone 201214, genomic survey sequence.//0.00085:203:66//B53732
- 10 F-PLACE1008630//Sequence 26 from Patent WO9517522.//9.7e-05:97:80//A45356
- F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP), complete cds.//1.4e-23:299:64//D38595
- F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//1.1e-133:622:99//AF04333
- 15 F-PLACE1008693//CIT-HSP-2346F2.TF CIT-HSP Homo sapiens genomic clone 2346F2, genomic survey sequence.//0.24:89:76//AQ060732
- F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//1.4e-94:420:97//AF038406
- F-PLACE1008715//CIT-HSP-2294K20.TR CIT-HSP Homo sapiens genomic clone 2294K20, genomic survey sequence.//2.1e-70:349:98//AQ007199
- 20 F-PLACE1008748//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.14:347:59//AC004260
- F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//7.9e-25:244:71//AC003037
- 25 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//4.5e-120:503:97//AF060543
- F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.00026:370:61//AF001549
- F-PLACE1008807//CIT-HSP-2334B19.TF CIT-HSP Homo sapiens genomic clone 2334B19, genomic survey sequence.//3.3e-08:220:65//AQ036643
- 30 F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//1.7e-120:470:97//AF030933
- F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//2.8e-87:504:89//AF032668
- F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-C4), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//4.0e-21:212:74//AL021920
- 35 F-PLACE1008854
- F-PLACE1008867//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//4.7e-77:477:84//Z82209
- F-PLACE1008887//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//3.4e-53:699:70//AC005539
- 40 F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds.//2.1e-06:164:68//M63660
- F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//6.4e-158:753:98//AB018308
- F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00013:400:63//AC002042
- 45 F-PLACE1008934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE.//7.4e-05:145:71//AL022312
- F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete cds.//4.3e-41:282:87//L15309
- F-PLACE1008947//Pseudorabies virus with upstream and downstream sequences.//5.9e-15:710:60//M34651
- F-PLACE1009020//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//1.9e-21:167:86//AQ253727
- 50 F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//4.1e-152:763:97//AL031117
- F-PLACE1009039//HS\_2034\_A2\_F08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, genomic survey sequence.//0.17:252:59//AQ230137
- 55 F-PLACE1009045//HS\_3185\_B2\_B03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=6 Row=D, genomic survey sequence.//1.9e-34:260:86//AQ172861
- F-PLACE1009048//Pig pituitary glycoprotein hormone alpha subunit gene, 5'flank and exon 1.//4.7e-70:463:80//D00766



- F-PLACE1009050//Homo sapiens 12q13.1 PAC RPC13-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.63:280:61//AC004241
- F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting protein X), complete CDS.//5.9e-113:725:85//AJ005073
- 5 F-PLACE1009090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1045J21, WORKING DRAFT SEQUENCE.//9.1e-27:222:84//AL021919
- F-PLACE1009091//Homo sapiens clone DJ0968116, complete sequence.//0.027:630:58//AC006016
- F-PLACE1009094
- F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cds.//2.1e-85:726:76//M36515
- 10 F-PLACE1009110
- F-PLACE1009111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 138B7, WORKING DRAFT SEQUENCE.//6.0e-12:362:64//Z98752
- F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//3.4e-138:671:97//AF035586
- 15 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds.//3.6e-23:718:59//D25215
- F-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* ,WORKING DRAFT SEQUENCE.//6.1e-142:684:98//AJ011929
- F-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//4.3e-36:227:77//AP000031
- 20 F-PLACE1009158//H.sapiens genomic sequence for ERCC2 gene 3'region involved in DNA excision repair.//1.0:173:60//X52222
- F-PLACE1009166
- F-PLACE1009172//Human BAC clone 7E17 from 12q, complete sequence.//4.0e-35:257:85//AC002070
- F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human BAC Library) complete sequence.//2.9e-19:288:72//AC004805
- 25 F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence.//0.053:388:60//AB008266
- F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxC1) mRNA, complete cds.//1.8e-50:317:89//AF061242
- 30 F-PLACE1009190//RPC11-81N5.TJ RPC11 Homo sapiens genomic clone R-81N5, genomic survey sequence.//0.91:114:67//AQ281881
- F-PLACE1009200//CITBI-E1-2509J16.TF CITBI-E1 Homo sapiens genomic clone 2509J16, genomic survey sequence.//2.8e-44:175:83//AQ262198
- F-PLACE1009230//H.sapiens gene for pregnancy specific beta-1 glycoprotein.//1.1e-106:495:88//X63203
- 35 F-PLACE1009246//HS\_3058\_B1\_A06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=11 Row=B, genomic survey sequence.//0.10:175:68//AQ185945
- F-PLACE1009298//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.8e-94:575:89//U47024
- F-PLACE1009308//Human clone mcag32 chromosome 7 CTG repeat region.//0.0017:350:62//U23862
- F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds.//3.0e-06:411:59//U83192
- 40 F-PLACE1009328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191P20, WORKING DRAFT SEQUENCE.//5.7e-138:830:86//AL034399
- F-PLACE1009335//Human (lambda) DNA for immunoglobulin light chain.//0.071:253:62//D87015
- F-PLACE1009338//RPC11-74N24 TV RPC11 Homo sapiens genomic clone R-74N24, genomic survey sequence.//2.4e-34:180:100//AQ268811
- 45 F-PLACE1009368
- F-PLACE1009375
- F-PLACE1009388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1014D13, WORKING DRAFT SEQUENCE.//2.0e-37:288:84//AL022311
- F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cds.//4.3e-78:730:74//M27878
- 50 F-PLACE1009404//SmD homolog [mice, liver, mRNA Partial, 199 nt].//0.16:95:71//S71494
- F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK\_142\_H\_19, complete sequence.//1.6e-150:701:99//AC005919
- F-PLACE1009434//Mus musculus clone OST431, genomic survey sequence.//2.9e-73:442:88//AF046700
- F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//0.012:582:56//AL022022
- 55 F-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds.//4.6e-21:146:93//AF012872
- F-PLACE1009459//Mus musculus clone OST9217, genomic survey sequence.//2.9e-31:264:81//AF046660

F-PLACE1009468//Sequence 1 from patent US 5580968.//1.9e-83:567:84//30536  
 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//1.9e-142:704:97//AC004531  
 F-PLACE1009477//Human 11p14.3 PAC clone pDJ939m16, complete sequence.//2.2e-09:235:68//AC004601  
 5 F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.9e-83:171:92//U91321  
 F-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Armo, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-69:175:92//Z94160  
 10 F-PLACE1009539//Mus musculus synaptotagmin 2 isoform alpha mRNA, complete cds.//7.0e-26:237:78//AF041862  
 F-PLACE1009542//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//3.1e-10:126:79//AL031587  
 15 F-PLACE1009571//RPC11-60K12.TK RPC11 Homo sapiens genomic clone R-60K12, genomic survey sequence.//1.4e-05:68:91//AQ195869  
 F-PLACE1009581  
 F-PLACE1009595//Homo sapiens chromosome 5, P1 clone 1029A7 (LBNL H15), complete sequence.//6.6e-19:309:70//AC003959  
 20 F-PLACE1009596//Rattus norvegicus platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta) gene, complete cds.//9.0e-09:485:59//AF016049  
 F-PLACE1009607//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//4.9e-43:714:66//Z83824  
 25 F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.017:655:57//AC004157  
 F-PLACE1009621  
 F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 791 Col=16 Row=J, genomic survey sequence.//2.7e-15:100:98//B33248  
 30 F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.63:130:67//AC005308  
 F-PLACE1009639//S.pombe chromosome II cosmid c24E9.//0.86:509:58//AL021816  
 F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.4e-171:816:98//AB011159  
 35 F-PLACE1009665//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.4e-67:437:87//AC005177  
 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.5e-147:701:98//AF062534  
 F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//1.5e-98:228:100//AC006011  
 F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//2.2e-130:736:91//AC000109  
 40 F-PLACE1009731//M.musculus mRNA for immunity associated protein 38.//1.1e-13:311:64//Y08026  
 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//4.2e-125:602:98//AF046024  
 F-PLACE1009794  
 F-PLACE1009798//Hnman DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.3e-73:271:84//AL030996  
 45 F-PLACE1009845  
 F-PLACE1009861//B.taurus cathepsin B mRNA, 3' end.//0.00023:147:65//M64620  
 F-PLACE1009879//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.//4.9e-27:725:63//AL034397  
 50 F-PLACE1009886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SEQUENCE.//8.2e-12:135:82//AL031427  
 F-PLACE1009888//F14G3-T7 IGF Arabidopsis thaliana genomic clone F14G3, genomic survey sequence.//0.0044:232:60//AQ251431  
 55 F-PLACE1009908//S.pombe chromosome I cosmid c3F10.//1.5e-19:559:59//Z69369  
 F-PLACE1009921//Homo sapiens cosmid clone HDAB (15149) insert DNA, complete cosmid.//5.9e-48:304:87//M63005  
 F-PLACE1009924//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-201104, WORKING DRAFT SE-

QUENCE, 4 unordered pieces.//2.4e-51:481:78//AC004529

F-PLACE1009925//nbxb0027C22r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0027C22r, genomic survey sequence.//0.98:220:67//AQ272066

F-PLACE1009935//Sequence 16 from patent US 552281.//0.030:152:67//I25655

5 F-PLACE1009947//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-12:322:67//AC006026

F-PLACE1009971

F-PLACE1009992//HS\_3178\_B1\_F04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=7 Row=L, genomic survey sequence.//4.9e-23:142:95//AQ150311

10 F-PLACE1009995//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00019:231:64//Z81029

F-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//7.9e-87:552:80//U48288

F-PLACE1010023

15 F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//6.9e-101:181:98//AL031775

F-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//2.3e-136:689:95//X84692

20 F-PLACE1010069//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING DRAFT SEQUENCE.//0.0090:383:60//Z95114

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//1.8e-166:792:98//AF065482

F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds.//7.5e-13:203:77//D25540

F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-152:727:98//AB007925

25 F-PLACE1010089//HS\_3111\_A1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3111 Col=15 Row=L, genomic survey sequence.//4.8e-07:124:78//AQ101268

F-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//1.2e-108:700:85//X64411

F-PLACE1010102//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-07:476:60//AC005506

30 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//3.6e-25:726:60//AF095959

F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome Xq22.//6.5e-25:488:63//Z93928

F-PLACE1010134//S.pombe chromosome I cosmid c29B12.//1.9e-13:238:67//Z99164

F-PLACE1010148//Homo sapiens partial human cDNA (660 bp).//4.8e-83:409:98//AJ222636

35 F-PLACE1010152//CIT-HSP-2381F24.TF CIT-HSP Homo sapiens genomic clone 2381F24, genomic survey sequence.//1.5e-28:163:98//AQ196757

F-PLACE1010181//Homo sapiens PAC clone DJ1139101 from Xq23, complete sequence.//2.4e-15:197:72//AC004973

F-PLACE1010194//Ictalurus punctatus tumor suppressor p53 mRNA, complete cds.//3.0e-14:181:74//AF074967

F-PLACE1010202//Homo sapiens mRNA for MBNL protein.//1.2e-27:509:66//Y13829

40 F-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SEQUENCE.//2.3e-101:194:95//AL033377

F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds.//5.8e-145:693:97//AB007917

F-PLACE1010270//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence; WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.1e-05:347:60//AC004710

45 F-PLACE1010274//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00040:231:64//Z81029

F-PLACE1010293//Homo sapiens chromosome 2 PAC RPC13-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.5e-25:344:70//AC004464

F-PLACE1010310//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//3.5e-10:185:67//AL031005

50 F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.010:524:58//Z84468

F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP Homo sapiens genomic clone 2335J21, genomic survey sequence.//9.1e-90:448:97//AQ041837

F-PLACE1010329//Apis mellifera ligustica complete mitochondrial genome.//2.8e-08:384:64//L06178

55 F-PLACE1010341//HS-1047-A2-C04-MR.abl CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=8 Row=E, genomic survey sequence.//4.1e-21:141:92//B38252

F-PLACE1010362//Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.//0.94:398:57//AL022121

F-PLACE1010364//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y102G3, WORKING DRAFT SEQUENCE.//0.11:404:56//AL020985

F-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//0.066:88:76//AC004675

5 F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP Homo sapiens genomic clone 2367K17, genomic survey sequence.//2.4e-71:454:88//AQ076825

F-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//7.5e-134:722:93//AF003927

F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//2.2e-150:702:99//AF039081

F-PLACE1010492

10 F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq28.//0.022:405:60//U82695

F-PLACE1010529//Sequence 1 from patent US 5776717.//2.9e-145:684:98//AR016417

F-PLACE1010547//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.0:283:61//AL031677

15 F-PLACE1010562//RPC111-651.6.TK RPC111 Homo sapiens genomic clone R-651.6, genomic survey sequence.//0.017:216:67//AQ200831

F-PLACE1010579//Homo sapiens full-length insert cDNA Y123D12.//3.9e-19:147:89//AF075014

F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//6.4e-96:559:89//L25125

F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds.//3.1e-146:707:97//AF045186

20 F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.045:454:59//AC005308

F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence.//9.1e-07:378:60//AL034558

F-PLACE1010624//Streptomyces coelicolor cosmid 5A7.//1.4e-05:518:61//AL031107

25 F-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.0e-137:675:97//AC004846

F-PLACE1010629//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//2.5e-17:187:80//AC004682

F-PLACE1010630//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence.//0.21:159:64//AB016872

30 F-PLACE1010631//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-144:720:97//AC005069

F-PLACE1010661

F-PLACE1010662//Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project).//0.90:257:61//AL021960

35 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds.//3.3e-73:697:74//U35376

F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.010:447:59//AC004583

40 F-PLACE1010720//Mouse TPA-induced T1S1 mRNA.//2.0e-86:535:88//X14678

F-PLACE1010739//HS\_2013\_B2\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=20 Row=D, genomic survey sequence.//5.7e-87:435:97//AQ235864

F-PLACE1010743//R.norvegicus mRNA for myr5.//1.7e-87:582:85//X77609

F-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//4.7e-45:235:99//AC005921

45 F-PLACE1010771//M.musculus HCNGP mRNA.//1.6e-135:801:88//X68061

F-PLACE1010786//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-15, complete sequence.//0.35:334:60//AL010221

F-PLACE1010800//RPC111-79H17.TV RPC111 Homo sapiens genomic clone R-79H17, genomic survey sequence.//5.8e-18:168:82//AQ284252

50 F-PLACE1010802//Human Chromosome X clone bWXD531, complete sequence.//1.6e-30:693:63//AC004384

F-PLACE1010811//RPC111-51N5.TK RPC111 Homo sapiens genomic clone R-51N5, genomic survey sequence.//8.3e-11:142:78//AQ052380

F-PLACE1010833//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467K16, WORKING DRAFT SEQUENCE.//7.3e-40:147:88//AL031283

55 F-PLACE1010856//M.musculus mRNA for utrophin.//7.3e-17:150:86//Y12229

F-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.4e-94:422:95//AB020868

- F-PLACE1010870//M.musculus mRNA for ZT3 zinc finger factor.//1.3e-93:530:90//Z67747  
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.1e-147:694:98//AB011182  
 F-PLACE1010891  
 F-PLACE1010896//Mouse BAC mbac20 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//3.9e-26:394:68//AC003997  
 F-PLACE1010900  
 F-PLACE1010916//HS\_2242\_A1\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=7 Row=E, genomic survey sequence.//1.0e-78:391:97//AQ146687  
 F-PLACE1010917  
 F-PLACE1010925//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.11:629:56//AC004688  
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.5e-138:653:98//AB011126  
 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds.//5.6e-90:437:98//AF064243  
 F-PLACE1010944//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-09:208:68//AF086247  
 F-PLACE1010947  
 F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP Homo sapiens genomic clone 2283D9, genomic survey sequence.//2.1e-29:190:91//B98965  
 F-PLACE1010960//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//0.00074:421:60//AL010226  
 F-PLACE1010965//CIT-HSP-2386K24:TF.1 CIT-HSP Homo sapiens genomic clone 2386K24, genomic survey sequence.//1.8e-84:412:99//AQ240696  
 F-PLACE1011026//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete sequence.//0.00037:257:64//AL008972  
 F-PLACE1011032//Homo sapiens chromosome 5, BAC clone 118L13 (LBNL H176), complete sequence.//3.8e-06:315:65//AC005348  
 F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds.//1.5e-56:286:98//U07669  
 F-PLACE1011046//Rat phospholipase C-1 mRNA, complete cds.//1.3e-24:278:76//M20636  
 F-PLACE1011054//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 98L123, WORKING DRAFT SEQUENCE.//3.8e-27:196:84//AL031686  
 F-PLACE1011056//Ovis aries bactinecin 11 (Bac11) gene, exon 4, and complete cds.//5.4e-06:182:67//U77049  
 F-PLACE1011057//protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA, 3255 nt].//3.2e-31:169:100//S75548  
 F-PLACE1011090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//5.1e-80:479:89//AL031687  
 F-PLACE1011109//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//2.3e-24:192:84//L14684  
 F-PLACE1011114//S.cerevisiae chromosome XI reading frame ORF YKR024c.//1.4e-14:346:60//Z28249  
 F-PLACE1011133//T7E9-T7.1 TAMU Arabidopsis thaliana genomic clone T7E9, genomic survey sequence.//0.010:345:60//B19698  
 F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00013:95:76//AQ109305  
 F-PLACE1011160//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.7e-111:692:87//AC004893  
 F-PLACE1011165//H.sapiens galactokinase (GK2) mRNA, complete cds.//8.4e-31:194:92//M84443  
 F-PLACE1011185//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-249B10, complete sequence.//3.1e-43:447:72//AC002288  
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds.//3.3e-124:584:99//AF038664  
 F-PLACE1011214//HS\_2046\_A2\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2046 Col=2 Row=C, genomic survey sequence.//2.0e-39:346:81//AQ305965  
 F-PLACE1011219  
 F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 Homo sapiens genomic clone 2513F18, genomic survey sequence.//2.4e-20:119:100//AQ279801  
 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds.//4.4e-146:675:99//AB011101  
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.7e-42:212:84//AC005014  
 F-PLACE1011273//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y37D8, WORKING DRAFT SEQUENCE.//1.0:214:60//Z92819

F-PLACE1011291//RPCI11-16P9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-16P9, genomic survey sequence.//8.0e-08:66.98//B81770

F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LANL), complete sequence.//0.027:135:67//AC004647

5 F-PLACE1011310//H.sapiens CpG island DNA genomic MseI fragment, clone 53c10, reverse read cpg53c10.rt1b.//1.4e-05:57:100//Z61496

F-PLACE1011325//Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds.//0.077:193:60//O2290

10 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//3.1e-150:699:99//AF102265

F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388\_F\_14, complete sequence.//2.4e-38:186:83//AC005375

F-PLACE1011371//Mus musculus PK-120 precursor (lith-4) mRNA, complete cds.//6.0e-35:689:63//AF023919

F-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.0e-88:584:86//AJ010310

15 F-PLACE1011399//paramedum species 7,325 mt dna dimer: replication init. region.//0.00011:255:63//K00919

F-PLACE1011419//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//0.067:337:62//AJ006996

F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.6e-157:743:98//AB011102

F-PLACE1011452//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*. WORKING DRAFT SEQUENCE.//1.1e-53:557:73//AJ011929

20 F-PLACE1011465//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//3.5e-71:498:80//AC004605

F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//4.8e-151:703:99//AB018255

F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//5.2e-145:675:99//AF065482

F-PLACE1011492//Ray (T.californica) acetylcholine receptor beta-subunit mRNA.//1.0:448:59//J00964

25 F-PLACE1011503

F-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//3.8e-147:692:99//AC004968

F-PLACE1011563//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//0.00036:296:61//X83546

F-PLACE1011567//Homo sapiens PAC clone DJ1164K10 from 7p21-p22, complete sequence.//1.1e-38:315:82//AC004984

30 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds.//1.3e-65:268:86//AF054180

F-PLACE1011586//Homo sapiens chromosome 17, clone HRP890E16, complete sequence.//2.0e-82:188:96//AC004477

35 F-PLACE1011635//Homo sapiens chromosome 17, clone hRPK.214\_O\_1, complete sequence.//1.8e-153:752:97//AC005224

F-PLACE1011641//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//4.8e-05:190:67//AE000660

F-PLACE1011643//Alcaligenes eutrophus phaP gene.//0.16:466:59//X85729

40 F-PLACE1011646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING DRAFT SEQUENCE.//9.1e-19:156:76//AL033383

F-PLACE1011649

F-PLACE1011650//Homo sapiens retinol dehydrogenase gene, complete cds.//6.4e-09:172:74//AF037062

F-PLACE1011664//D.melanogaster crn mRNA.//1.1e-52:650:68//X58374

45 F-PLACE1011675//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.11:443:58//AC005507

F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//0.31:127:71//AL008719

50 F-PLACE1011719//Human BAC clone RG369K23 from 7q31, complete sequence.//4.6e-52:461:77//AC002487

F-PLACE1011725

F-PLACE1011729//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:320:62//AC004737

F-PLACE1011749//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00031:544:59//AC004157

55 F-PLACE1011762//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-115:682:90//AC004003

F-PLACE1011778//RPCI11-22D17.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22D17, genomic survey sequence.//2.7e-114:611:93//AQ008944

F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP Homo sapiens genomic clone 2317N1, genomic survey sequence.//2.3e-17:120:94//AQ042330

F-PLACE1011858//Gallus domesticus filamin mRNA, complete cds.//4.1e-24:565:64//U00147

5 F-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312, complete sequence.//2.5e-141:678:98//AC004478

F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds.//1.6e-108:526:98//AB011152

F-PLACE1011891//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING DRAFT SEQUENCE.//0.0014:330:62//AL021392

10 F-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//1.4e-89:678:82//U61969

F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.069:246:61//U81400

F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//1.2e-138:664:98//AF059617

F-PLACE1011962//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//2.4e-07:154:74//AQ175369

15 F-PLACE1011964//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//3.7e-22:369:69//AL023799

F-PLACE1011982//HS-1041-A1-B01-MR. abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=1 Row=C, genomic survey sequence.//0.44:309:58//B36529

20 F-PLACE1011995//Homo sapiens Xq28 BAC RPC11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//8.8e-53:687:71//AC006054

F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.2e-146:690:98//AB018256

F-PLACE20000033//Homo sapiens chromosome 17, clone hRPC.318\_A\_15, complete sequence.//1.7e-62:293:88//AC005837

25 F-PLACE2000006//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//1.4e-116:261:91//AC006057

F-PLACE2000007

F-PLACE2000011//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//5.2e-102:489:99//AC005578

F-PLACE2000014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//0.0095:307:62//AL022574

30 F-PLACE2000015//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.0e-36:316:81//AC005069

F-PLACE2000017//HS\_3042\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=15 Row=K, genomic survey sequence.//1.0:184:61//AQ098074

35 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//4.6e-84:844:72//AF082556

F-PLACE2000030//Human Chromosome 11 Cosmid cSRL16b6, complete sequence.//2.3e-22:233:77//U73638

F-PLACE2000033//C.capitata mRNA for chorion protein s18.//0.0019:342:62//Y08913

40 F-PLACE2000034//Rattus norvegicus transmembrane receptor Robo1 mRNA, complete cds.//2.8e-13:335:63//AF041082

F-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//7.7e-84:489:90//L08505

F-PLACE2000047//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.0e-28:327:76//U95626

45 F-PLACE2000050//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.1e-32:527:68//AC003101

F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP Homo sapiens genomic clone 2346L20, genomic survey sequence.//1.1e-05:89:83//AQ059010

50 F-PLACE2000062//Human membrane-associated lectin type-C mRNA.//9.0e-113:662:86//M98457

F-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//2.2e-133:631:98//AF027219

F-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-16:119:93//AC005910

55 F-PLACE2000100//HS\_3184\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=11 Row=G, genomic survey sequence.//1.5e-80:409:97//AQ150004

F-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//1.0e-172:830:98//AL031848

F-PLACE2000111//Homo sapiens DNA, trinucleotide repeats region.//1.0:200:64//AB018491

F-PLACE2000115

- F-PLACE2000124//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//6.2e-43:362.80//AC004531
- F-PLACE2000132//RPCI11-79F15.TV RPCI11 Homo sapiens genomic clone R-79F15, genomic survey sequence.//5.4e-35:206.94//AQ284166
- 5 F-PLACE2000136//Human BAC clone 7E17 from 12q, complete sequence.//2.7e-12:814.59//AC002070
- F-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//3.6e-165:799.97//AL020995
- F-PLACE2000164//Canine histamine H2 receptor gene, complete cds.//0.10:392:56//M32701
- F-PLACE2000170
- 10 F-PLACE2000172//Homo sapiens PAC clone DJ0811017 from 7q21-22, complete sequence.//3.9e-91:552.88//AC006005
- F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence.//0.98:201:64//AC004032
- F-PLACE2000187
- 15 F-PLACE2000216
- F-PLACE2000223//RPCI11-12L17.TP RPCI-11 Homo sapiens genomic clone RPCI-11-12L17, genomic survey sequence.//0.00039:325.58//B75888
- F-PLACE2000235//Human Chromosome 16 BAC clone CIT987SK-254P9, complete sequence.//7.5e-55:237.78//AC003003
- 20 F-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//2.4e-92:236.94//AC005902
- F-PLACE2000264//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudo-genes similar to ribosomal protein, ESTs, GSSs, complete sequence.//1.4e-32:331.78//AL031577
- F-PLACE2000274//Anthracidaris crassispina mRNA for B2HC, partial cds.//8.5e-48:765.66//AB012308
- 25 F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//8.3e-08:662.58//US2064
- F-PLACE2000305//Homo sapiens clone DJ1129L24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.4e-08:95.81//AC006021
- F-PLACE2000317//HS\_3183\_B2\_F05\_MR CIT Approved Human Genomic Sperm-Library D Homo sapiens genomic clone Plate=3183 Col=10 Row=L, genomic survey sequence.//2.5e-71:346.99//AQ172747
- 30 F-PLACE2000335//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.7e-14:402.65//AC004952
- F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.//4.5e-77:555.82//AF026554
- 35 F-PLACE2000342//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial cds.//1.6e-14:259.71//U66829
- F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmids R32543., and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//6.0e-34:376.74//AC003006
- F-PLACE2000359//RPCI11-23J20.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23J20, genomic survey sequence.//8.4e-21:288.69//AQ013849
- 40 F-PLACE2000366//Human Tigger1 transposable element, complete consensus sequence.//5.0e-114:692.80//U49973
- F-PLACE2000371//Homo sapiens 12p13.3 PAC RPCI1-29K11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.38:356.58//AC005182
- 45 F-PLACE2000373//RPCI11-49C18.TJ RPCI11 Homo sapiens genomic clone R-49C18, genomic survey sequence.//0.064:132.68//AQ051776
- F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.6e-130:776.88//AC003658
- F-PLACE2000394//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//5.4e-113:808.83//AC005909
- 50 F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosophila 'period' gene.//0.87:286.63//X06967
- F-PLACE2000399
- F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence.//2.9e-59:532.68//Z36238
- 55 F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds.//0.44:553.56//U89984
- F-PLACE2000419//Human adenosine deaminase (ADA) gene, complete cds.//1.4e-56:303.86//M13792
- F-PLACE2000425//HS\_3047\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-



nomic clone Plate=3047 Col=9 Row=O, genomic survey sequence.//2.8e-42:224:97//AQ126949  
 F-PLACE2000427  
 F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//1.1e-19:363:67//AC005821  
 5 F-PLACE2000435//HS\_3036\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=L, genomic survey sequence.//3.1e-06:184:66//AQ096999  
 F-PLACE2000438//Caenorhabditis elegans cosmid Y45F10D, complete sequence.//4.6e-23:550:62//AL021492  
 F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//1.0e-78:604:80//AC006025  
 10 F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//8.2e-05:330:63//AC002300  
 F-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.7e-168:816:97//AC005740  
 15 F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//4.3e-33:296:79//AC002037  
 F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//3.4e-59:598:74//AC005057  
 F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds.//7.6e-49:361:84//U81602  
 F-PLACE3000009//Human placenta (Diff48) mRNA, complete cds.//3.0e-58:713:69//U49187  
 20 F-PLACE3000020//R.norvegicus type III adenylyl cyclase mRNA, complete cds.//6.1e-103:600:89//M55075  
 F-PLACE3000029  
 F-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//4.4e-115:718:86//Y17267  
 F-PLACE3000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.8e-17:250:74//AC005368  
 25 F-PLACE3000103//Caenorhabditis elegans cosmid C13F10.//4.6e-07:408:61//U97006  
 F-PLACE3000119//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.5e-58:291:86//AC004670  
 F-PLACE3000121//Rattus norvegicus rsec15 mRNA, complete cds.//8.1e-81:837:71//AF032668  
 F-PLACE3000124//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//1.8e-48:330:79//AC005695  
 30 F-PLACE3000136  
 F-PLACE3000142//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//0.011:294:62//AL033520  
 F-PLACE3000145//Gallus gallus tensin mRNA, 3' end.//6.9e-52:659:68//L06662  
 35 F-PLACE3000147//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//5.1e-37:305:81//AL031053  
 F-PLACE3000148//Homo sapiens chromosome Y, clone 47511, complete sequence.//4.7e-32:766:63//AC004474  
 F-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//7.4e-173:822:98//AC005277  
 40 F-PLACE3000156//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-81:783:74//AC003682  
 F-PLACE3000157  
 F-PLACE3000158//, complete sequence.//1.0e-180:845:97//AC005500  
 F-PLACE3000160//CIT978SK-152K7.TV CIT978SK Homo sapiens genomic clone 152K7, genomic survey sequence.//0.080:259:59//B50878  
 45 F-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//9.8e-158:749:98//AC006130  
 F-PLACE3000194  
 F-PLACE3000197//F.rubripes GSS sequence, clone 075N04bB7, genomic survey sequence.//1.4e-08:164:68//AL003352  
 50 F-PLACE3000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//0.0019:277:58//Z82207  
 F-PLACE3000207//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//6.6e-21:312:67//AC005013  
 55 F-PLACE3000208//Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds.//1.0:279:61//L23982  
 F-PLACE3000218//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//9.3e-43:383:79//AC004086

F-PLACE3000220//RPCI11-54B4, TV RPCI11 Homo sapiens genomic clone R-54B4, genomic survey sequence.//2.4e-36:381:76//AQ082056

F-PLACE3000221//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-135:721:91//AC005231

5 F-PLACE3000226

F-PLACE3000230//Homo sapiens c1cr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//3.3e-80:498:78//U95626

F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs and genomic marker DXS8032, complete sequence.//2.6e-54:254:92//Z98046

10 F-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.4e-139:850:86//X80169

F-PLACE3000254//Atelinae herpesvirus 3 complete genome.//1.3e-10:399:61//AF083424

F-PLACE3000271//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//1.8e-21:350:68//AF001548

15 F-PLACE3000276//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//5.7e-45:376:81//AQ231147

F-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//1.6e-138:650:99//AC005328

20 F-PLACE3000310

F-PLACE3000322//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-41:379:77//AL034379

F-PLACE3000322//Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complete sequence.//3.3e-35:419:68//AC005822

25 F-PLACE3000331//CIT-HSP-2347D24, TR CIT-HSP Homo sapiens genomic clone 2347D24, genomic survey sequence.//2.7e-20:119:99//AQ061543

F-PLACE3000339//Rhodobacter sphaeroides magnesium chelatase subunits Bchl (bchl) and BchD (bchD) genes, complete cds; and BchO (bchO) gene, partial cds.//0.99:310:58//AF017642

F-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//7.5e-159:752:98//AC006055

30 F-PLACE3000350//Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds.//2.3e-107:592:92//AF084205

F-PLACE3000352//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//2.1e-37:480:70//Z83732

35 F-PLACE3000353

F-PLACE3000362//Homo sapiens chromosome 17, clone hRPK.215\_P\_18, complete sequence.//0.00011:373:60//AC005969

F-PLACE3000363

F-PLACE3000365//Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.//0.074:279:61//Z81007

40 F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-118:653:92//Z92545

F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//2.2e-25:288:71//AC005154

45 F-PLACE3000399//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//2.3e-69:303:86//Z97630

F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence.//0.0063:435:58//Z93239

F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.8e-25:292:73//AC006023

50 F-PLACE3000402//RPCI11-20D6, TVB RPCI-11 Homo sapiens genomic clone RPCI-11-20D6, genomic survey sequence.//1.1e-10:154:74//AQ008761

F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.9e-41:515:72//AC005701

55 F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone cSRL-179E11, genomic survey sequence.//2.8e-91:540:89//B03443

F-PLACE3000413

F-PLACE3000416//F19L8-Sp6 IGF Arabidopsis thaliana genomic clone F19L8, genomic survey sequence.//

0.0018:664:55//B11305

F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//1.1e-16:284:70//AL022719

F-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//3.6e-146:732:96//AL031284

F-PLACE3000475//HS\_2164\_A2\_H10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=20 Row=O, genomic survey sequence.//1.5e-07:159:71//AQ132983

F-PLACE3000477//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//2.9e-11:213:70//Z83843

F-PLACE400009//Sequence 93 from patent US 5616500.//9.9e-08:692:60//I39845

F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//1.1e-116:331:100//AB018352

F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.0e-05:244:63//AC004131

F-PLACE4000049//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//1.2e-37:385:74//AC005926

F-PLACE4000052//M.musculus abci mRNA.//1.5e-110:671:88//X75926

F-PLACE4000063

F-PLACE4000089//M.musculus BOX DNA for regulatory element and promoter region related to EC cell differentiation.//3.7e-12:114:85//X74311

F-PLACE4000093//CIT-HSP-2380K5.TF CIT-HSP Homo sapiens genomic clone 2380K5, genomic survey sequence.//0.11:245:60//AQ108342

F-PLACE4000100//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//2.9e-19:384:65//AL031848

F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds.//1.2e-145:684:99//AB007931

F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//3.7e-62:541:78//AF091234

F-PLACE4000129

F-PLACE4000131//HS\_3139\_B2\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence.//2.3e-14:221:70//AQ183207

F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.2-23. Contains part of the COL4A5 gene for Collagen Alpha 5(V) Chain Precursor. Contains GSSs, complete sequence.//0.28:412:58//AL031622

F-PLACE4000156//Human zinc finger protein ZNF136.//7.2e-88:764:76//U09367

F-PLACE4000192

F-PLACE4000211

F-PLACE4000222//344J1.TVB CIT978SKA1 Homo sapiens genomic clone A-344J01, genomic survey sequence.//1.2e-14:177:76//B17158

F-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//9.8e-116:662:89//AF030430

F-PLACE4000233//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//5.2e-54:363:70//AC003973

F-PLACE4000247

F-PLACE4000250//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.0053:229:65//AC004673

F-PLACE4000252

F-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//2.0e-25:191:87//Z70200

F-PLACE4000261//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.6e-23:314:71//AF084259

F-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//5.5e-122:734:88//AF032667

F-PLACE4000270

F-PLACE4000300

F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete cds.//1.4e-21:135:96//L34075

F-PLACE4000323//HS\_2165\_B1\_B02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence.//4.3e-08:170:71//AQ125036

F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//2.8e-06:311:63//M10296

F-PLACE4000344//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.014:252:60//AE001401

F-PLACE4000367

- F-PLACE4000369  
F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 2350B9, genomic survey sequence.//9.2e-46:282:86//AQ062661  
F-PLACE4000387//CIT-HSP-2382F11.TR CIT-HSP Homo sapiens genomic clone 2382F11, genomic survey sequence.//0.96:102:70//AQ080649
- 5 F-PLACE4000392//Rattus norvegicus polymorphic marker D20UJA1 sequence.//1.2e-05:222:68//AF054088  
F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds.//9.6e-46:605:71//AB014540  
F-PLACE4000411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984
- 10 F-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//4.0e-44:263:92//Z70200  
F-PLACE4000445//HS-1053-B1-D02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=3 Row=H, genomic survey sequence.//0.070:47:100//B41346  
F-PLACE4000450  
F-PLACE4000465//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//2.3e-07:273:65//AC005065
- 15 F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//4.1e-34:351:70//AC005821  
F-PLACE4000489//HS\_3012\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3012 Col=9 Row=N, genomic survey sequence.//2.0e-36:220:92//AQ095537
- 20 F-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC005865  
F-PLACE4000521//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* ,WORKING DRAFT SEQUENCE.//1.6e-163:770:98//AJ011929  
F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch2-C, partial cds.//4.0e-124:686:90//U47645
- 25 F-PLACE4000548  
F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:435:59//X12747  
F-PLACE4000581  
F-PLACE4000590//Homo sapiens chromosome Y, clone 47511, complete sequence.//3.6e-20:747:59//AC004474
- 30 F-PLACE4000593//Caenorhabditis elegans cosmid F25D7, complete sequence.//5.6e-16:326:65//Z78418  
F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.7e-163:785:97//AC005281  
F-PLACE4000638//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.7e-74:707:74//AC006039
- 35 F-PLACE4000650  
F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267  
F-PLACE4000670//Sequence 13 from patent US 5712381.//1.0:311:59//I82816  
F-SKNMC1000011//Gallus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577  
F-SKNMC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59//M25312
- 40 F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.6e-147:706:98//AB014554  
F-SKNMC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//AR020616  
F-SKNMC1000091//Human NK homeobox protein (Nkx6.1) gene, exon 1.//0.0018:375:60//U66797  
F-THYRO1000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//6.6e-97:542:84//U91561
- 45 F-THYRO1000026//Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence.//3.5e-46:353:82//AL008637  
F-THYRO1000034//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353
- 50 F-THYRO1000035//Human Chromosome X clone bWDX187, complete sequence.//1.2e-39:303:83//AC004383  
F-THYRO1000040  
F-THYRO1000070//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//1.3e-05:613:58//AC005383  
F-THYRO1000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.7e-84:722:77//AB014557
- 55 F-THYRO1000085  
F-THYRO1000092//CIT-HSP-2013L16.TFB CIT-HSP Homo sapiens genomic clone 2013L16, genomic survey sequence.//0.31:186:61//B60606  
F-THYRO1000107

F-THYRO1000111//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:690:87//Z93403

F-THYRO1000132//Rattus norvegicus CTD-binding SIR-like protein rA8 mRNA, complete cds.//1.4e-127:816:85//U49055

5 F-THYRO1000124//H.sapiens CpG island DNA genomic MseI fragment, clone 72a7, forward read cp972a7.ft1a.//9.5e-26:169:94//Z62724

F-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e-154:732:98//AF087142

F-THYRO1000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//3.7e-39:315:82//AC002096

10 F-THYRO1000156//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.2e-21:335:71//AL023574

F-THYRO1000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-AA-218C7, complete sequence.//8.4e-52:301:88//AC002331

F-THYRO1000173//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//4.0e-89:821:74//M62419

15 F-THYRO1000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207

F-THYRO1000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57//X06214

F-THYRO1000190//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//0.38:184:64//AC005746

20 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.5e-174:805:99//AJ005698

F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.2e-86:616:84//AB014552

F-THYRO1000206//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.51:331:63//AQ099134

F-THYRO1000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC004157

25 F-THYRO1000241//Gallus gallus genome fragment with pentamer tandem repeats.//0.43:191:62//X00186

F-THYRO1000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156

F-THYRO1000253//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//AC006055

30 F-THYRO1000270

F-THYRO1000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664

F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179:848:98//AB016068

F-THYRO1000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complete cds.//1.0e-44:331:83//AF036894

35 F-THYRO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//5.7e-112:641:91//L35233

F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.2e-162:763:98//AB018333

F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//2.2e-32:177:84//U29091

40 F-THYRO1000368//Caenorhabditis elegans cosmid W09G3, complete sequence.//0.97:206:60//Z82080

F-THYRO1000381//Arthrobacter sp. gicl gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668

F-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:98//AC006019

F-THYRO1000394//HS\_2061\_A2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey sequence.//1.6e-29:202:91//AQ247672

45 F-THYRO1000395//Drosophila melanogaster ring canal protein and ORF2 mRNA, complete cds.//4.3e-15:512:59//L08483

F-THYRO1000401 3.2e-116:504:80//AF051908

F-THYRO1000438//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-09:539:59//AC005308

50 F-THYRO1000452//RPCI11-1C19.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1C19, genomic survey sequence.//0.27:132:64//B49573

F-THYRO1000471//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.3e-38:332:81//AC005229

55 F-THYRO1000484//Homo sapiens BAC378, complete sequence.//2.2e-37:254:76//U85196

F-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//6.3e-130:327:97//AC005740

F-THYRO1000501//H.sapiens Staf50 mRNA.//9.8e-74:615:77//X82200

F-THYRO1000502//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//0.076:380:59//Z94056

F-THYRO 1000505

5 F-THYRO1000558//Human PAC clone 127H14 from 12q, complete sequence.//2.4e-27:412:69//AC002563

F-THYRO1000569//HS\_2178\_B2\_E03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=6 Row=J, genomic survey sequence.//1.9e-27:326:74//AQ307499

F-THYRO1000570

10 F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//7.4e-167:808:97//AF075587

F-THYRO1000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//0.99:280:61//U91323

F-THYRO1000602//HS\_3037\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence.//1.2e-05:109:75//AQ097057

15 F-THYRO1000605//Homo sapiens map Zp11.2; 83cM from GATA85A06 repeat region, complete sequence.//1.0:84:70//AF067777

F-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//3.4e-174:820:98//AC005546

F-THYRO1000637//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//3.6e-38:289:84//AL024474

20 F-THYRO1000641//Plasmodium falciparum MAL3P7, complete sequence.//6.8e-07:540:56//AL034559

F-THYRO1000658//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//1.1e-08:468:84//AC005696

F-THYRO1000662//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0072:141:70//AB016874

25 F-THYRO1000666//Mus musculus mRNA for motor domain of KIF9, partial cds.//4.7e-58:367:87//AB001437

F-THYRO1000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//1.2e-36:396:71//AC005778

F-THYRO1000684//Fugu rubripes cosmid 165K09 DNA for GRM7, TRIP, Sand, PRGFR3 genes.//6.6e-13:236:69//AJ010317

30 F-THYRO1000699//RPC111-50D4.TK RPC111 Homo sapiens genomic clone R-50D4, genomic survey sequence.//2.7e-09:135:78//AQ052641

F-THYRO1000712//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//5.2e-17:290:67//AC005053

35 F-THYRO1000715//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.6e-08:517:60//L14320

F-THYRO1000734//HS\_3233\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D-Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence.//6.0e-72:463:89//AQ182143

F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds.//9.7e-34:339:74//AB007871

40 F-THYRO1000756//M.musculus mRNA for Gal beta1, 3GalNAc alpha2,3-sialyltransferase.//0.00034:349:60//X73523

F-THYRO1000777//S.griseus strO gene and sts gene cluster.//8.2e-05:625:59//Y08763

F-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//4.0e-70:860:69//U37373

45 F-THYRO1000787//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366D1, WORKING DRAFT SEQUENCE.//5.3e-09:221:66//Z97986

F-THYRO1000793

F-THYRO1000796//Cristatella mucedo clone 5.9 microsatellite sequence.//0.34:173:63//AF085422

F-THYRO1000805//Homo sapiens Xp21 PAC RPC11-37A12 containing exons 10 to 16 of the Duchenne Muscular Dystrophy gene, complete sequence.//7.8e-43:677:66//AC004468

50 F-THYRO1000815//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//5.5e-43:405:77//AC005914

F-THYRO1000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence.//2.0e-20:159:88//AQ240053

55 F-THYRO1000843

F-THYRO1000852//Homo sapiens chromosome 19, cosmid R31855, complete sequence.//1.8e-33:445:72//AC005782

F-THYRO1000855//Mus musculus potassium channel alpha subunit (Kv9.1) mRNA, complete cds.//0.038:208:

- 64//AF008573  
F-THYRO1000865//Homo sapiens PAC clone DJ0283M22 from 14, complete sequence.//1.9e-30:286:74//AC005477
- 5 F-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 385E7, WORKING DRAFT SEQUENCE.//2.8e-18:186:80//AL031720  
F-THYRO1000916//Homo sapiens clone DJ096K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-78:432:93//AC006015  
F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.2e-178:839:98//AF079529
- 10 F-THYRO1000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:759:63//M77836  
F-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229  
F-THYRO1000952  
F-THYRO1000974//HS\_3238\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//12.4e-26:154:96//AQ219846  
F-THYRO1000975//Plasmodium falciparum Topoli gene.//0.32:491:58//X79345  
F-THYRO1000983//Mwv9A3 exon amplification products from BACs in Mwv region Mus musculus genomic, genomic survey sequence.//7.0e-16:112:94//AQ010457  
F-THYRO1000984//CIT-HSP-2167O17.TR CIT-HSP Homo sapiens genomic clone 2167O17, genomic survey sequence.//0.00015:186:66//B91313
- 20 F-THYRO1000988//Human Chromosome 11q12.2 PAC clone pDJ756b9 containing human ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.024:267:63//AC004588  
F-THYRO1001003  
F-THYRO1001031//Homo sapiens chromosome 17, clone hRPC.859\_O\_20, complete sequence.//1.1e-55:543:72//AC003695
- 25 F-THYRO1001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328 (section 5 of 148) of the complete genome.//0.94:445:58//AE000799  
F-THYRO1001062//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320  
F-THYRO1001093//Homo sapiens chromosome 9, clone hRPC.202\_H\_3, complete sequence.//4.9e-34:353:76//AC006241  
F-THYRO1001100//Human DNA-binding protein mRNA, 3'end.//1.1e-72:742:74//L14787  
F-THYRO1001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522
- 35 F-THYRO1001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 671O14, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595  
F-THYRO1001133//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//4.0e-35:349:76//AC004996  
F-THYRO1001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486  
F-THYRO1001142//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178  
F-THYRO1001173  
F-THYRO1001177//Human pigment epithelium-derived factor gene, complete cds.//1.9e-42:250:86//U29953
- 45 F-THYRO1001189//HS\_3171\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=20 Row=L, genomic survey sequence.//1.8e-28:246:83//AQ302330  
F-THYRO1001204//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//4.9e-39:657:64//U34925  
F-THYRO1001213//, complete sequence.//1.7e-45:257:84//AC005300
- 50 F-THYRO1001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.5e-40:274:87//AP000036  
F-THYRO1001271//Streptomyces coelicolor cosmid 1A6.//0.033:364:61//AL023496  
F-THYRO1001287//Drosophila melanogaster cosmid clone 86E4.119.6e-49:586:69//AL021086  
F-THYRO1001290//HS\_2045\_B1\_H09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2045 Col=17 Row=P, genomic survey sequence.//4.4e-13:156:78//AQ248237
- 55 F-THYRO1001313//S. lavendulae bla gene for beta-lactamase, complete cds.//1.0:229:64//D12693  
F-THYRO1001320//Homo sapiens Chromosome 22q11.2 PAC Clone p\_n5 in BCRL2-GGT Region, complete sequence.//1.1e-88:672:82//AC002472

- F-THYRO1001321//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.2e-115:740:87//AC000114  
 F-THYRO1001322//HS\_3205\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=24 Row=F, genomic survey sequence.//0.00031:285:61//AQ304025  
 F-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//2.2e-43:638:64//AB018288  
 5 F-THYRO1001363//Homo sapiens PAC clone DJ0845121 from 7q11.21-q11.23, complete sequence.//1.0e-09:189:74//AC004905  
 F-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map-10q25, complete sequence.//7.6e-168:821:97//AC005660  
 10 F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//2.3e-155:740:97//AB014607  
 F-THYRO1001401//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//3.2e-07:138:73//AC005239  
 F-THYRO1001403//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//3.6e-70:360:86//AC005845  
 F-THYRO1001405//Bos taurus mRNA for NDP52, complete cds.//2.6e-14:559:63//AB008852  
 15 F-THYRO1001406//Mus musculus putative steroid dehydrogenase (KIK-1) mRNA, complete cds.//1.0e-91:631:82//AF064635  
 F-THYRO1001411//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//5.5e-42:509:71//AC006126  
 20 F-THYRO1001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118122) from chromosome 11: HTGS phase 1, WORKING DRAFT SEQUENCE.//2.7e-31:172:81//AL002553  
 F-THYRO1001434//Human Chromosome 11 pac pDJ393c15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.0:98:70//AC000384  
 F-THYRO1001458//Bos taurus non-muscle myosin heavy chain mRNA, partial cds.//1.9e-58:653:71//U87265  
 25 F-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-42:357:80//AC006001  
 F-THYRO1001487//H.sapiens DNA sequence.//0.92:160:64//Z22449  
 F-THYRO1001534//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-47:266:80//AC004666  
 F-THYRO1001537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//1.3e-79:479:89//AL031687  
 30 F-THYRO1001541//Human DNA sequence from clone 399M14 on chromosome Xq26.1-26.3. Contains ESTs, an STS and GSSs, complete sequence.//0.0034:106:77//Z96074  
 F-THYRO1001559//Rattus norvegicus simple sequence repeat D18Mco6.//1.6e-09:351:63//AF006056  
 F-THYRO1001570//RPCI11-49B23.TJ RPCI11 Homo sapiens genomic clone R-49B23, genomic survey sequence.//1.4e-65:384:91//AQ052105  
 35 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA.//8.2e-104:546:95//AF070572  
 F-THYRO1001584//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498  
 40 F-THYRO1001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//8.7e-145:779:93//AL023808  
 F-THYRO1001602//Homo sapiens chromosome 17, clone hRPC.786\_O\_4, complete sequence.//2.9e-26:393:68//AC005863  
 F-THYRO1001605//Dictyostelium discoideum filopodin (talA) gene, complete cds.//0.0012:436:58//U14576  
 F-THYRO1001617//Homo sapiens full-length insert cDNA clone ZD69D05.//8.6e-43:342:82//AF086381  
 45 F-THYRO1001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10 unordered pieces.//6.2e-15:318:66//AC004950  
 F-THYRO1001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.5e-05:147:68//AC004827  
 F-THYRO1001661  
 50 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//2.5e-164:780:98//AJ225089  
 F-THYRO1001673//Homo sapiens clone RG161A02, complete sequence.//4.4e-40:770:64//AC005071  
 F-THYRO1001703//S.coelicolor plasmid SCP2 transfer region DNA.//0.14:414:59//X72857  
 F-THYRO1001706//Homo sapiens BAC clone RG281B09 from 7q21.1-q31.1, complete sequence.//2.6e-43:308:75//AC004745  
 55 F-THYRO1001721//, complete sequence.//9.9e-134:770:91//AC005500  
 F-THYRO1001738//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 355C18, WORKING DRAFT SEQUENCE.//0.99:163:61//AL022327



F-THYRO1001745  
 F-THYRO1001746  
 F-THYRO1001772//HS\_3069\_B1\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3069 Col=9 Row=F, genomic survey sequence.//1.5e-61:360:91//AQ171021  
 5 F-THYRO1001793//B.taurus mRNA for beta-subunit of rod photoreceptor CNG-channel.//0.028:446:58//X89626  
 F-THYRO 1001809  
 F-THYRO1001828//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 110F11, WORKING DRAFT SEQUENCE.//1.3e-175:841:98//AL033526  
 10 F-THYRO1001854//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.9e-07:445:59//AC003664  
 F-THYRO1001895  
 4.4e-13:248:68//AB012576  
 F-THYRO1001907//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.9e-15:144:77//AC005058  
 15 F-VESEN1000122//HS\_3075\_B1\_C09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=F, genomic survey sequence.//1.1e-16:130:90//AQ143749  
 F-Y79AA1000013  
 F-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//2.9e-95:300:94//AC006027  
 20 F-Y79AA1000037//Human prot-oncogene (BMI-1) mRNA, complete cds.//2.4e-19:230:66//L13689  
 F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds.//2.2e-38:629:64//U78521  
 F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers DXS6791 and DXS8038 on chromosome X contains EST.//5.3e-10:117:83//Z72005  
 25 F-Y79AA1000131//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//7.6e-10:381:64//U92893  
 F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//1.4e-165:732:99//AL031864  
 F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.//9.1e-20:339:65//AC005115  
 30 F-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//3.7e-72:397:93//AC004854  
 F-Y79AA1000230  
 F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cds.//8.5e-151:833:90//AF053232  
 F-Y79AA1000258//Leishmania donovani histidine secretory acid phosphatase (SACP-1) gene, complete cds.//0.0099:547:58//U78522  
 35 F-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//4.0e-11:424:62//AF035207  
 F-Y79AA1000313  
 F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//5.9e-07:173:69//B55085  
 40 F-Y79AA1000342//RPC111-57J6 TK.1 RPC111 Homo sapiens genomic clone R-57J6, genomic survey sequence.//5.2e-27:151:99//AQ115511  
 F-Y79AA1000346//B.primigenius mRNA for coat protein gamma-cop.//5.7e-69:694:71//X92987  
 F-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//1.8e-98:535:92//X84692  
 F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-21:129:85//AC005484  
 45 F-Y79AA1000368//H.sapiens CpG island DNA genomic MseI fragment, clone 12f1, reverse read cpG12f1.r1tc.//0.00016:53:98//Z56610  
 F-Y79AA1000405//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P4, WORKING DRAFT SEQUENCE.//0.069:366:59//AL031747  
 50 F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome X.//1.0e-25:235:80//Z86061  
 F-Y79AA1000420//H.sapiens CpG island DNA genomic MseI fragment, clone 82c3, forward read cpG82c3.ft1a.//2.0e-36:194:98//Z63378  
 F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds.//8.5e-121:696:89//U41736  
 55 F-Y79AA1000480//HS\_2175\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175 Col=22 Row=O, genomic survey sequence.//2.5e-26:178:89//AQ307693  
 F-Y79AA1000538//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.67:111:72//AC004980

- F-Y79AA1000539//HS\_2237\_B2\_F10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, genomic survey sequence.//1.2e-14:168:77//AQ153503
- F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.94:127:67//AC005193
- 5 F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//1.7e-114:776:84//X14972
- F-Y79AA1000574//M.musculus tex23 mRNA (5'region).//1.8e-23:291:75//X80424
- F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//8.6e-153:755:97//AF091080
- F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.//5.2e-135:644:98//AF060503
- F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//6.9e-148:902:86//X69942
- 10 F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assembly factor, complete cds.//4.8e-180:850:98//AB018080
- F-Y79AA1000748//Caenorhabditis elegans cosmid F25B5.//0.00019:308:60//U23172
- F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein.//1.7e-40:513:68//AJ003023
- F-Y79AA1000774
- 15 F-Y79AA1000782
- F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//3.5e-177:847:97//AF098799
- F-Y79AA1000794//H.sapiens CpG island DNA genomic Mse1 fragment, clone 45a4, forward read cpq45a4.ft1a.//2.5e-13:104:92//Z61120
- F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds.//0.98:244:60//AF056085
- 20 F-Y79AA1000802
- F-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//9.3e-76:528:85//U73642
- F-Y79AA1000824//RPCI11-26B4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-26B4, genomic survey sequence.//4.4e-14:99:95//B84538
- F-Y79AA1000827//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117715, WORKING DRAFT SEQUENCE.//1.5e-08:249:69//AL022315
- 25 F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin.//1.8e-103:603:89//X04757
- F-Y79AA1000850
- F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//0.038:468:59//Z82203
- 30 F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.7e-150:865:89//AF071314
- F-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//6.4e-122:717:88//U38253
- F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence.//1.0:155:63//AC002397
- 35 F-Y79AA1000976//Caenorhabditis elegans cosmid F54C1.//4.3e-06:130:73//U88165
- F-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//2.4e-44:428:77//U05823
- F-Y79AA1001023
- F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds.//2.3e-13:90:100//U63329
- 40 F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds.//2.6e-28:772:60//D43682
- F-Y79AA1001061//Homo sapiens chromosome 4 clone B331M8 map 4q25, complete sequence.//9.4e-36:292:82//AC004701
- F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [Streptomyces lividans, Genomic, 1146 nt].//0.17:537:59//S64314
- 45 F-Y79AA1001077//Zea mays mRNA for aldehyde oxidase-2, complete cds.//0.17:231:64//D88452
- F-Y79AA1001078
- F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete cds.//3.1e-63:529:77//D26173
- F-Y79AA1001145//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.3e-23:228:76//AC005015
- 50 F-Y79AA1001167
- F-Y79AA1001177//M.musculus mRNA for NfX1-protein.//4.0e-10:398:64//Y07688
- F-Y79AA1001185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING DRAFT SEQUENCE.//1.1e-113:666:90//Z93015
- 55 F-Y79AA1001211//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//5.5e-12:87:96//AQ187492
- F-Y79AA1001216
- F-Y79AA1001228//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//0.028:188:67//

AL021841

F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogenase mRNA, complete cds.//3.5e-24:731:60//M36263

F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNL1101133Q7 (RZPD Berlin)).//1.2e-133:441:97//AJ005892

F-Y79AA1001281//HS\_2241\_B2\_F09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2241 Col=18 Row=L, genomic survey sequence.//5.0e-27:169:94//AQ271497

F-Y79AA1001299//Human Inl1 mRNA, complete cds.//6.7e-115:323:93//U04847

F-Y79AA1001312

F-Y79AA1001323

F-Y79AA1001384

F-Y79AA1001391//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//5.8e-42:245:74//U59322

F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequence.//7.8e-18:636:58//Z48583

F-Y79AA1001402//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-110:738:85//AC005924

F-Y79AA1001493//H.sapiens DNA sequence.//2.0e-27:254:82//Z22497

F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.1e-158:804:95//AL034430

F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//1.7e-100:820:78//D14336

F-Y79AA1001541//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//5.1e-28:218:86//AQ150183

F-Y79AA1001548//Homo sapiens chromosome 19, cosmid R28738, complete sequence.//5.4e-21:167:86//AC004151

F-Y79AA1001555//R.norvegicus mRNA for drebrin A.//0.88:643:59//X59267

F-Y79AA1001581//FMR1 (CGG repeats) [human, Fragile X syndrome patient, Genomic, 429 nt].//0.00051:252:65//S74494

F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds.//7.2e-33:375:76//M26434

F-Y79AA1001594

F-Y79AA1001603//Homo sapiens PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence.//4.2e-06:338:66//AF064861

F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds.//0.024:520:57//AB014583

F-Y79AA1001647//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.014:331:61//Z92860

F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.99:273:63//Z84468

F-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//1.2e-97:682:81//M22743

F-Y79AA1001692//Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1292 nt, segment 1 of 4].//5.6e-05:426:59//S37712

F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polyprotein (containing putative helicase and putative RNA-dependent RNA polymerase domains), complete cds.//1.0:437:60//D32136

F-Y79AA1001705//M.musculus fhx-5 gene.//0.18:153:64//X71943

F-Y79AA1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//5.4e-76:191:98//AL022240

F-Y79AA1001781//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15, WORKING DRAFT SEQUENCE.//0.99:227:63//AP000017

F-Y79AA1001805//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpg13d12.rt1c.//2.6e-13:88:100//Z64565

F-Y79AA1001827//Oryctolagus cuniculus PIUS mRNA, complete cds.//3.7e-130:775:88//U74297

F-Y79AA1001846//CIT-HSP-2300M6.TR CIT-HSP Homo sapiens genomic clone 2300M6, genomic survey sequence.//8.3e-17:218:76//AQ012369

F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds.//4.2e-10:378:62//AB002388

F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (Rkr1) mRNA, complete cds.//6.9e-41:441:71//U41164

F-Y79AA1001874//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.00017:412:62//AF029779

- F-Y79AA1001875//CTT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271.67//AQ042654
- F-Y79AA1001923//H.sapiens CpG island DNA genomic MseI fragment, clone 193c12, forward read cp913c12.fl1a.//0.0031:108.75//Z60186
- 5 F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184
- F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340
- 10 F-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 526114, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214
- F-Y79AA1002089
- F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 mRNA, partial cds.//1.2e-112:678:88//U43548
- 15 F-Y79AA1002103//HS\_3052\_B1\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014
- F-Y79AA1002115
- F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693
- F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358
- 20 F-Y79AA1002204//HS\_2235\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260
- F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397
- F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719
- 25 F-Y79AA1002210//Homo sapiens chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615
- F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043
- F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738
- 30 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045
- F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.3e-174:821:98//AB014592
- F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.50:470:60//AC005015
- 35 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6.8e-159:748:98//AB014555
- F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds.//0.036:278:62//U10886
- F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.4e-129:622:97//AB014534
- F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877
- 40 F-Y79AA1002351//S.clavuliger pah and cas genes.//1.0:369:58//X84101
- F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//5.4e-105:762:80//Y18208
- F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.0e-159:411:100//AC005920
- F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//1.1e-118:609:84//AC004662
- 45 F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPSH) mRNA, complete cds.//4.4e-90:529:88//U49385
- F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, complete cds.//1.0:166:66//U36196
- F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917
- 50 F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC301323), complete sequence.//1.9e-13:242:69//AC006116
- F-Y79AA1002482//Homo sapiens full-length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022
- F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677
- 55 Homology Search Result Data 3.

**[0303]** The result of the homology search of the GenBank using the clone sequence of 3'-end except EST and STS.  
**[0304]** Data include

the name of clone,  
 definition of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

5

[0305] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0306] Data are not shown for the clones in which the P-value was higher than 1.

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R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.6e-60:504:78//L16953  
 R-HEMBA1000030//F.rubripes GSS sequence, clone 063K10bD3, genomic survey sequence.//0.28:117:68//Z88864

R-HEMBA1000042//RPC11-77G23.TV RPC11 Homo sapiens genomic clone R-77G23, genomic survey sequence.//1.3e-56:292:97//AQ268240

15

R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence.//9.8e-56:401:82//U82696

R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455.//0.0010:175:68//L31948

R-HEMBA1000076//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.9e-41:364:79//AC005520

R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//4.7e-30:229:84//AC003684

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R-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//2.4e-93:503:93//AC003104

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//6.5e-99:514:94//AB018340

R-HEMBA1000150//Homo sapiens clone RG086D03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.7e-37:289:83//AC005060

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R-nnnnnnnnnnn//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64//L43631

R-HEMBA1000158

R-nnnnnnnnnnn

R-HEMBA1000180//Plasmodium falciparum encoding Pfg27/25.//0.073:292:56//X84904

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R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.3e-40:286:85//AC006146

R-HEMBA1000193

R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y17126

R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF100655

35

R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//2.5e-31:269:79//AF001548

R-nnnnnnnnnnn

R-HEMBA1000231//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//4.3e-24:400:68//AL009181

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R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.3e-19:319:69//AC004526

R-HEMBA1000244

R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds; transfer RNA-His gene; 16S ribosomal RNA gene; ND3 gene, complete cds; cytochrome b (cytb) gene, 5' end of cds.//0.16:338:60//L76262

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R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012

R-nnnnnnnnnnn//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//3.5e-10:238:70//AC003037

R-HEMBA1000282//Arabidopsis thaliana BAC IG002P16.//0.71:344:60//AF007270

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R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//4.8e-33:267:82//AC003046

R-HEMBA1000290//Homo sapiens chromosome 17, clone HRC837J1, complete sequence.//2.2e-15:249:69//AC004223

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R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP Homo sapiens genomic clone 2173N10, genomic survey sequence.//1.0:215:61//B95105

R-nnnnnnnnnnn//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//1.0e-77:551:82//AF030131

R-nnnnnnnnnnn//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//2.0e-96:546:90//U16802

- R-HEMBA1000307//Mus musculus mRNA for CDV-1 protein.//3.8e-36:315:68//Y10496  
 R-nnnnnnnnnnn//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.078:379:59//AC005505
- 5 R-HEMBA1000338//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//2.0e-33:399:72//AL031667  
 R-HEMBA1000351//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//1.7e-39:272:87//AJ003147  
 R-HEMBA1000355//Human primary Alu transcript.//0.0045:67:85//U67829
- 10 R-HEMBA1000357//Homo sapiens (subclone 9\_h8 from PI H16) DNA sequence.//8.7e-93:426:88//L42086  
 R-HEMBA1000366//Homo sapiens PAC clone DJ094216 from 7q11, complete sequence.//1.7e-12:130:83//AC006012  
 R-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//1.9e-69:355:97//AL031587
- 15 R-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-39315 (BC301323), complete sequence.//3.7e-66:410:89//AC006116  
 R-HEMBA1000387//Homo sapiens chromosome 17, clone HCIT169H, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:363:81//AC002993  
 R-HEMBA1000390//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//4.6e-23:417:69//AC005053
- 20 R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence.//6.2e-05:174:68//AC004582  
 R-HEMBA1000396//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//1.4e-62:564:77//AL022575
- 25 R-HEMBA1000411  
 R-HEMBA1000418//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.94:210:60//X04465  
 R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP Homo sapiens genomic clone 2382A6, genomic survey sequence.//4.4e-12:98:92//AQ078233  
 R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//2.0e-93:526:90//Z95400
- 30 R-HEMBA1000434//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-07:452:60//AC004826  
 R-HEMBA1000442//E. caballus microsatellite DNA, clone HMB4.//0.39:135:62//Y07733  
 R-HEMBA1000456//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//2.6e-05:174:70//AL010226
- 35 R-HEMBA1000459//Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), putative acyl-coA dehydrogenase (AtG6), and calcium dependent protein kinase genes, complete cds; and unknown genes.//0.013:212:63//AF049236
- 40 R-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//8.6e-114:556:98//AC004839  
 R-HEMBA1000464//Caenorhabditis elegans cosmid C34B7, complete sequence.//0.086:334:61//Z83220  
 R-HEMBA1000469//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.8e-52:472:79//AC005104
- 45 R-HEMBA1000488//, complete sequence.//3.3e-68:200:99//AC005500  
 R-HEMBA1000490//Caenorhabditis elegans cosmid Y53C12B, complete sequence.//0.97:233:61//Z99278  
 R-HEMBA1000491  
 R-HEMBA1000504//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, complete sequence.//1.7e-08:440:60//AL009014
- 50 R-HEMBA1000505//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11.//0.37:189:62//AB020858  
 R-HEMBA1000508//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//1.1e-25:248:80//Z70280  
 R-HEMBA1000518//RPC111-6022.TV RPC1-11 Homo sapiens genomic clone RPC1-11-6022, genomic survey sequence.//0.0035:293:61//B49544
- 55 R-HEMBA1000519  
 R-HEMBA1000520//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//0.30:255:63//AC006232

- R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds.//1.2e-53:203:92//U15782
- R-HEMBA1000531//CIT-HSP-388J17. TR CIT-HSP Homo sapiens genomic clone 388J17, genomic survey sequence.//2.7e-24:137:99//B55638
- 5 R-HEMBA1000540//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044
- R-HEMBA1000545//Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.//6.9e-87:552:87//AC004103
- 10 R-nnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//8.9e-121:584:98//AL034555
- R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//5.7e-45:307:87//AC004381
- R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence.//1.3e-43:279:90//AF046762
- 15 R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//3.8e-05:506:56//AE001368
- R-HEMBA1000568//RPC111-49P8.TK.11 RPC111 Homo sapiens genomic clone R-49P8, genomic survey sequence.//1.7e-101:498:97//AQ116293
- R-nnnnnnnnnnn
- 20 R-HEMBA1000575//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 754E20, WORKING DRAFT SEQUENCE.//1.3e-47:458:75//AL022335
- R-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.9e-62:447:81//AF045573
- R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.2e-111:591:9411A.J007509
- 25 R-HEMBA1000592//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//3.5e-09:421:60//AL010216
- R-HEMBA1000594//Homo sapiens clone RG004N09, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-15:421:66//AC005044
- R-HEMBA1000604//HS\_2220\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=19 Row=M, genomic survey sequence.//1.0e-51:306:92//AQ151991
- 30 R-HEMBA1000608
- R-HEMBA1000622//H.sapiens CpG island DNA genomic MseI fragment, clone 155e4, reverse read cpg155e4.r11a.//4.5e-16:105:98//Z56962
- R-HEMBA1000636//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//4.8e-62:421:86//AP000008
- 35 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.2e-97:443:97//AB014590
- R-HEMBA1000655//Homo sapiens chromosome 19, cosmid R26349, complete sequence.//9.8e-61:311:90//AC005953
- R-HEMBA1000657
- R-HEMBA1000662
- 40 R-HEMBA1000673//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//1.0e-13:351:63//Z97196
- R-HEMBA1000682//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-50:298:79//AC005377
- 45 R-HEMBA1000686//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00048:210:62//AQ093513
- R-HEMBA1000702//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.7e-54:317:88//AC005000
- R-HEMBA1000705//Glossonotus uhivittatus 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//0.080:138:65//U77850
- 50 R-HEMBA1000719//Rattus norvegicus mRNA for TESK1, complete cds.//0.96:291:58//D50864
- R-HEMBA1000722
- R-HEMBA1000726//Homo sapiens PAC clone DJ0701016 from 7q33-q36, complete sequence.//4.4e-26:284:77//AC005531
- R-HEMBA1000727//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//9.1e-05:351:60//AL010266
- 55 R-HEMBA1000747//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.5e-16:123:93//AL021326

R-HEMBA1000749//Human Chromosome 16 BAC clone CIT987SK-327024, complete sequence.//2.8e-32:298:79//AC003108

R-HEMBA1000752//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-90:542:90//Z92545

R-HEMBA1000769//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-36:405:75//AC005031

R-HEMBA1000773//HS\_3050\_A2\_B08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3050 Col=16 Row=C, genomic survey sequence.//0.00053:268:60//AQ105619

R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//4.7e-46:338:85//AC004690

R-HEMBA1000791//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//5.3e-47:279:91//U14571

R-HEMBA10008177//Sequence 1 from Patent WO 8904839.//0.86:148:67//I09339

R-HEMBA1000822//T.brucei kinetoplast maxicircle variable region DNA.//0.00061:246:61//Z15118

R-HEMBA1000827//Homo sapiens Ser(Arg)-related nuclear matrix protein (SRM160) mRNA, complete cds.//6.9e-43:228:98//AF048977

R-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.7e-41:319:84//AL022394

R-HEMBA1000851//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.40:168:67//AC004260

R-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.5e-112:572:96//AC005295

R-HEMBA1000867//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//0.11:121:71//AC004938

R-HEMBA1000869//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-22:186:76//AC002042

R-HEMBA1000870//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//0.0060:283:63//AC002528

R-HEMBA1000872//Rattus norvegicus polymorphic satellite repetitive elements.//3.8e-05:269:61//M98801

R-HEMBA1000876//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-38:327:77//AC006057

R-HEMBA1000908//CIT-HSP-237314.TR CIT-HSP Homo sapiens genomic clone 237314, genomic survey sequence.//5.0e-34:221:90//AQ108658

R-HEMBA1000910//T.pigmentosa UM1060 macronuclear rDNA telomeric region 3' term.//0.19:280:61//X04205

R-HEMBA1000918//RPCI11-68E14.TK RPCI11 Homo sapiens genomic clone R-68E14, genomic survey sequence.//1.3e-32:172:100//AQ267293

R-HEMBA1000919

R-HEMBA1000934//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.6e-18:284:71//AL021997

R-HEMBA1000942//Homo sapiens clone RG350L10, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.4e-17:217:76//AC005098

R-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_L15, complete sequence.//9.0e-113:586:95//AC005324

R-HEMBA1000946//T5N8TFB TAMU Arabidopsis thaliana genomic clone T5N8, genomic survey sequence.//0.030:369:59//B26224

R-HEMBA1000960//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-52:494:77//AC005096

R-HEMBA1000968//Homo sapiens P1 clone 797a11 containing MHC class II DQ-beta (HLA-DQB) and MHC class II DC-alpha (HLA-DCA) genes, complete cds.//3.5e-77:568:83//U92032

R-HEMBA1000971//RPCI11-54D1.TJ RPCI11 Homo sapiens genomic clone R-54D1, genomic survey sequence.//2.3e-27:153:98//AQ081552

R-HEMBA1000972//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//7.3e-43:375:79//AL023876

R-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//2.8e-104:521:97//AC004817



- R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//8.0e-22:352:68//AL031311
- R-HEMBA1000985//Homo sapiens PAC clone DJ0797C05 from Tq31, complete sequence.//8.5e-05:306:63//AC004888
- 5 R-HEMBA1000986//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.7e-37:296:83//AC005632
- R-HEMBA1000991//RPC111-22017. TVB RPC1-11 Homo sapiens genomic clone RPC1-11-22017, genomic survey sequence.//6.5e-44:162:90//AQ008952
- 10 R-HEMBA1001007
- R-HEMBA1001008//Homo sapiens chromosome 16, P1 clone 79-2A (LANL), complete sequence.//0.082:313:60//AC005365
- R-HEMBA1001009//O. sativa csr40g2 gene.//0.99:203:62//Y08987
- R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//1.0e-113:587:95//AB007937
- 15 R-HEMBA1001019//Bos taurus cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, complete cds.//7.4e-24:215:82//L26547
- R-HEMBA1001020//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//2.8e-18:449:64//AL008722
- R-HEMBA1001022
- 20 R-HEMBA1001024//Homo sapiens BAC clone 393122 from 8q21, complete sequence.//6.6e-48:536:74//AF070717
- R-HEMBA1001026//T33H14TF TAMU Arabidopsis thaliana genomic clone T33H14, genomic survey sequence.//0.013:180:66//B97363
- R-nnnnnnnnnnn//Caenorhabditis elegans cosmid R10H10, complete sequence.//1.2e-25:438:65//Z70686
- 25 R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPC13-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.3e-38:188:89//AC004217
- R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region.//2.4e-24:279:74//X04751
- R-HEMBA1001060//HS\_2056\_B1\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence.//4.1e-14:137:83//AQ245004
- R-HEMBA1001071//M.musculus COL3A1 gene for collagen alpha-1.//6.9e-38:513:70//X52046
- 30 R-HEMBA1001077//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.9e-22:507:61//AL022318
- R-HEMBA1001080
- R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase Iix genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.2e-43:317:83//AC004586
- 35 R-HEMBA1001088//Caenorhabditis elegans cosmid C18H7.//0.46:301:60//AF067607
- R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//5.3e-98:501:96//AC005105
- R-HEMBA1001099
- R-HEMBA1001109//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE.//3.1e-39:335:80//AL033527
- 40 R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2.//9.8e-11:122:81//U81833
- R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence.//0.0024:284:63//Z98551
- R-HEMBA1001123//Human NFE genomic fragment.//3.6e-26:318:72//M98511
- R-HEMBA1001133
- 45 R-HEMBA1001137//Homo sapiens full-length insert cDNA clone ZD29F04.//4.2e-88:426:98//AF086241
- R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-41:304:84//AC005077
- R-HEMBA1001172//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//3.7e-36:261:85//Z98304
- 50 R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.0:219:58//AE001398
- R-HEMBA1001197
- R-HEMBA1001208//HS\_2233\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey sequence.//0.083:174:68//AQ170789
- 55 R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-59:553:75//AC005377
- R-HEMBA1001235//RPC111-50E6.TJ RPC111 Homo sapiens genomic clone R-50E6, genomic survey sequence.//2.6e-08:97:76//AQ052866
- R-HEMBA1001247//Caenorhabditis elegans cosmid C01F1.//2.4e-05:319:63//U58761



- R-HEMBA1001446//HS\_3207\_A1\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey sequence.//8.9e-06:119:73//AQ175385
- R-HEMBA1001450//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//0.0043:266:63//AC005065
- 5 R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from 7q31, complete sequence.//7.1e-25:210:82//AC004855
- R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640\_15, complete sequence.//2.7e-08:316:62//AC005324
- 10 R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, complete sequence.//0.57:219:60//AC005208
- R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//9.3e-50:252:80//AC004840
- R-HEMBA1001478
- R-HEMBA1001497
- 15 R-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//3.5e-41:282:86//U89337
- R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//1.9e-79:529:86//Z98753
- R-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//4.3e-18:335:71//AC004549
- 20 R-HEMBA1001522
- R-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG islands.//5.6e-08:265:67//Z98258
- R-HEMBA1001533//Human DNA sequence from PAC 179M20 on chromosome 20q12-13.1. Contains adenosine deaminase (ADA), placental protein Diff33, CA repeat, ESTs, STS.//7.8e-16:235:72//Z97053
- 25 R-HEMBA1001557
- R-HEMBA1001566//Human Chromosome X clone bWXD187, complete sequence.//2.2e-44:416:78//AC004383
- R-HEMBA1001569//Sequence 15 from patent US 5693476.//1.8e-59:389:88//I77040
- R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//1.1e-44:316:87//AC004453
- 30 R-HEMBA1001579//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0047:437:60//AC005506
- R-HEMBA1001581//P.falciparum complete gene map of plastid-like DNA (IR-B).//2.3e-07:491:58//X95276
- R-HEMBA1001585//Caenorhabditis elegans cosmid C06A6.//0.68:224:62//U41012
- 35 R-HEMBA1001589
- R-HEMBA1001595//CIT-HSP-2349G19.TF CIT-HSP Homo sapiens genomic clone 2349G19, genomic survey sequence.//8.0e-89:337:99//AQ060483
- R-HEMBA1001608//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//9.5e-59:514:78//AC005177
- 40 R-HEMBA1001620//S.polymorpha mRNA for D-myo-inositol-3-phosphate synthase.//4.5e-12:289:65//Z11693
- R-nnnnnnnnnnn//HS\_2195\_A1\_E09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=17 Row=I, genomic survey sequence.//5.8e-09:358:58//AQ292688
- R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA, complete cds.//0.77:225:59//U04270
- 45 R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 6p21. Contains ETS related protein TEL like and GS2 like genes, ESTs and an STS.//6.0e-49:404:79//Z84484
- R-nnnnnnnnnnn
- R-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.1e-103:532:95//AC005368
- 50 R-HEMBA1001658//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.0:197:64//AL023808
- R-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.5e-100:457:93//AC005740
- R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//1.2e-90:496:91//AF072247
- 55 R-HEMBA1001675
- R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds.//1.3e-101:534:94//AF038962

- R-HEMBA1001681//CIT-HSP-2345M7.TF CIT-HSP Homo sapiens genomic clone 2345M7, genomic survey sequence.//0.21:124.68//AQ056593
- R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPC1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//8.3e-06:279:63//AC004801
- 5 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds.//1.9e-96:483:96//AB014598
- R-HEMBA1001711//Human HepG2 3' region cDNA, clone hmd2b02.//2.3e-31:169:100//D16886
- R-HEMBA1001712//HS-1015-B1-E01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 790 Col=1 Row=J, genomic survey sequence.//0.0025:200:65//B32577
- 10 R-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//6.6e-27:316:75//U12250
- R-HEMBA1001718//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//3.1e-41:167:87//B89781
- R-HEMBA1001723//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//0.53:275:61//AF018261
- 15 R-HEMBA1001731//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//2.9e-48:292:84//AL023799
- R-HEMBA1001734//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-33:290:81//AC005959
- R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21 Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs, GSSs and retroviral sequence, complete sequence.//0.98:203:62//AL022067
- 20 R-HEMBA1001745//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//0.00019:312:59//AC005084
- R-HEMBA1001746//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.045:457:61//AC004153
- 25 R-HEMBA1001761//Homo sapiens chromosome X, clone hCIT.200\_L\_4, complete sequence.//3.8e-39:331:80//AC006121
- R-HEMBA1001781//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//0.0062:245:60//AC004554
- 30 R-HEMBA1001784//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.1e-22:370:63//AC005740
- R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-50:408:80//AL023575
- R-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//9.0e-37:335:77//AQ009222
- 35 R-HEMBA1001803//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.86:536:56//AC005506
- R-nnnnnnnnnnnn/Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//2.9e-93:553:89//M21977
- 40 R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//2.8e-112:548:98//AB007969
- R-HEMBA1001809
- R-HEMBA1001815//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//2.6e-48:363:84//AC004025
- R-HEMBA1001819//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SEQUENCE.//1.1e-15:275:68//AJ009612
- 45 R-HEMBA1001820//HS\_3022\_B1\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=17 Row=B, genomic survey sequence.//0.00054:335:59//AQ165107
- R-nnnnnnnnnnnn/Xenopus laevis intersectin mRNA, complete cds.//1.4e-19:533:63//AF032118
- R-HEMBA1001824//IS clavuligerus linear plasmid pSCL (complete sequence).//0.62:189:65//X54107
- 50 R-HEMBA1001835//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//1.0:450:60//AL024507
- R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene, complete cds.//1.6e-07:170:68//UJ05871
- R-HEMBA1001847
- R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//3.3e-108:553:96//AB014517
- 55 R-HEMBA1001864//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463
- R-HEMBA1001866//HS\_2258\_B2\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=H, genomic survey sequence.//2.8e-39:397:75//AQ221138

- R-nnnnnnnnnnn/Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//5.9e-56:303:94//AC005065
- R-HEMBA1001888/Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.7e-43:281:88//AC006210
- 5 R-HEMBA1001896  
R-HEMBA1001910  
R-HEMBA1001912/Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//10.10:307:61//AC004775  
R-HEMBA1001913
- 10 R-HEMBA1001915/HS\_2037\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=23 Row=I, genomic survey sequence.//0.071:206:64//AQ233106  
R-HEMBA1001918/Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.97:449:59//AC004775  
R-HEMBA1001921/Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.0e-105:534:96//AF000145  
15 R-HEMBA1001939/Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508115, WORKING DRAFT SEQUENCE.//4.6e-13:120:82//AL021707  
R-HEMBA1001940/Homo sapiens clone DJ109316, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-36:301:81//AC005629
- 20 R-HEMBA1001942/Human PAC clone DJ0205E24 from Xq23, complete sequence.//1.9e-10:208:68//AC003013  
R-HEMBA1001945/Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//1.2e-06:393:60//AE001433  
R-HEMBA1001950/R. prowazekii genomic DNA fragment (clone A437R).//0.33:122:66//Z82646  
R-HEMBA1001960/Borrelia afzelii VS461 outer surface protein D (ospD) gene, complete cds.//0.0086:427:59//U05329
- 25 R-HEMBA1001962/Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//4.5e-07:176:70//AC004069  
R-HEMBA1001964/HS\_2215\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2215 Col=1 Row=P, genomic survey sequence.//7.3e-25:215:74//AQ151931
- 30 R-HEMBA1001967/Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//1.7e-51:209:95//AL031178  
R-HEMBA1001979/CIT-HSP-2387112.TF.1 CIT-HSP Homo sapiens genomic clone 2387112, genomic survey sequence.//4.9e-06:153:71//AQ240461
- 35 R-HEMBA1001987/Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//3.1e-46:437:77//AL033521  
R-HEMBA1001991/Human DNA sequence from PAC 42618 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-48:446:78//AL020997  
R-HEMBA1002003/Homo sapiens mRNA for protein phosphatase 2C (beta).//5.1e-90:448:97//AJ005801
- 40 R-HEMBA1002008/Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GTG and GTG repeat polymorphisms, complete sequence.//3.2e-42:317:84//Z97181  
R-HEMBA1002018/HS\_3006\_B1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=19 Row=H, genomic survey sequence.//1.0:63:74//AQ089717  
R-HEMBA1002022/Homo sapiens chromosome 18, clone hRPK.453\_M\_1, complete sequence.//0.93:339:59//AC006203
- 45 R-HEMBA1002035/Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.4e-11:285:67//AC003694  
R-HEMBA1002039  
R-HEMBA1002049/Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117715, WORKING DRAFT SEQUENCE.//5.3e-52:266:84//AL022315
- 50 R-HEMBA1002084/CIT-HSP-2357L11.TR CIT-HSP Homo sapiens genomic clone 2357L11, genomic survey sequence.//0.0013:185:66//AQ063078  
R-HEMBA1002092/Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//2.7e-70:479:86//U92703
- 55 R-HEMBA1002100/Homo sapiens thyroid receptor interactor (TRIP7) mRNA, 3' end of cds.//8.5e-32:206:91//L40357  
R-HEMBA1002102/Homo sapiens Chromosome 15q26.1 PAC clone pDJ427d15, complete sequence.//4.3e-42:302:85//AC005800

- R-HEMBA1002113//Human chromosome 12p13 sequence, complete sequence.//1.6e-64:550:80//U47924  
 R-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.2e-92:435:92//AC000378  
 R-HEMBA1002125  
 R-HEMBA1002139//Human nebulin mRNA, partial cds.//0.056:68:88//U35637  
 5 R-HEMBA1002144//Homo sapiens Chromosome 11p14.3 PAC clone 6-130a9 containing tryptophan hydroxylase gene, complete sequence.//2.0e-26:323:70//AC005728  
 R-HEMBA1002150//Human DNA sequence from clone 742C19 on chromosome 22q12.3-13.1. Contains a pseudogene similar to Cytochrome C Oxidase Polypeptide VB and (parts of) up to four novel genes, two with homology to Phorbolins genes and one a novel Chromobox protein gene. Contains ESTs, an STS, GSSs and putative CpG islands, complete sequence.//1.0:371:61//AL031846  
 10 R-HEMBA1002151  
 R-HEMBA1002153//Human BAC 367D17 from chromosome 18, complete sequence.//2.4e-21:322:70//AC003971  
 R-HEMBA1002160//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of *S.cerevisiae*, DNA binding protein similar to URE-B1, ESTs and STS.//2.5e-38:216:84//Z97054  
 15 R-HEMBA1002161//CIT-HSP-2163F10. TF CIT-HSP Homo sapiens genomic clone 2163F10, genomic survey sequence.//3.1e-58:284:80//B89969  
 R-HEMBA1002162//Caenorhabditis elegans cosmid F48C11, complete sequence.//0.0079:286:57//Z80789  
 R-HEMBA1002166//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//5.9e-53:326:80//AC002980  
 20 R-HEMBA1002177  
 R-HEMBA1002185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745I14, WORKING DRAFT SEQUENCE.//9.5e-37:356:76//AL033532  
 R-HEMBA1002189//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.4e-43:244:77//AC003684  
 25 R-HEMBA1002191//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.3e-37:323:78//AC005077  
 R-HEMBA1002199//Human Cosmid g5129g124 from 7q31.3, complete sequence.//1.4e-89:564:87//AC002498  
 R-HEMBA1002204//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g in IGLC Region, complete sequence.//1.5e-31:313:71//AC000053  
 30 R-HEMBA1002212//K.lactis mitochondrial COX1 and A8 genes for cytochrome oxidase subunit I and ATPase subunit 8.//0.0023:346:60//X57546  
 R-HEMBA1002215//M.musculus mRNA for testin.//4.7e-61:414:84//X78989  
 R-HEMBA1002226//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING DRAFT SEQUENCE.//4.6e-46:375:77//AL033529  
 35 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.6e-46:238:98//AF089814  
 R-HEMBA1002237//Homo sapiens 12q13 PAC RPC1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.3e-26:469:67//AC004242  
 40 R-HEMBA1002253//Homo sapiens BAC clone GSHB-519E5 from 7q31, complete sequence.//5.1e-23:162:82//AC005016  
 R-HEMBA1002257  
 R-HEMBA1002267//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//4.6e-44:300:88//AF03 8127  
 45 R-HEMBA1002270//Human BAC clone RG067M09 from 7q21-7q22, complete sequence.//1.9e-19:176:85//AC000057  
 R-HEMBA1002321  
 R-HEMBA1002328//HS\_3061\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=11 Row=G, genomic survey sequence.//1.0:151:65//AQ127617  
 50 R-HEMBA1002337//Saccharomyces cerevisiae RNA polymerase II holoenzyme component (SRB7) gene, complete cds.//3.7e-07:328:63//U23811  
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-128:642:96//AB018314  
 R-HEMBA1002348//Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence.//3.7e-07:587:58//AL031256  
 55 R-HEMBA1002349//Leishmania tarentolae maxicircle DNA fragment.//0.018:341:58//X02438  
 R-NNNNNNNNNN//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//1.2e-121:661:93//AF092563  
 R-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and

non-small cell lung cancer, segment 11/11.//1.1e-70:559:79//AB020868  
 R-HEMBA1002389//HS\_3218\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=J, genomic survey sequence.//0.0011:122:72//AQ213602  
 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//4.2e-81:232:97//AC005954  
 R-HEMBA1002419//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.50:231:64//AC004848  
 R-HEMBA1002430//P.falcalparum complete gene map of plastid-like DNA (IR-B).//0.0023:604:56//X95276  
 R-HEMBA1002439//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-23:183:80//AC006026  
 R-HEMBA1002458//Human DNA sequence from clone 146H21 on chromosome Xq22 Contains cleavage stimulation factor, 64 KD subunit, gene similar to CYTOCHROME B-245 HEAVY CHAIN, pseudogene similar to hnRNP A1 protein and ESTs, complete sequence.//7.7e-32:161:83//Z83819  
 R-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//2.6e-100:305:100//AC005378  
 R-HEMBA1002462//Sequence 43 from patent US 5708157 //2.0e-10:131:77//I80068  
 R-nnnnnnnnnnn  
 R-HEMBA1002477//Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence.//6.6e-33:279:80//AC004841  
 R-HEMBA1002486//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.//2.1e-50:290:92//I14573  
 R-HEMBA1002495//CITBI-E1-2515J10. TR CITBI-E1 Homo sapiens genomic clone 2515J10, genomic survey sequence.//1.0:122:68//AQ261762  
 R-HEMBA1002498//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//2.8e-22:210:78//AC004963  
 R-HEMBA1002503//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//2.7e-17:435:58//AC003043  
 R-HEMBA1002508//Homo sapiens, clone hRPK, 15\_A\_1, complete sequence.//3.7e-09:408:61//AC006213  
 R-nnnnnnnnnnnnn/Homo sapiens mRNA for histone deacetylase-like protein (JM21).//7.1e-112:456:92//AJ011972  
 R-HEMBA1002515  
 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds.//1.6e-104:564:93//AB007923  
 R-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//2.8e-25:186:86//AQ188792  
 R-HEMBA1002547//Mus musculus agrin gene, exon 36.//0.0095:93:75//M92658  
 R-HEMBA1002552//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-49:308:90//AC005378  
 R-HEMBA1002555//Homo sapiens full-length insert cDNA clone YR87G10.//8.3e-65:318:99//AF085957  
 R-HEMBA1002558//, complete sequence.//2.3e-38:264:89//AC005409  
 R-HEMBA1002561//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.1e-44:192:80//AL008634  
 R-nnnnnnnnnnnnn/Homo sapiens protein associated with Myc mRNA, complete cds.//4.5e-119:587:97//AF075587  
 R-HEMBA1002583  
 R-HEMBA1002590//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p3delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p3beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-42:248:88//Z95152  
 R-HEMBA1002592//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//2.6e-56:302:84//AC004510  
 R-HEMBA1002621  
 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//6.7e-76:380:97//AB018351  
 R-HEMBA1002628//P.falcalparum complete gene map of plastid-like DNA (IR-A).//8.8e-05:327:60//X95275  
 R-HEMBA1002629//Mus musculus clone OST16705, genomic survey sequence.//4.3e-06:205:66//AF046247  
 R-HEMBA1002645//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.1e-39:281:84//U14567  
 R-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//1.1e-104:500:95//AC004839  
 R-HEMBA1002659//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//1.2e-61:280:92//AL022323  
 R-HEMBA1002661//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 225E12, WORKING DRAFT SEQUENCE.//3.2e-41:325:81//AL031772  
 R-HEMBA1002666//Homo sapiens full-length insert cDNA clone YY74A07.//0.00037:79:84//AF088008  
 R-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORK-

ING DRAFT SEQUENCE.//2.3e-107:561:94//AL034421  
 R-nnnnnnnnnnn//CIT-HSP-2287E8.TF CIT-HSP Homo sapiens genomic clone 2287E8, genomic survey sequence.//5.4e-17:137:88//B99281  
 R-HEMBA1002688//Homo sapiens chromosome 5, P1 clone 1354A7 (LBNL H47), complete sequence.//0.033:146:70//AC004503  
 R-HEMBA1002696  
 R-HEMBA1002712//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//6.2e-44:302:87//AC003982  
 R-HEMBA1002716//Mus musculus mRNA for ELM1, complete cds.//1.1e-31:332:76//AB004873  
 R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds.//1.2e-35:287:81//AB014521  
 R-HEMBA1002730//D. discoideum actin M6 gene, 5' flank.//0.018:233:66//M29109  
 R-HEMBA1002742//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108H3, WORKING DRAFT SEQUENCE.//2.6e-13:419:62//AL033525  
 R-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//0.019:202:65//AC003694  
 R-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING DRAFT SEQUENCE.//0.046:263:60//AL023883  
 R-HEMBA1002750//Human DNA sequence from PAC 452H17 on chromosome X contains sodium-and chloride-dependent glycine transporter 1 (GLYT-1) like, ESTs.//0.052:421:58//Z96810  
 R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//1.2e-104:545:95//AB011126  
 R-HEMBA1002770//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.0e-07:523:59//AC005140  
 R-HEMBA1002777  
 R-HEMBA1002779//Human HepG2 3' region Mbol cDNA, clone hmd1e03m3.//9.4e-25:158:93//D17139  
 R-HEMBA1002780//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//1.6e-42:463:75//AL022344  
 R-HEMBA1002794//Plasmodium falciparum MAL3P8, complete sequence.//2.2e-05:417:59//AL034560  
 R-HEMBA1002801//Meloidogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes, ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS.//0.00055:444:59//L76261  
 R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//4.4e-115:559:97//AF071185  
 R-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.3e-88:329:94//AC005043  
 R-HEMBA1002826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//1.9e-22:262:67//AP000041  
 R-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//1.3e-79:396:97//AC004707  
 R-HEMBA1002850//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.013:393:61//AC005506  
 R-HEMBA1002863//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//4.1e-73:489:85//AC005562  
 R-HEMBA1002876//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.21:549:55//AL034557  
 R-HEMBA1002886//CIT-HSP-2013C4.TR CIT-HSP Homo sapiens genomic clone 2013C4, genomic survey sequence.//0.30:431:56//B53836  
 R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds.//3.9e-106:541:95//AF037261  
 R-HEMBA1002921  
 R-HEMBA1002924//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10.//4.6e-19:139:78//AB020875  
 R-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//7.5e-45:282:89//AL031681  
 R-HEMBA1002935//CIT-HSP-2282P14.TFB CIT-HSP Homo sapiens genomic clone 2282P14, genomic survey sequence.//1.5e-102:514:97//AQ008584  
 R-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745114, WORKING DRAFT SEQUENCE.//3.3e-87:444:97//AL033532  
 R-HEMBA1002939  
 R-HEMBA1002944//HS\_3107\_A1\_C05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=9 Row=E, genomic survey sequence.//6.3e-21:250:73//AQ103952  
 R-HEMBA1002951//Xeromyces miniatil mitochondrial 12S rRNA gene.//0.013:228:63//AJ008020



- R-HEMBA1002954//HS\_3246\_A2\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=18 Row=M, genomic survey sequence.//5.8e-42:258:91//AQ218005
- R-HEMBA1002968//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//4.2e-38:300:83//AC005553
- 5 R-HEMBA1002970//Slime mold (D. discoideum) prestalk D11 gene, complete cds.//5.0e-05:541:57//M11012
- R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds.//7.2e-29:162:99//AB014579
- R-HEMBA1002973//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//9.1e-36:520:69//AC006128
- 10 R-nnnnnnnnnnn//Homo Sapiens Chromosome X clone BWXD691, complete sequence.//0.00040:504:59//AC004386
- R-HEMBA1002999//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.7e-66:556:79//U19614
- R-HEMBA1003021//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-44:530:70//AC000406
- 15 R-HEMBA1003033//Homo sapiens full-length insert cDNA clone ZC34B10.//4.6e-78:414:94//AF086194
- R-HEMBA1003034//Homo sapiens chromosome 19, cosmid R29351, complete sequence.//9.0e-52:322:75//AC004026
- R-HEMBA1003035//HS\_2008\_A2\_G08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=16 Row=M, genomic survey sequence.//4.0e-68:343:97//AQ269839
- 20 R-HEMBA1003037//347G15.TVB CIT978SKA1 Homo sapiens genomic clone A-347G15, genomic survey sequence.//0.57:188:58//B17694
- R-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//6.3e-30:350:72//AC004983
- 25 R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//4.1e-118:578:97//AF054182
- R-HEMBA1003064//Human cosmid LL12NC01-N-136B11, located centromeric to the ETV6 gene, chromosome 12p12-13.//0.0018:271:60//U59962
- R-HEMBA1003067//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 633019, WORKING DRAFT SEQUENCE.//5.3e-48:464:76//AL022302
- 30 R-HEMBA1003071//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.19:48:87//AQ110136
- R-HEMBA1003077//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.9e-69:494:84//U42975
- 35 R-HEMBA1003078//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.1e-11:331:64//Z97054
- R-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//4.6e-116:576:98//AC004673
- 40 R-HEMBA1003083//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-43:280:83//AC005798
- R-HEMBA1003086//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3-unordered pieces.//1.2e-43:281:88//AC006039
- R-HEMBA1003096//Human DNA sequence from clone J506G21, WORKING DRAFT SEQUENCE.//0.00037:421:59//Z82213
- 45 R-HEMBA1003098//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.4e-30:303:78//AC005598
- R-HEMBA1003117
- R-HEMBA1003129//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F11, WORKING DRAFT SEQUENCE.//7.9e-11:109:85//AL022329
- 50 R-HEMBA1003133//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.9e-99:484:98//AC004472
- R-HEMBA1003136//CIT-HSP-2281L22.TF CIT-HSP Homo sapiens genomic clone 2281L22, genomic survey sequence.//2.0e-10:93:92//B99861
- R-HEMBA1003142//Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.8e-40:270:87//AC004024
- 55 R-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//1.1e-116:586:96//AJ005670
- R-HEMBA1003166//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//6.4e-35:364:70//Z83822

- R-HEMBA1003175//Human IFNAR gene for interferon alpha/beta receptor.//1.9e-30:282:77//X60459  
R-HEMBA1003197
- 5 R-HEMBA1003199//HS\_2166\_A1\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=23 Row=I, genomic survey sequence.//0.00026:271:61//AQ164162  
R-HEMBA1003202//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.4e-44:291:83//AC005480  
R-HEMBA1003204//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//3.1e-10:293:62//AC000118
- 10 R-HEMBA1003212//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.0:118:69//AC006148  
R-HEMBA1003220//HS\_3092\_B1\_F09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=17 Row=L, genomic survey sequence.//0.00014:59:91//AQ128202  
R-HEMBA1003222//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y43F8, WORKING DRAFT SEQUENCE.//0.84:214:62//Z95393
- 15 R-HEMBA1003229//RPCI11-16F15.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16F15, genomic survey sequence.//0.42:167:64//B83610  
R-HEMBA1003235//CIT-HSP-2320G19.TF CIT-HSP Homo sapiens genomic clone 2320G19, genomic survey sequence.//3.6e-36:195:81//AQ037231  
R-HEMBA1003250//HS\_2168\_A2\_C09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=18 Row=E, genomic survey sequence.//1.4e-22:158:89//AQ125356
- 20 R-HEMBA1003257//Human PCP4 gene, exon 3 and complete cds.//0.96:268:61//U53709  
R-HEMBA1003273//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//1.0e-32:255:84//AC002549  
R-HEMBA1003276//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0044:212:60//AC005308
- 25 R-HEMBA1003278//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-34:286:74//AC002395  
R-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.8e-53:428:83//AC005840
- 30 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//3.0e-115:551:99//AB011109  
R-HEMBA1003296//CIT-HSP-2196L16.TR CIT-HSP Homo sapiens genomic clone 2196L16, genomic survey sequence.//2.9e-20:337:65//AQ003073  
R-HEMBA1003304//Sequence 230 from patent US 5552281//1.8e-31:179:97//U25662
- 35 R-HEMBA1003309//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence.//0.00019:334:60//AB017061  
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//2.8e-111:545:97//AB001872  
R-HEMBA1003322//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.60:274:61//AL022153
- 40 R-HEMBA1003327//Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.//0.00028:172:65//AC005099  
R-HEMBA1003328//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.2e-44:268:90//AC005081  
R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds.//2.7e-61:312:97//AF026029
- 45 R-HEMBA1003348//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.2e-38:186:83//U14567  
R-HEMBA1003369//Caenorhabditis elegans cosmid F59C6, complete sequence.//0.00012:465:59//Z79600  
R-HEMBA1003370//Homo sapiens chromosome 17, clone hRPC867C24, complete sequence.//3.2e-42:301:87//AC002558
- 50 R-HEMBA1003373//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.4e-34:375:74//AL022721
- 55 R-HEMBA1003376//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//1.6e-46:309:88//AC004651  
R-HEMBA1003380//HS\_3184\_B2\_E06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=12 Row=J, genomic survey sequence.//1.0e-35:237:88//AQ189144

- R-HEMBA1003384//HS\_2193\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=16 Row=P, genomic survey sequence.//0.00029:96:76//AQ032212
- R-HEMBA1003395//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.6e-21:139:86//AC002993
- 5 R-HEMBA1003402//CIT-HSP-2166E19, TR CIT-HSP Homo sapiens genomic clone 2166E19, genomic survey sequence.//0.99:144:61//B91549
- R-nnnnnnnnnnn
- R-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//2.5e-112:547:98//AL031321
- 10 R-HEMBA1003418//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//0.082:352:59//AC004879
- R-HEMBA1003433//Homo sapiens cell cycle regulatory protein p95 (NBS1) mRNA, complete cds.//9.9e-114:544:98//AF058696
- R-HEMBA1003461
- 15 R-HEMBA1003463
- R-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//9.1e-106:533:96//AC005041
- R-HEMBA1003528
- R-HEMBA1003531//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//3.4e-08:333:64//AC002454
- 20 R-HEMBA1003538//Human mRNA for complement component C1r.//1.4e-23:333:68//X04701
- R-HEMBA1003545//Zebrafish mRNA for zfls-2 (insulin gene enhancer binding protein homolog), complete cds.//0.030:144:68//D38453
- R-HEMBA1003548//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0017:487:57//AC004153
- 25 R-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 371H6, WORKING DRAFT SEQUENCE.//2.8e-99:503:96//AL031718
- R-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//1.6e-114:574:97//AC005913
- R-HEMBA1003560//Diplolepis rosae microsatellite clone DR04096.//0.24:116:67//AF034416
- 30 R-HEMBA1003568//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.9e-05:422:63//AC006036
- R-HEMBA1003569//Homo sapiens full-length insert cDNA clone ZD82D06.//8.7e-108:545:95//AF086450
- R-HEMBA1003571//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//4.6e-51:570:71//AC004914
- 35 R-HEMBA1003579//HS\_3237\_B2\_E05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237 Col=10 Row=J, genomic survey sequence.//8.5e-97:495:95//AQ029302
- R-HEMBA1003581//Mouse mRNA for talin.//8.3e-12:128:82//X56123
- R-HEMBA1003591//Homo sapiens chromosome 16, BAC clone 2603 (LANL), complete sequence.//2.9e-87:251:95//AC005774
- 40 R-HEMBA1003595//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a ggtt repeat polymorphism, complete sequence.//4.5e-52:384:83//AL008715
- R-HEMBA1003597//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.6e-41:442:74//Z84480
- 45 R-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.8e-23:177:88//AC005153
- R-HEMBA1003615
- R-HEMBA1003617//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:494:57//AC005139
- 50 R-HEMBA10036211\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0052122, HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.3e-26:309:75//AC004599
- R-HEMBA1003622//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//7.1e-56:545:75//AC002980
- 55 R-HEMBA1003630//Homo sapiens CC chemokine gene cluster, complete sequence.//2.8e-32:546:68//AF088219
- R-HEMBA1003637//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//8.0e-25:457:68//AC002454
- R-HEMBA1003640//Homo sapiens chromosome X, PAC 671D9, complete sequence.//2.8e-40:280:86//AF031078

- R-HEMBA1003645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//1.7e-33:297:82//AL023693
- R-HEMBA1003646//Plasmodium falciparum MAL3P7, complete sequence.//0.44:319:59//AL034559
- 5 R-HEMBA1003656//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-36:242:80//AC004382
- R-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//8.6e-117:588:96//AC005746
- R-HEMBA1003667//Sequence 8 from patent US 5420245.//1.8e-21:170:88//I12222
- 10 R-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.6e-22:180:87//AC005065
- R-HEMBA1003680//C. elegans cosmid ZK353.//1.1e-06:270:61//L15313
- R-HEMBA1003684//Colias alexandra alexandra cytochrome oxidase subunit I (cox1) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.77:171:66//AF044872
- 15 R-HEMBA1003690//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-104:523:97//AC004466
- R-HEMBA1003692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//1.7e-41:414:77//AL021707
- R-HEMBA1003711//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-29:304:77//AC000406
- 20 R-HEMBA1003714
- R-HEMBA1003715//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-685D8, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-63:578:77//AC005136
- R-HEMBA1003720//Homo sapiens, WORKING DRAFT SEQUENCE, 135 unordered pieces.//2.4e-36:350:78//AC002353
- 25 R-HEMBA1003725//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//6.3e-42:250:75//AC004699
- R-HEMBA1003729//RPCI11-22D14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22D14, genomic survey sequence.//1.0:234:62//B86158
- R-HEMBA1003733//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.7e-80:558:83//AL008634
- 30 R-HEMBA1003742//HS\_3080\_B2\_H06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=12 Row=P, genomic survey sequence.//3.4e-55:331:91//AQ139179
- R-HEMBA1003758//Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains ESTs, CA repeat, STS and CpG Island.//4.5e-59:521:75//Z97876
- 35 R-HEMBA1003760
- R-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//2.6e-72:467:86//U17343
- R-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.0e-77:557:81//AF084259
- 40 R-HEMBA1003784
- R-HEMBA1003799//Homo sapiens PAC clone DJ1032B10 from 7p15.3-p21, complete sequence.//2.1e-49:390:72//AC004455
- R-HEMBA1003803
- 45 R-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//9.4e-99:359:99//AC004596
- R-HEMBA1003805//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.0e-113:567:96//AL031781
- 50 R-HEMBA1003807//Bovine dinucleotide microsatellite HUJ177.//5.4e-18:194:78//M96348
- R-HEMBA1003836//Human DNA from overlapping chromosome 19 cosmids R31396, F2545L and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//3.4e-40:256:85//AC002115
- R-HEMBA1003838//CIT-HSP-2380F18.TF CIT-HSP Homo sapiens genomic clone 2380F18, genomic survey sequence.//9.7e-25:150:96//AQ196624
- 55 R-HEMBA1003856//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//4.8e-33:486:68//Z93929
- R-HEMBA1003864//, complete sequence.//4.4e-100:531:94//AC005300

- R-HEMBA1003866//HS\_3203\_B2\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=2 Row=F, genomic survey sequence.//2.6e-05:206:64//AQ180298  
R-HEMBA1003879//Human sapiens chromosome 10 clone CIT987SK-1119P3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.7e-17:170:79//UB2207
- 5 R-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//7.8e-103:526:96//AP000036  
R-HEMBA1003885//Human apolipoprotein apoC-IV (APOC4) gene, complete cds.//3.5e-45:299:87//U32576  
R-HEMBA1003893//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE.//1.1e-41:386:77//AL034421
- 10 R-HEMBA1003902//HS\_3031\_B2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3031 Col=14 Row=J, genomic survey sequence.//5.3e-50:293:93//AQ165549  
R-HEMBA1003908//CIT-HSP-2367K7.TR CIT-HSP Homo sapiens genomic clone 2367K7, genomic survey sequence.//1.2e-32:220:92//AQ076795  
R-HEMBA1003926//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//3.1e-58:294:85//AC005368  
R-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//8.0e-111:590:93//AF109718  
R-HEMBA1003939  
R-HEMBA1003942//Homo sapiens clone DJ0828F13, complete sequence.//2.2e-08:474:58//AC004904  
R-HEMBA1003950//Plasmodium vivax from Brazil cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.034:258:62//AF069619
- 20 R-HEMBA1003953//Plasmodium falciparum MAL3P8, complete sequence.//0.096:492:57//AL034560  
R-HEMBA1003958//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING DRAFT SEQUENCE.//7.3e-40:382:78//AL031668  
R-HEMBA1003959//Amaranthus hypochondriacus betaine aldehyde dehydrogenase (ahyd4h4) gene, complete cds.//0.11:428:60//AF000132
- 25 R-HEMBA1003976//Homo sapiens PAC clone DJ0724E13 from 7p11.2-p12, complete sequence.//1.0:222:62//AC004414  
R-HEMBA1003978//Sequence 31 from patent US 5708157.//1.9e-14:159:77//B0060  
R-HEMBA1003985//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.6e-14:136:83//AC004804  
R-HEMBA1003987//Human chromosome 12p13 sequence, complete sequence.//3.2e-26:268:79//U47924  
R-HEMBA1003989//RPCI11-52K22.TJ RPCI11 Homo sapiens genomic clone R-52K22, genomic survey sequence.//2.2e-86:443:95//AQ052484  
R-HEMBA1004000  
R-HEMBA1004011
- 35 R-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//4.7e-38:284:85//AC005670  
R-HEMBA1004015//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//0.48:460:58//AL023575  
R-HEMBA1004024//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.5e-21:159:80//AC005081  
R-HEMBA1004038//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.9e-10:231:66//AC006054  
R-HEMBA1004042//Homo sapiens clone DJ096816, complete sequence.//0.00071:263:68//AC006016
- 45 R-HEMBA1004045//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//8.8e-23:196:69//AC006143  
R-HEMBA1004048//CIT-HSP-2288N20.TF CIT-HSP Homo sapiens genomic clone 2288N20, genomic survey sequence.//0.013:162:67//AQ007283  
R-HEMBA1004049//Human hsp 70 gene 3' region for 70 kDa heat shock protein.//7.7e-30:176:96//X04677  
R-HEMBA1004055//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.4e-05:395:63//AC005504  
R-HEMBA1004056//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-61:551:77//AC005484  
R-HEMBA1004074//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.98:275:63//AC004952
- 55 R-HEMBA1004086//Sequence 65 from patent US 5691147.//2.8e-54:313:92//76237  
R-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//1.8e-11:323:63//AF091234  
R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds.//9.3e-42:534:69//D50918

- R-HEMBA1004132//Homo sapiens chromosome 17, done hCIT211\_P\_7, complete sequence.//6.0e-49:491:76//AC003665
- R-HEMBA1004133//HS\_3229\_B2\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=18 Row=J, genomic survey sequence.//1.1e-72:374:97//AQ192003
- 5 R-HEMBA1004138//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING DRAFT SEQUENCE.//3.1e-09:277:66//AL024498
- R-HEMBA1004143//Plasmodium falciparum MAL3P4, complete sequence.//0.53:239:61//AL0008970
- 10 R-HEMBA1004146//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.0e-35:165:88//AC004820
- R-HEMBA1004150//CITBI-E1-2517I2.TR CITBI-E1 Homo sapiens genomic clone 2517I2, genomic survey sequence.//0.56:379:59//AQ277616
- R-HEMBA1004164//Human BAC clone GS200K05 from 7q21-q22, complete sequence.//4.6e-49:448:77//AC002429
- 15 R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//2.4e-110:563:96//AF067855
- R-HEMBA1004199//S.pombe chromosome I cosmid c8A4.//0.73:187:64//Z66569
- R-HEMBA1004200//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//6.3e-30:293:77//AC004552
- R-HEMBA1004202//rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].//3.0e-64:517:80//S72304
- 20 R-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.0e-97:303:98//AC005488
- R-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.6e-116:573:97//U50748
- R-HEMBA1004225//Drosophila melanogaster mitochondrial DNA with 12 tRNAs and 7 genes.//5.4e-11:493:60//M37275
- 25 R-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//6.1e-76:443:86//AF095927
- R-HEMBA1004238//Homo sapiens chromosome 19, cosmid R28341, complete sequence.//1.1e-42:330:83//AC005763
- R-HEMBA1004241
- 30 R-HEMBA1004246//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//1.1e-45:288:85//AP000011
- R-HEMBA1004248//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.2e-09:516:61//AC004903
- R-HEMBA1004264
- 35 R-HEMBA1004267//HS\_2255\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=24 Row=O, genomic survey sequence.//8.6e-59:318:95//AQ068854
- R-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCIS-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-113:576:96//AC005831
- R-nnnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence.//4.4e-110:553:96//AF091081
- 40 R-HEMBA1004276
- R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//1.9e-106:538:97//AF022795
- R-HEMBA1004289//RPC111-74010.TJ RPC111 Homo sapiens genomic clone R-74010, genomic survey sequence.//2.3e-37:248:76//AQ266668
- 45 R-HEMBA1004295//Baboon apolipoprotein A-VI mRNA, 3' end.//0.0016:273:64//L13174
- R-HEMBA1004306//HS\_3175\_B2\_F01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3175 Col=2 Row=L, genomic survey sequence.//1.6e-28:190:77//AQ169206
- R-HEMBA1004312//Human BAC clone RG119P24 from 7q31, complete sequence.//6.3e-36:267:82//AC003088
- R-HEMBA1004321//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 10155, WORKING DRAFT SEQUENCE.//4.1e-111:576:95//AJ009611
- 50 R-HEMBA1004323//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//2.7e-42:136:91//AQ114933
- R-HEMBA1004327//CIT-HSP-2303L24.TF CIT-HSP Homo sapiens genomic clone 2303L24, genomic survey sequence.//1.0:78:67//AQ017600
- 55 R-HEMBA1004330//Homo sapiens clone DJ1173120, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-119:580:98//AC004987
- R-HEMBA1004334//Pimpinella brachycarpa Phylb mRNA, complete cds.//3.3e-14:238:69//AF082024
- R-HEMBA1004335//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.8e-

21:291:71//AC004638  
R-HEMBA1004341  
R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds.//4.1e-74:444:90//D89667  
R-HEMBA1004354//Human DNA from overlapping chromosome 19-specific cosmid R29515 and R28253, genomic sequence, complete sequence.//7.0e-38:287:82//AC003002  
5 R-HEMBA1004356//Sequence 2 from patent US 5652144.//3.7e-108:588:92//58611  
R-HEMBA1004366//WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-14:446:63//AC005949  
R-HEMBA1004372//CIT-HSP-2005C13.TF CIT-HSP Homo sapiens genomic clone 2005C13, genomic survey sequence.//0.010:334:61//B55811  
10 R-HEMBA1004389//Homo sapiens full-length insert cDNA clone ZE09A11.//1.5e-19:170:83//AF086540  
R-HEMBA1004394//Human (D21S198) DNA segment containing (TG)23 repeat.//1.0:50:84//X58124  
R-HEMBA1004396//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//8.2e-34:459:69//AC004057  
15 R-HEMBA1004405//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//2.8e-42:314:84//AC005030  
R-HEMBA1004408  
R-HEMBA1004429//M.musculus of DNA encoding DNA-binding protein.//1.6e-66:449:82//Z54200  
R-HEMBA1004433//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//7.2e-32:460:68//AJ011930  
20 R-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.9e-113:581:96//AC004846  
R-HEMBA1004461//HS\_3244\_A2\_F12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=24 Row=K, genomic survey sequence.//8.0e-83:397:99//AQ220876  
R-HEMBA1004479//Homo sapiens PAC clone DJ094216 from 7q11, complete sequence.//1.7e-40:485:70//AC006012  
25 R-HEMBA1004482//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//2.2e-11:513:59//AE001370  
R-HEMBA1004502//Homo sapiens chromosome 17, clone hRPK.372\_K\_20, complete sequence.//2.0e-08:245:66//AC005951  
30 R-HEMBA1004506//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34606, WORKING DRAFT SEQUENCE.//4.2e-81:582:83//Z84487  
R-HEMBA1004507//Caenorhabditis elegans cosmid C40C9, complete sequence.//0.56:235:64//Z70266  
R-HEMBA1004509  
R-HEMBA1004534//Sequence 58 from patent US 5691147.//1.9e-61:430:83//I76230  
35 R-HEMBA1004538//HS\_3189\_B2\_C03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=6 Row=F, genomic survey sequence.//6.1e-21:140:92//AQ170330  
R-HEMBA1004554//CIT-HSP-712K9.TP CIT-HSP Homo sapiens genomic clone 712K9, genomic survey sequence.//1.7e-16:116:93//B73329  
40 R-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//2.2e-14:213:71//D87457  
R-HEMBA1004573  
R-HEMBA1004577//Human DNA sequence from cosmid L247F6, Huntington's Disease Region, chromosome 4p16.3 contains protein similar to Mouse SH3 binding protein 3BP2, multiple ESTs and a CpG island.//1.0:352:60//Z68279  
R-HEMBA1004586  
45 R-nnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.0012:359:60//Z98551  
R-HEMBA1004610//S. pombe chromosome II cosmid c354.//0.0011:362:62//AL022071  
R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501.14e-50:327:85//AB007970  
R-HEMBA1004629//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human BAC Library) complete sequence.//4.4e-13:527:63//AC004805  
50 R-HEMBA1004631//Rattus norvegicus Nc1one10 mRNA.//2.9e-24:364:71//U31866  
R-HEMBA1004632  
R-HEMBA1004637//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-117:573:98//AC005534  
55 R-HEMBA1004638//H. sapiens mRNA for DGCR2.//3.8e-19:118:99//X84076  
R-HEMBA1004666//Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence.//0.00013:501:58//AC005171  
R-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel

genes, ESTs, GSSs and CpG islands, complete sequence.//1.5e-120:571-98//AL031432  
 R-HEMBA1004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING  
 DRAFT SEQUENCE.//4.4e-12:110:88//Z93241  
 R-HEMBA1004672//Human DNA sequence from PAC 308I13 on chromosome 1p35-1p36.3.//3.4e-38:324:81//  
 Z99291  
 R-HEMBA1004693//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//  
 0.86:309:57//AB006702  
 R-HEMBA1004697//T33B22TF TAMU Arabidopsis thaliana genomic clone T33B22, genomic survey sequence.//  
 0.29:331:61//B97342  
 R-HEMBA1004705//Plasmodium falciparum MAL3P7, complete sequence.//0.051:424:58//AL034559  
 R-HEMBA1004709//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.7e-  
 49:497:76//AC004638  
 R-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//1.6e-38:362:  
 79//AC005562  
 R-HEMBA1004725  
 R-HEMBA1004730//Homo sapiens Chromosome 17p13 Cosmid Clone cos26, complete sequence.//1.1e-58:489:  
 79//AC02085  
 R-HEMBA1004733  
 R-HEMBA1004734//Human DNA sequence from clone 273N12 on chromosome 6q16.1-16.3. Contains the gene  
 for the N-Oct5a (N-Oct3, N-Oct5b) POU domain proteins and an unknown gene. Contains a putative CpG island,  
 ESTs, STS; and GSSs, complete sequence.//0.0030:362:61//AL022395  
 R-HEMBA1004736//Homo sapiens clone DJ0981007, complete sequence.//1.9e-58:282:87//AC006017  
 R-HEMBA1004748//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//3.6e-34:287:  
 81//AC004953  
 R-HEMBA1004751//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S riboso-  
 mal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//5.3e-40:266:89//Z98950  
 R-HEMBA1004752//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 495010, WORKING  
 DRAFT SEQUENCE.//3.3e-39:281:85//AL031121  
 R-HEMBA1004753//Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.//2.6e-65:475:84//  
 L06498  
 R-HEMBA1004756//Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone  
 genes H2A1, H2B.1A, H4, H2A.1b, H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG  
 island.//1.8e-08:516:59//AL021807  
 R-HEMBA1004758//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//5.1e-45:577:  
 72//AC004057  
 R-HEMBA1004763  
 R-HEMBA1004768//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1  
 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Amino-  
 transferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2)  
 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-60:435:78//AL022310  
 R-HEMBA1004770//Plasmodium falciparum chromosome 2, section 8 of 73 of the complete sequence.//8.7e-05:  
 476:61//AE001371  
 R-HEMBA1004771//Homo sapiens Xp22 Cosmid U152D7 (Lawrence Livermore human cosmid library) complete  
 sequence.//5.0e-08:113:80//AC003047  
 R-HEMBA1004776  
 R-HEMBA1004778//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-35:288:84//U14567  
 R-nnnnnnnnnnn/HS\_3192\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic  
 clone Plate=3192 Col=17 Row=L, genomic survey sequence.//1.9e-44:233:98//AQ155855  
 R-HEMBA1004803//Homo sapiens minisatellite ms31 repeat region.//3.0e-67:318:87//AF048728  
 R-HEMBA1004806  
 R-HEMBA1004807//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-  
 20:333:69//AC005015  
 R-HEMBA1004816//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE  
 LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.  
 Contains polymorphic CA repeat.//6.3e-13:148:77//Z92545  
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds.//1.5e-12:141:85//M74002  
 R-HEMBA1004847//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//7.6e-80:297:85//  
 X53744



R-HEMBA1004850  
 R-HEMBA1004863/Human DNA sequence from PAC 345P10 on chromosome 22q12-qter contains ESTs and STS and polymorphic CA repeat D22S927.//2.0e-14:159:79//Z82201  
 R-HEMBA1004864  
 5 R-HEMBA1004865/Homo sapiens Xp22-149 BAC RPC111-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.90:76:76//AC005297  
 R-HEMBA1004880/Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-49:551:73//AC004826  
 10 R-HEMBA1004889/Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 223B1, WORKING DRAFT SEQUENCE.//0.0021:189:65//AL031943  
 R-HEMBA1004900/Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//6.6e-11:144:7711AC005972  
 R-HEMBA1004909/Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//7.6e-46:341:83//Z98052  
 15 R-HEMBA1004918/Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 994L9, WORKING DRAFT SEQUENCE.//1.6e-54:301:89//AL034554  
 R-HEMBA1004923/Homo sapiens 47kB DNA fragment from Xq28, proximal to MTM1 gene.//2.0e-07:182:69//Y15994  
 R-HEMBA1004929  
 20 R-HEMBA1004930/Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.7e-66:547:79//AC005848  
 R-HEMBA1004933/H. sapiens Humig mRNA.//0.13:233:62//X72755  
 R-HEMBA1004934/CIT-HSP-2021116.TF CIT-HSP Homo sapiens genomic-clone 2021116, genomic survey sequence.//0.66:268:62//B65345  
 25 R-HEMBA1004944/CIT-HSP-22811L12.TR CIT-HSP Homo sapiens genomic clone 22811L12, genomic survey sequence.//3.8e-20:104:82//B99849  
 R-HEMBA1004954/Homo sapiens chromosome 17, clone hRPK.146\_P\_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00082:385:60//AC005341  
 R-HEMBA1004956/CIT-HSP-2305H22.TF CIT-HSP Homo sapiens genomic clone 2305H22, genomic survey sequence.//1.6e-84:411:99//AQ020408  
 30 R-HEMBA1004960/Human DNA sequence from PAC 358H7 on chromosome X.//3.3e-22:249:74//Z77249  
 R-HEMBA1004972/hnxb0003aF01f CUGI Rice BAC Library Oryza sativa genomic clone hnxb0003K01f, genomic survey sequence.//0.52:171:64//AQ049982  
 R-HEMBA1004973/\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.69:179:64//AC003656  
 35 R-HEMBA1004977/Caenorhabditis elegans cosmid F08G2, complete sequence.//7.6e-07:492:58//Z81495  
 R-HEMBA1004978/Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.20:427:60//AL024509  
 40 R-HEMBA1004980/CIT-HSP-2379K5.TF CIT-HSP Homo sapiens genomic clone 2379K5, genomic survey sequence.//1.6e-53:331:88//AQ108614  
 R-HEMBA1004983/Genomic sequence from Human 17, complete sequence.//0.00061:473:58//AC000389  
 45 R-HEMBA1004995/Homo sapiens chromosome 16, cosmid clone 306E5 (LANL), complete sequence.//1.6e-90:527:89//AC004224  
 R-HEMBA1005007/Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudogenes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//5.4e-65:357:83//AL031663  
 50 R-HEMBA1005009/Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//5.6e-107:550:96//AF041474  
 R-HEMBA1005019/Homo sapiens mRNA for KIAA0648 protein, partial cds.//6.3e-104:542:94//AB014548  
 55 R-HEMBA1005029/Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal Protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c),

H4FFP (H4f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//3.1e-67.493:83//AL009179  
R-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//7.4e-101:537:94//AC004596

5 R-HEMBA1005039//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//9.5e-30:446:68//AL031650

R-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//1.4e-34:229:88//Z22819

R-HEMBA1005050//Human Chromosome X PAC RPC1.290C9 from the Pieter de Jong Human PAC library; complete sequence.//4.0e-43:371:80//AC002404

10 R-HEMBA1005062//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//2.3e-15:269:66//AC004675

R-HEMBA1005066//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-30:305:74//AC006030

R-HEMBA1005075

15 R-HEMBA1005079//Homo sapiens clone HS.19.11 Alu-Ya5 sequence.//6.5e-48:245:91//AF015156

R-HEMBA1005083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.3e-15:142:83//AL034423

R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//5.3e-110:545:96//AF080561

20 R-HEMBA1005113//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53C10, WORKING DRAFT SEQUENCE.//0.026:252:64//Z93340

R-HEMBA1005123//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//7.1e-55:306:82//AL022336

25 R-HEMBA1005133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//6.4e-45:309:87//AL022345

R-HEMBA1005149//Human cosmid LL12NC01-95H4, ETV6 gene, exon 2 and partial cds.//3.2e-31:310:76//U81834

R-HEMBA1005152//Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.//1.4e-33:361:79//AL021407

30 R-HEMBA1005159//Human DNA sequence from clone 163016 on chromosome 1p35.1-36.13 Contains CA repeat, STS, complete sequence.//2.7e-22:440:66//AL031279

R-HEMBA1005185//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE.//0.0017:381:58//AL022594

35 R-HEMBA1005201//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.5e-05:457:57//X95276

R-HEMBA1005202//Human 18S ribosomal RNA.//4.7e-38:236:91//X03205

R-HEMBA1005219

R-HEMBA1005223//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//1.0:209:65//AC004854

40 R-HEMBA1005232//Homo-sapiens chromosome Y, clone 264.M.20, complete sequence.//0.0040:439:58//AC004617

R-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//4.2e-111:568:96//AC005154

45 R-HEMBA1005244//HS\_3092\_B2\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=22 Row=F, genomic survey sequence.//4.9e-12:116:84//AQ127947

R-HEMBA1005251//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//3.2e-27:210:84//AC004548

R-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//4.6e-105:437:97//AC005837

50 R-HEMBA1005274//Slime mold mitochondrial DNA, binding region to the membrane system.//0.011:339:59//D86630

R-HEMBA1005275//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//3.4e-17:269:71//AC004914

R-HEMBA1005293//Human DNA sequence from PAC 130N4, BRCA2 gene region chromosome 13q12-13 contains xs7 mRNA, ESTs.//6.9e-20:193:73//Z57887

55 R-HEMBA1005296//HS\_3037\_B1\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=1 Row=H, genomic survey sequence.//0.26:184:64//AQ117120

R-HEMBA1005304//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//

- 1.5e-58:445:78//AC006146  
 R-HEMBA1005311//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796E4, WORKING DRAFT SEQUENCE.//9.3e-42:383:78//AL022337  
 R-HEMBA1005314//Caenorhabditis elegans cosmid F23H11.//0.80:179:65//AF003389  
 5 R-HEMBA1005315//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-40:409:71//AC006030  
 R-HEMBA1005318//S.pombe chromosome I cosmid c2E11.//0.97:370:61//AL031181  
 R-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//1.9e-112:577:95//AC005803  
 10 R-HEMBA1005353//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 429E7, WORKING DRAFT SEQUENCE.//8.9e-80:406:97//AL031722  
 R-HEMBA1005359//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-50:320:84//AC005412  
 R-HEMBA1005367//RPC111-85E23.TV RPC111 Homo sapiens genomic clone R-85E23, genomic survey sequence.//0.39:148:67//AQ281915  
 15 R-HEMBA1005372//Homo sapiens full-length insert cDNA YH93B03.//2.6e-108:557:95//AF074997  
 R-HEMBA1005374//Homo sapiens full-length insert cDNA clone ZA95D11.//1.9e-110:531:98//AF086142  
 R-HEMBA1005389//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Txp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RS (X-linked juvenile retinosis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//6.0e-41:432:75//Z92542  
 20 R-HEMBA1005394//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 681N20, WORKING DRAFT SEQUENCE.//4.9e-107:585:93//AL031670  
 R-HEMBA1005403//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//5.1e-118:586:97//AL034379  
 25 R-HEMBA1005408//Bos taurus retina membrane guanylate cyclase ROS-GC2 mRNA, complete cds.//1.6e-06:204:68//U95958  
 R-HEMBA1005410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//1.2e-23:452:66//AL008722  
 30 R-HEMBA1005411//RPC111-66N19.TK RPC111 Homo sapiens genomic clone R-66N19, genomic survey sequence.//2.2e-38:222:79//AQ237442  
 R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//5.6e-117:453:99//AF041248  
 35 R-HEMBA1005426//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//0.86:278:60//Z97196  
 R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment.//5.4e-46:305:87//L40391  
 R-HEMBA1005447//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//3.3e-79:531:86//AL031054  
 40 R-HEMBA1005468//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//4.0e-27:469:66//AC004894  
 R-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//7.2e-40:410:76//AC005212  
 R-HEMBA1005472//Human DNA Sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1090E8, WORKING DRAFT SEQUENCE.//3.1e-40:296:85//AL033524  
 45 R-HEMBA1005475//HS\_2266\_B2\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=8 Row=F, genomic survey sequence.//0.49:209:61//AQ069377  
 R-HEMBA1005497  
 R-HEMBA1005500//Homo sapiens PAC clone DJ1093O17 from 7q11.23-q21, complete sequence.//4.5e-116:580:97//AC004957  
 50 R-HEMBA1005506//Arabidopsis thaliana BAC T26D22.//0.0050:442:59//AF058826  
 R-HEMBA1005508//Sigalaphus sp. 16S ribosomal RNA gene, partial sequence.//0.020:391:59//AF003509  
 R-HEMBA1005511//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.44:195:63//Z96811  
 55 R-HEMBA1005517//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.44:470:57//L14320  
 R-HEMBA1005518//M.musculus mRNA for paladin gene.//6.2e-29:183:81//X99384  
 R-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-40:281:86//AC004913

- R-HEMBA1005528//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//3.9e-40:482:73//Z97985
- R-HEMBA1005528//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//3.8e-84:309:99//AB020860
- 5 R-HEMBA1005530//Homo sapiens PAC clone 946B23 SCA2 region, SP6 end, genomic sequence, genomic survey sequence.//8.1e-25:154:94//U84091
- R-HEMBA1005548//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 970A17, WORKING DRAFT SEQUENCE.//5.3e-105:534:96//AL034431
- 10 R-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//2.8e-69:432:88//AC004743
- R-HEMBA1005558
- R-HEMBA1005568//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//5.9e-33:367:74//AC004087
- R-HEMBA1005570//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin. ESTs and GSSs, complete sequence.//2.2e-67:399:91//AL020989
- 15 R-HEMBA1005576//Homo sapiens chromosome 16, BAC clone 97H22 (LANL), complete sequence.//1.0:156:631//AC005737
- R-HEMBA1005577
- R-HEMBA1005581//Homo sapiens mRNA for MEGFS, partial cds.//9.7e-27:561:64//AB011538
- 20 R-HEMBA1005582//Torulopsis glabrata mitochondrial intergenic region ATPase 9-cytochrome oxidase 2 genes.//2.3e-10:404:62//X02171
- R-HEMBA1005583//HS\_3014\_B1\_D05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=9 Row=H, genomic survey sequence.//3.0e-81:442:94//AQ154499
- R-HEMBA1005588//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains an Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//1.8e-54:490:77//Z98046
- 25 R-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//2.2e-28:262:79//AC005746
- R-HEMBA1005595//HS\_2224\_A2\_G03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2224 Col=6 Row=M, genomic survey sequence.//3.6e-48:263:95//AQ033446
- R-HEMBA1005606//Human PAC clone DJ0093103 from Xq23, complete sequence.//2.5e-08:355:63//AC003983
- R-HEMBA1005609//HS\_2182\_B1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=P, genomic survey sequence.//2.2e-82:400:99//AQ023130
- 35 R-HEMBA1005616//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 124K22, WORKING DRAFT SEQUENCE.//0.80:308:60//AL031176
- R-HEMBA1005621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//7.4e-76:338:98//AL031731
- R-HEMBA1005627//Homo sapiens full-length insert cDNA clone ZD53D02.//4.5e-72:398:93//AF086321
- 40 R-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//3.8e-17:548:60//AC004460
- R-HEMBA1005632//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.4e-13:172:75//AL020269
- R-HEMBA1005634//RPC111-13015.TVB RPC1-11 Homo sapiens genomic clone RPC1-11-13015, genomic survey sequence.//1.0e-28:153:82//B73293
- 45 R-HEMBA1005666//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//4.5e-51:343:87//AL021786
- R-HEMBA1005670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//2.5e-33:288:78//AL020995
- R-HEMBA1005679//Human esterase D mRNA, 3'end.//4.2e-49:322:88//M13450
- 50 R-HEMBA1005680//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.0e-36:285:83//AC005924
- R-HEMBA1005685//H. sapiens (MAR8) chromosome 19 DNA, 343bp.//0.022:65:86//Z35281
- R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds.//5.4e-46:376:84//U66406
- 55 R-HEMBA1005705//RPC111-13014.TP RPC1-11 Homo sapiens genomic clone RPC1-11-13014, genomic survey sequence.//0.071:182:59//B76186
- R-HEMBA1005717//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.

Contains polymorphic CA repeat.//1.0:189:66//Z92545

R-HEMBA1005732//Human Chromosome 11q12 pac pDJ363p2, WORKING DRAFT SEQUENCE, 22 unordered pieces.//2.1e-47:449:75//AC003023

R-HEMBA1005737

R-nnnnnnnnnnn//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//0.11:174:63//X91255

R-HEMBA1005755//Human DNA-sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//0.15:160:65//AL008634

R-HEMBA1005765//Human Xq28 cosmids U225B5 and U236A12, complete sequence.//5.2e-39:422:74//U71148

R-HEMBA1005780//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.037:261:61//AP000010

R-HEMBA1005813//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.7e-26:242:80//AL023808

R-HEMBA1005815//Bufo boreas MVZ 145227 c-mos gene, partial cds.//0.17:199:62//U52805

R-HEMBA1005822//Plasmodium falciparum MAL3P7, complete sequence.//0.26:437:56//AL034559

R-HEMBA1005829//Human Cosmid g1572c035, complete sequence.//3.8e-05:366:61//AC000124

R-HEMBA1005834//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.2e-107:551:96//AL031781

R-HEMBA1005852//F.ribripes GSS sequence, clone 163A22aA4, genomic survey sequence.//2.6e-17:225:72//AL018730

R-HEMBA1005853//Human Chromosome 15 pac pDJ24m8, complete sequence.//1.1e-27:314:75//AC000379

R-HEMBA1005884//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.6e-20:328:67//AC006207

R-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//2.0e-102:543:95//AC004945

R-HEMBA1005894

R-HEMBA1005909

R-HEMBA1005911//CIT-HSP-2342E5.TR CIT-HSP Homo sapiens genomic clone 2342E5, genomic survey sequence.//0.0012:315:60//AQ058081

R-HEMBA1005921//P.chrysogenum mitochondrion genes for tRNA-Arg, tRNA-Asn, tRNA-Tyr, small subunit rRNA, and ATPase subunit 6.//0.0090:445:58//Z23072

R-HEMBA1005931//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-46:351:83//Z98304

R-HEMBA1005934//Homo sapiens chromosome 17, clone hRPK.261\_A\_13, complete sequence.//0.0052:179:71//AC005138

R-HEMBA1005962//Homo sapiens clone RG012D21, complete sequence.//1.1e-11:149:74//AC005045

R-HEMBA1005963//HS\_3055\_A1\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//5.4e-79:403:97//AQ147357

R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//6.9e-112:580:95//AF082516

R-HEMBA1005991//Human DNA sequence from clone 58A9 on chromosome 1q24.1-24.3. Contains STSs, GSSs, genomic marker D1S210 and a ca repeat polymorphism, complete sequence.//2.6e-39:299:82//AL031285

R-HEMBA1005999//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.1e-29:260:70//AC004859

R-HEMBA1006002//Rattus norvegicus s-nexilin mRNA, complete cds.//6.3e-15:174:78//AF056035

R-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//2.6e-112:574:95//AF036405

R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds.//7.6e-27:444:67//AB018268

R-HEMBA1006035//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.025:373:60//AC005139

R-HEMBA1006036//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//0.0056:535:59//AC004125

R-HEMBA1006042//HS\_2169\_A1\_B11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2169 Col=21 Row=C, genomic survey sequence.//1.7e-73:390:95//AQ132995

R-nnnnnnnnnnn

R-HEMBA1006081

R-HEMBA1006090//HS\_2262\_A2\_A01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=2 Row=A, genomic survey sequence.//2.1e-70:360:97//AQ162324

R-HEMBA1006091

R-HEMBA1006100/Homo sapiens DNA sequence from PAC 212G6 on chromosome Xp11.3-p11.4. Contains synapsin 1, brain protein 4.1, properdin, tyrosine kinase (ELK1) oncogene, ESTs, STS, GSS, complete sequence.//1.6e-36:354:77//AL009172

R-HEMBA1006108

R-HEMBA1006121

R-HEMBA1006124/Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//1.3e-12:327.64//Z95113

R-HEMBA1006130/WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.60:326:62//AC005948

R-nnnnnnnnnnn/Homo sapiens chromosome 19, cosmid F16403, complete sequence.//4.3e-52:321:80//AC005777

R-HEMBA100614211, complete sequence.//1.0e-13:160:78//AC005500

R-HEMBA1006155/Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0013:389.60//AC004688

R-HEMBA1006158/Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.4e-119:574:98//AF048693

R-HEMBA1006173/Mus musculus protein tyrosine phosphatase STEP61 mRNA, complete cds.//4.1e-43:307:86//U28217

R-HEMBA1006182/Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.7e-30:300:71//AC004491

R-HEMBA1006198/\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.3e-36:284:85//U14567

R-HEMBA1006235/Homo sapiens clone 24422 mRNA sequence.//2.1e-110:545:97//AF070557

R-HEMBA1006248/Homo sapiens mRNA for KIAA0667 protein, partial cds.//0.46:365:58//AB014567

R-HEMBA1006252/Human Chromosome 16 BAC clone C1T987SK-A-972D3, complete sequence.//2.8e-41:438:71//U91323

R-HEMBA1006253/Homo sapiens 45kDa splicing factor mRNA, complete cds.//1.8e-28:179:91//AF083384

R-HEMBA1006259/RPC111-44N14.TJ RPC111 Homo sapiens genomic clone R-44N14, genomic survey sequence.//1.5e-48:348:85//AQ203161

R-HEMBA1006268

R-HEMBA1006272/Human DNA sequence from clone 1198H6 on chromosome 1p36.11-36.31. Contains two Melanoma Preferentially Expressed Antigen PRAME LIKE genes. Contains GSSs and ESTs, complete sequence.//2.8e-73:273:87//AL023753

R-nnnnnnnnnnn/H.sapiens PAP mRNA.//1.6e-54:585:71//X76770

R-HEMBA1006283/Sequence 7 from patent US 5776683.//9.7e-18:113:98//AR016240

R-HEMBA1006284/Homo sapiens chromosome 17, clone hRPC.1028\_K\_7, complete sequence.//0.97:447:59//AC004585

R-HEMBA1006291/Homo sapiens full-length insert cDNA clone ZB76B10.//2.9e-94:454:98//AF086161

R-HEMBA1006293/Sequence 8 from patent US 5721351.//8.1e-10:111:72//H89415

R-HEMBA1006309/Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.6e-37:288:84//AC005412

R-HEMBA1006310/Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.5e-29:132:81//AF076183

R-HEMBA1006328/Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 894K16, WORKING DRAFT SEQUENCE.//3.3e-50:340:75//AL034429

R-HEMBA1006334

R-HEMBA1006344/Rattus norvegicus nitizin mRNA, partial cds.//8.7e-22:259:72//AF087945

R-HEMBA1006347/Human prostaticin gene, complete cds.//1.8e-78:170:100//U33446

R-HEMBA1006349/Rat brain calcium channel alpha-1 subunit mRNA, complete cds.//0.00051:120:73//M57682

R-HEMBA1006359/CITBI-E1-2516C16.TR CITBI-E1 Homo sapiens genomic clone 2516C16, genomic survey sequence.//4.7e-74:576:82//AQ277951

R-HEMBA1006364/IG.gallus gene for transforming growth factor-beta2, exons 5-7.//2.5e-21:118:85//X59080

R-HEMBA1006377/Homo sapiens chromosome 19, cosmid F23149, complete sequence.//5.7e-68:367:85//AC005239

R-HEMBA1006380/Human BAC clone RG007J15 from 7q31, complete sequence.//6.1e-47:300:83//AC003989

R-HEMBA1006381/Homo sapiens chromosome 5, BAC clone 189 (LBNL H135), complete sequence.//1.5e-47:336:86//AC005914

R-HEMBA1006398/Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.5e-67:501:83//AC005609

- R-HEMBA1006416//Homo sapiens chromosome 17, clone 347\_H\_5, complete sequence.//4.4e-37:319:76//AC002119
- R-HEMBA1006419//Homo sapiens chromosome 17, clone HCIT542B22, complete sequence.//2.9e-50:502:75//AC004253
- 5 R-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.//4.1e-116:572:97//AF107885
- R-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//9.4e-117:57:97//AL031781
- 10 R-HEMBA1006426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//2.2e-08:353:63//Z93017
- R-HEMBA1006438//HS\_2008\_A1\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=7 Row=G, genomic survey sequence.//1.2e-29:194:91//AQ245162
- 15 R-HEMBA1006445//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:330:60//AC005075
- R-HEMBA1006446//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.032:256:61//AE001398
- R-HEMBA1006461//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//5.6e-35:229:77//AC002364
- 20 R-HEMBA1006467//Homo sapiens Chromosome 9p22 Cosmid clone 34a5, complete sequence.//1.1e-14:354:63//AC002052
- R-HEMBA1006471
- R-HEMBA1006474//p40, p24 [Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Genomic RNA, 1138 nt, segment 1 of 3].//1.1e-14:442:60//S67502
- 25 R-HEMBA1006483//Homo sapiens chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//3.7e-37:290:82//U95742
- R-HEMBA1006485//H. sapiens mRNA for aminopeptidase.//7.6e-91:517:91//Y07701
- R-HEMBA1006486//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-33:289:81//AC005089
- 30 R-HEMBA1006489//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//6.0e-07:485:60//AL020989
- R-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//4.3e-112:572:95//AC005828
- 35 R-HEMBA1006494//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.3e-10:186:67//AC002994
- R-HEMBA1006497//RPCI11-16L10.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16L10, genomic survey sequence.//1.5e-10:75:100//B88015
- R-HEMBA1006502//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//3.3e-36:516:70//Z93929
- 40 R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//1.2e-115:570:96//AB014566
- R-HEMBA1006521//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//2.2e-20:266:71//Z98304
- 45 R-HEMBA1006530//RPCI11-52M1.TJ RPCI11 Homo sapiens genomic clone R-52M1, genomic survey sequence.//0.00015:227:64//AQ052526
- R-HEMBA1006535//HS\_2234\_B1\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=13 Row=D, genomic survey sequence.//7.5e-33:191:95//AQ129525
- 50 R-HEMBA1006540//Homo sapiens clone GS051M12, complete sequence.//0.026:497:58//AC005007
- R-HEMBA1006546//Homo sapiens chromosome 19, cosmid R33496, complete sequence.//5.2e-41:289:86//AC004603
- R-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//3.4e-64:551:78//U06944
- R-HEMBA1006562//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//5.7e-09:266:66//AC002554
- 55 R-HEMBA1006566//HS\_2171\_B1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=7 Row=D, genomic survey sequence.//0.012:306:61//AQ125421
- R-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//3.8e-70:529:82//U39357
- R-HEMBA1006579//Homo sapiens BAC clone NH0115E20 from Y, complete sequence.//1.0:141:65//AC006032

- R-HEMBA1006583//CIT-HSP-2377M16.TR CIT-HSP Homo sapiens genomic clone 2377M16, genomic survey sequence.//1.7e-31:271:76//AQ111875
- R-HEMBA1006595//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.093:270:61//AC004709
- 5 R-HEMBA1006597//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-45:371:80//AC005031
- R-HEMBA1006612
- R-nnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 8B22, WORKING DRAFT SEQUENCE.//2.1e-20:229:77//AL031737
- 10 R-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//4.8e-40:321:83//AL023284
- R-HEMBA1006631//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 202O6, WORKING DRAFT SEQUENCE.//1.5e-45:477:77//AL031848
- 15 R-HEMBA1006635//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//8.0e-40:245:91//U14572
- R-HEMBA1006639
- R-HEMBA1006643
- R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds.//2.5e-106:567:94//U40282
- 20 R-HEMBA1006652//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//8.7e-54:334:76//AC002089
- R-HEMBA1006653//Homo sapiens 7q telomere, complete sequence.//5.0e-36:207:89//AF027390
- R-HEMBA1006665//HS\_3213\_B2\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=8 Row=H, genomic survey sequence.//1.2e-21:235:67//AQ175625
- 25 R-HEMBA1006674//H.sapiens telomeric DNA sequence, clone 9QTEL023, read 9QTELOO023.seq.//2.6e-32:212:83//Z96776
- R-HEMBA1006676//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-10:436:60//Z98551
- R-HEMBA1006682//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//6.1e-06:477:59//L40608
- 30 R-HEMBA1006695//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.8e-30:266:80//AC005096
- R-HEMBA1006696
- R-HEMBA1006708
- R-HEMBA1006709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 715N11, WORKING DRAFT SEQUENCE.//6.8e-14:139:82//AL031674
- 35 R-HEMBA1006717
- R-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//9.9e-18:365:66//AC005828
- R-HEMBA1006744//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.3e-37:380:75//AC003108
- 40 R-HEMBA1006754//Homo sapiens chromosome 5, P1 clone 962c5 (LBNL H87), complete sequence.//2.1e-75:338:85//AC003951
- R-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//1.2e-112:579:95//AC005752
- 45 R-HEMBA1006767//Plasmodium falciparum MAL3P6, complete sequence.//0.00022:528:58//Z98551
- R-HEMBA1006779//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.3e-46:305:87//AC005701
- R-HEMBA10067801//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//7.2e-39:305:82//AL023232
- 50 R-HEMBA1006789//Streptomyces coelicolor cosmid 6G4.//0.0085:449:61//AL031317
- R-HEMBA1006795//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//4.1e-43:355:801//AC006120
- R-HEMBA1006796//HS\_3038\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=22 Row=P, genomic survey sequence.//0.99:158:63//AQ102483
- 55 R-HEMBA1006807//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//8.4e-47:481:75//AC004854
- R-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62\_O\_9, complete sequence.//3.0e-08:84:90//AC004797



- R-HEMBA1006824//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.7e-54.496:76//Z93023
- R-HEMBA1006832//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, complete sequence.//0.70:206:65//AC005668
- 5 R-HEMBA1006849//Homo sapiens 12q24.1 PAC RPI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-46:281:91//AC004217
- R-HEMBA1006865//Mus musculus clone 101 B1 repeat region sequence.//0.61:115:70//AF056074
- R-nnnnnnnnnnn//Mus musculus mRNA for oxysterol-binding protein, complete cds.//3.3e-102:618:87//AB017026
- 10 R-HEMBA1006885 4.2e-14:379:63//AG006839
- R-HEMBA1006900//CIT-HSP-2006M20.TR CIT-HSP Homo sapiens genomic clone 2006M20, genomic survey sequence.//2.6e-07:230:66//B56395
- R-HEMBA1006921//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//2.1e-68:267:86//AC005154
- 15 R-HEMBA1006926
- R-HEMBA1006929//HS\_3244\_A2\_C01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=2 Row=E, genomic survey sequence.//6.9e-21:191:83//AQ207500
- R-HEMBA1006936
- R-HEMBA1006938//Colias philodice eriphyle large subunit ribosomal RNA gene, partial sequence; tRNA-Vai gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//0.11:309:59//AF044853
- 20 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//2.0e-75:371:98//AJ010841
- R-HEMBA1006949//Homo sapiens PAC clone DJ0777G09 from 7q34-q36, complete sequence.//0.47:240:63//AC005518
- R-HEMBA1006973//HS\_2009\_A2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=24 Row=A, genomic survey sequence.//9.6e-05:407:60//AQ232302
- 25 R-HEMBA1006976//RPI11-49L11.TJ RPI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//0.0018:184:63//AQ051701
- R-HEMBA1006993//Human thrombopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thrombopoietin beta.//1.9e-47:394:79//U18271
- 30 R-HEMBA1006996//CIT-HSP-2172D17.TF CIT-HSP Homo sapiens genomic clone 2172D17, genomic survey sequence.//1.8e-07:365:62//B93406
- R-HEMBA1007002//Plasmodium falciparum MAL3P2, complete sequence.//0.0012:505:56//AL034558
- R-HEMBA1007017//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//5.6e-41:437:71//AC005277
- 35 R-HEMBA1007018//G. gallus mRNA for dynein light chain-A.//8.2e-73:556:80//X79088
- R-HEMBA1007045
- R-HEMBA1007051//Human DNA sequence from cosmid N69F4 on chromosome 22q11.2-qter contains EST.//9.9e-27:342:71//Z72006
- 40 R-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//5.4e-85:558:87//U85056
- R-HEMBA1007062
- R-HEMBA1007066
- R-HEMBA1007073//Homo sapiens chromosome 17, clone hRPK.421\_E\_14, complete sequence.//2.0e-66:476:85//AC006141
- 45 R-HEMBA1007078//Homo sapiens chromosome 17, clone hRPK.60\_A\_24, complete sequence.//1.0e-38:179:82//AC005325
- R-HEMBA1007085//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.2e-49:551:73//AC006015
- R-HEMBA1007087//Human Chromosome 11 pac pDJ392a17, complete sequence.//1.0:261:61//AC000385
- R-HEMBA1007112//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//0.043:295:62//AC004803
- 50 R-HEMBA1007113//Homo sapiens (subclone 6\_a8 from P1 H16) DNA sequence.//1.4e-52:307:87//L43392
- R-HEMBA1007129//Human DNA sequence from PAC 863K19 on chromosome X. Contains STS.//1.2e-08:131:75//Z92547
- R-HEMBA1007147//H. sapiens CpG island DNA genomic MseI fragment, clone 65f1, reverse read cp65f1.r1ta.//0.16:187:64//Z62246
- 55 R-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//7.6e-108:543:96//AC005239
- R-HEMBA1007151//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.14:323:58//

AC004875

R-nnnnnnnnnnn/Homo sapiens epsilon 2a mRNA, complete cds.//5.1e-103.529.94//AF062085

R-HEMBA1007178/Homo sapiens chromosome 12p13.3 clone RPC11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//5.4e-106.537.96//AC005911

5 R-HEMBA1007194/Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.1e-39.262.80//AC003035

R-HEMBA1007203/Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.3e-61.332.95//D86987

R-HEMBA1007206/Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//1.9e-50.436.81//Z93023

10 R-HEMBA1007224/Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.3e-96.471.97//AB018340

R-HEMBA1007251/Homo sapiens chromosome 5, PAC clone 247F3 (LBNL H85), complete sequence.//0.011:349.62//AC004777

R-HEMBA1007256/Homo sapiens PAC clone DJ0676L20 from 7q35-q36, complete sequence.//2.8e-10.224.70//AC004856

15 R-HEMBA1007267/Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.4e-53.362.86//AC005924

R-HEMBA1007273

R-HEMBA1007279/Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4.//0.042:454:57//AJ235273

20 R-HEMBA1007281/Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.09:288:60//AJ235272

R-HEMBA1007288/Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//7.4e-107.554.95//AL031003

R-HEMBA1007300/Caenorhabditis elegans cosmid C48C5.//0.22:474:59//U939994

25 R-HEMBA1007301

R-HEMBA1007319/Campylobacter jejuni repetitive DNA, clone pINT.//4.9e-08.524:58//Y14425

R-HEMBA1007320/Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//3.4e-16:244:71//AP000043

R-HEMBA1007322/Homo sapiens BAC clone RG324D18 from 7p15-p21, complete sequence.//3.9e-83:383.85//AC005251

30 R-HEMBA1007327/Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 7706, WORKING DRAFT SEQUENCE.//1.6e-38:533:71//Z96804

R-HEMBA1007341/Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268D13, WORKING DRAFT SEQUENCE.//3.6e-21:394:66//AL023513

35 R-HEMBA1007342/Human BAC clone GS368F15 from 7q31, complete sequence.//1.7e-15:190:73//AC003080

R-HEMBA1007347/Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone N38G6, WORKING DRAFT SEQUENCE.//2.2e-47:455:77//Z96802

R-HEMBA1000005/Homo sapiens 3p21.1-9 PAC RPC14-793P23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-62:539:79//AC006208

40 R-HEMBA1000008/Homo sapiens chromosome 17, clone hCIT.211\_p\_7, complete sequence.//1.2e-36:285:83//AC003665

R-HEMBA1000018/Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-51:416:79//AC004820

45 R-HEMBA1000024/Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//3.9e-18:211:79//Z95113

R-HEMBA1000025/Hs\_3064\_B2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=14 Row=D, genomic survey sequence.//5.9e-40:254:90//AQ132765

R-HEMBA1000030/Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein family member), Ndr protein kinase gene similar to yeast suppressor protein SRP40, EST and GSS, complete sequence.//1.5e-32:452:70//Z85986

50 R-HEMBA1000036/CIT-HSP-2024L15.TF CIT-HSP Homo sapiens genomic clone 2024L15, genomic survey sequence.//9.3e-63:541:77//B66264

R-HEMBA1000037/Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//7.6e-91:467:97//AF084928

55 R-HEMBA1000039/Homo sapiens chromosome 17, clone hRPK.401\_0\_9, complete sequence.//2.4e-44:456:68//AC005291

R-HEMBA1000044/Human BAC clone RG016J04 from 7q21, complete sequence.//1.4e-54:307:80//AC002064

R-HEMBA1000048/Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//3.8e-

09:330:63//AC002300

R-HEM000050//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR1). Contains ESTs, an STS and GSSs, complete sequence.//6.7e-12:225:65//Z94056

R-HEM000054//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//8.9e-76:557:82//AL033521

R-HEM000055//Human housekeeping (Q1Z 7F5) gene, exons 2 through 7, complete cds.//1.6e-88:350:86//M81806

R-HEM000059//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.9e-12:356:65//AC006009

R-HEM000083//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.7e-41:311:82//AC004840

R-HEM000089//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-34:314:78//AC005520

R-HEM000099//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a ggtt repeat polymorphism, complete sequence.//8.8e-32:434:71//AL008715

R-HEM000103//Human DNA sequence from BAC 445C9 on chromosome 22q12.1. Contains CRYBB1, beta B1 crystallin, CRYBA4, beta A4 crystallin, high mobility group-1 protein (HMG-1), ESTs.//2.5e-16:207:74//Z95115

R-HEM000113//HS\_3013\_A1\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3013 Col=15 Row=C, genomic survey sequence.//0.94:211:63//AQ118730

R-HEM000119//Homo sapiens ASMTL gene.//1.9e-106:531:96//Y15521

R-HEM000136//Human Chromosome X, complete sequence.//0.00073:359:59//AC002407

R-HEM000141//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//6.8e-41:280:74//AF043945

R-HEM000144//Homo sapiens chromosome 17, clone hCIT.507\_E\_2, complete sequence.//0.00083:206:66//AC004134

R-HEM000173//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//2.5e-82:401:90//AC004085

R-HEM000175

R-HEM000198//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.91:428:56//AL021368

R-HEM000215//Homo sapiens DNA sequence from PAC 69E11 on chromosome 1q23-24. Contains a NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ) LIKE pseudogene, a 60S Ribosomal protein L34 LIKE pseudogene, an unknown gene similar to yeast YPR037W and worm C02C2.6 predicted genes, a predicted CpG island, ESTs and an STS, complete sequence.//4.4e-54:298:91//AL021397

R-HEM000217

R-HEM000218//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.8e-32:517:70//AC004216

R-HEM000226//Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin HVR and CpG island.//2.5e-77:450:92//Z69706

R-HEM000240//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//4.1e-05:310:62//AF029308

R-HEM000244//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//1.3e-43:278:85//AL034420

R-HEM000250//Human DNA sequence from clone 34B20 on chromosome 6p21.31-22.2. Contains seventeen Histone (pseudo)genes and a 40S Ribosomal protein S10 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-16:484:64//AL031777 R-HEM000258//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//4.3e-11:286:67//U91328

R-HEM000264//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//1.2e-42:406:79//AF079765

R-HEM000266//RPC111-76C20.TV RPC111 Homo sapiens genomic clone R-76C20, genomic survey sequence.//1.0:232:59//AQ265533

- R-HEMBA1000272//HS\_3032\_B1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=11 Row=P, genomic survey sequence.//0.0082:209:62//AQ096702
- R-HEMBA1000274//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g in IGLC Region, complete sequence.//1.6e-45:277:72//AC000053
- 5 R-HEMBA1000284//Homo sapiens full-length insert cDNA clone YY88A05.//6.9e-112:572:96//AF088018
- R-HEMBA1000307//Homo sapiens chromosome 17, clone hRPK.471\_L\_13, complete sequence.//5.7e-96:523:93//AC005244
- R-HEMBA1000312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//7.5e-21:218:67//AL023693
- 10 R-HEMBA1000317//Toxoplasma gondii chloroplast, complete genome.//0.062:354:58//U87145
- R-HEMBA1000318//Human DNA sequence from PAC 292H14 on chromosome Xp21. Contains STS and CA repeat polymorphism.//4.5e-52:302:81//AL008710
- R-HEMBA1000335//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//1.9e-16:139:84//AC005179
- 15 R-HEMBA1000336//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//0.0062:231:64//AJ003147
- R-HEMBA1000337//CIT-HSP-2329010.TF CIT-HSP Homo sapiens genomic clone 2329010, genomic survey sequence.//1.2e-31:192:92//AQ035976
- R-HEMBA1000338//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//1.9e-39:477:71//AC004605
- 20 R-HEMBA1000339//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//4.1e-54:357:76//AL031681
- R-HEMBA1000341//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.8e-19:501:63//AC002350
- 25 R-HEMBA1000343//Homo sapiens chromosome 16, cosmid clone 367E12 (LANL), complete sequence.//3.6e-41:457:72//AC004644
- R-HEMBA1000354//Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS.//7.2e-36:325:74//Z98751
- R-HEMBA1000369//Homo sapiens chromosome 4 clone B366O24 map 4q25, complete sequence.//9.0e-25:179:79//AC004067
- 30 R-HEMBA1000374//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 75N14, WORKING DRAFT SEQUENCE.//8.4e-58:332:79//Z97199
- R-HEMBA1000376//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.1e-47:309:88//D87675
- R-HEMBA1000391//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-46:302:85//AC005080
- 35 R-HEMBA1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//1.0e-107:531:97//AF076838
- R-HEMBA1000402//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//1.1e-25:441:67//Z98052
- 40 R-HEMBA1000404//HS\_2246\_A2\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2246 Col=2 Row=G, genomic survey sequence.//0.0025:196:63//AQ084251
- R-HEMBA1000420//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g in IGLC Region, complete sequence.//1.2e-29:358:72//AC000053
- R-HEMBA1000434//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.8e-51:299:89//AC004069
- 45 R-HEMBA1000438//HS\_2239\_B2\_E08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2239 Col=16 Row=J, genomic survey sequence.//1.3e-10:76:100//AQ067700
- R-HEMBA1000441//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//4.4e-60:281:90//Z82207
- 50 R-HEMBA1000449//Homo sapiens clone DJ0898018, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.8e-11:228:68//AC004920
- R-HEMBA1000455//Homo sapiens clone GS051M12, complete sequence.//3.1e-14:388:65//AC005007
- R-HEMBA1000472//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//4.9e-34:320:79//AC003104
- 55 R-HEMBA1000480//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//3.4e-36:285:82//Z83849
- R-HEMBA1000487

- R-HEM BB1000490//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.5e-34:281:81//AL034423
- R-HEM BB1000491//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//8.5e-37:483:72//Z93023
- 5 R-HEM BB1000493//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.6e-14:217:71//AL022721
- 10 R-HEM BB1000510//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//7.1e-44:221:80//AL033397
- R-HEM BB1000518//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//3.5e-51:280:90//AC002477
- 15 R-HEM BB1000523//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//1.7e-53:304:82//AC004079
- R-HEM BB1000530//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence.//4.2e-74:428:92//AC006236
- R-HEM BB1000550//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.6e-13:112:80//U91321
- 20 R-HEM BB1000554//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//5.1e-14:239:63//Z83824
- R-HEM BB1000556//Homo sapiens envoplaikin (EVPL) mRNA, complete cds.//0.031:275:60//U53786
- R-HEM BB1000564//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//3.1e-17:227:76//AC005914
- 25 R-HEM BB1000573//Borrelia afzelii (strain NT28) DNA, Internal transcribed spacer.//0.078:161:63//D84405
- R-HEM BB1000575//Homo sapiens chromosome 17, clone hRPC.859\_O\_20, complete sequence.//7.2e-52:260:80//AC003695
- R-HEM BB1000586//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//2.0e-33:305:79//Z70280
- 30 R-HEM BB1000589//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, complete sequence.//1.3e-14:409:65//AC005208
- R-HEM BB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//6.2e-39:493:71//AC005184
- R-HEM BB1000592//Homo sapiens 12p13.3 PAC RPC15-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.6e-08:254:64//AC005831
- 35 R-HEM BB1000598//Homo sapiens chromosome 11 pac pDJ1590i, complete sequence.//3.3e-38:407:76//AC000381
- R-HEM BB1000623//CIT-HSP-2374P17.TR CIT-HSP Homo sapiens genomic clone 2374P17, genomic survey sequence.//1.3e-41:212:100//AQ109717
- 40 R-HEM BB1000630//Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs, complete sequence.//5.2e-31:319:78//AL022724
- R-HEM BB1000631//Sequence 28 from patent US 5708157.//6.8e-20:208:80//I80058
- 45 R-HEM BB1000632//Homo sapiens Cosmid C4, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.4e-47:457:75//AC004176
- R-HEM BB1000637//Human BAC clone RG094H21 from 7q21-q22, complete sequence.//2.9e-45:263:87//AC003085
- R-HEM BB1000638//Genomic sequence from Human 6, complete sequence.//9.1e-34:375:73//AC002112
- 50 R-HEM BB1000643//HS\_2242\_A2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=14 Row=C, genomic survey sequence.//0.010:239:60//AQ065993
- R-HEM BB1000649//Homo sapiens RBP56/hTAFII68 gene, exon 7.//8.3e-63:306:100//AB010061
- R-HEM BB1000652//Human DNA sequence from PAC 467D16 on chromosome 6p22.3-24.1. Contains the 3' part of the SCA1 (ataxin-1) gene with a poly-glutamine (CAG repeat) polymorphism, the 3' part of the GMPR (GMP reductase, Guanosine 5'-monophosphate oxidoreductase) gene, ESTs and an STS with a polymorphic C A repeat.//3.3e-14:450:64//AL009031
- 55 R-HEM BB1000665//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence.//0.98:251:63//AB005247
- R-HEM BB1000671//Human DNA sequence from PAC 106C24, between markers DXS294 and DXS730 on chro-

- mosome X.//6.8e-58:296:85//Z83313  
 R-HEMBB1000673//CITBI-E1-2506F20. TR CITBI-E1 Homo sapiens genomic clone 2506F20, genomic survey sequence.//0.98:71:76//AQ264731
- 5 R-HEMBB1000684//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//2.6e-11:153:77//AL031584  
 R-nnnnnnnnnnn/Homo sapiens neuroan1 mRNA, complete cds.//2.0e-50:287:93//AF040723  
 R-HEMBB1000705//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.4e-18:340:65//AC005943
- 10 R-HEMBB1000706//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462C17, WORKING DRAFT SEQUENCE.//4.7e-10:358:64//AL033380  
 R-HEMBB1000709//RPC11-79A8.TV RPC11 Homo sapiens genomic clone R-79A8, genomic survey sequence.//1.4e-40:262:89//AQ282374  
 R-HEMBB1000725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence.//0.00018:386:60//AB017066
- 15 R-HEMBB1000726//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//1.5e-48:316:88//AC004990  
 R-HEMBB1000738//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.1e-53:382:85//AC004875  
 R-HEMBB1000749//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.5e-51:438:80//AC005069
- 20 R-HEMBB1000763//Plasmid Col Ib-P9 (from E.coli K12) colicin Ib promoter region and 5' coding region.//1.0:115:63//K02071  
 R-HEMBB1000770//Human Rhesus blood group antigen (RHCE) gene, intron 6, partial sequence.//5.6e-24:183:86//U83205
- 25 R-HEMBB1000781//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//0.00054:154:67//AC003046  
 R-HEMBB1000789//RPC11-2114.TVB RPC11-11 Homo sapiens genomic clone RPC11-2114, genomic survey sequence.//3.0e-09:299:64//B63628  
 R-HEMBB1000790//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//4.5e-46:185:85//U95740
- 30 R-HEMBB1000794//HS\_3253\_A1\_G06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=11 Row=M, genomic survey sequence.//5.7e-13:172:65//AQ216291  
 R-HEMBB1000807  
 R-HEMBB1000810//Human BAC clone RG114A06 from 7q31, complete sequence.//1.3e-24:385:71//AC002542
- 35 R-HEMBB1000821  
 R-HEMBB1000822//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//4.5e-08:278:64//AQ279944  
 R-HEMBB1000826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//1.2e-44:521:72//AP000043
- 40 R-HEMBB1000827//Homo sapiens clone DJ098I007, complete sequence.//6.8e-43:319:84//AC006017  
 R-HEMBB1000831//HS\_3247\_B2\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=18 Row=B, genomic survey sequence.//5.5e-74:381:96//AQ223850  
 R-HEMBB1000835//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceroldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//4.2e-17:167:80//AL021368
- 45 R-HEMBB1000840//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-26:220:73//AC005283  
 R-HEMBB1000848//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//7.8e-39:356:79//AC004086
- 50 R-HEMBB1000852//HS\_3075\_A2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=14 Row=C, genomic survey sequence.//3.4e-11:151:75//AQ138816  
 R-HEMBB1000870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 72E17, WORKING DRAFT SEQUENCE.//1.8e-44:454:75//AL033523
- 55 R-HEMBB1000876//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//0.0016:227:65//AL024474  
 R-HEMBB1000883//Homo sapiens chromosome 19, cosmid F19678, complete sequence.//0.62:238:62//

AC005621

R-HEMBA1000887//Synthetic human/adenovirus type 5 recombination junction.//9.9e-24:27.5:76//M34061

R-HEMBA1000888//CIT-HSP-2282A13. TR CIT-HSP Homo sapiens genomic clone 2282A13, genomic survey sequence.//2.4e-05:31.60//AC000826

5 R-HEMBA1000890//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//6.5e-44:305:84//AC005995

R-HEMBA1000893//Homo sapiens BAC clone RG363E19 from 7q31.1, complete sequence.//3.7e-30:265:80//AC004492

10 R-HEMBA1000908//RPC11-13P12. TV RPC1-11 Homo sapiens genomic clone RPC1-11-13P12, genomic survey sequence.//0.98:183:61//B76199

R-HEMBA1000910//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//1.7e-28:302:76//AC000024

R-HEMBA1000913//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//4.1e-34:314:76//AC003037

15 R-HEMBA1000915//Homo sapiens chromosome 16p11.2-p12 BAC clone CIT987SK-224D6 complete sequence.//6.3e-09:536:59//U95739

R-HEMBA1000917//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 169I5, WORKING DRAFT SEQUENCE.//1.6e-47:234:86//Z93015

R-HEMBA1000927

20 R-HEMBA1000947//CIT-HSP-2287M13. TF CIT-HSP Homo sapiens genomic clone 2287M13, genomic survey sequence.//0.090:115:69//B99228

R-HEMBA1000959//Homo sapiens chromosome 17, clone HRC905N1, complete sequence.//5.7e-89:544:90//AC003098

25 R-HEMBA1000973//Arabidopsis thaliana chromosome II BAC F219 genomic sequence, complete sequence.//0.038:377:58//AC005560

R-HEMBA1000975//Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence.//1.0e-05:342:62//AC006234

R-HEMBA1000981//CIT-HSP-2386J13. TF.1 CIT-HSP Homo sapiens genomic clone 2386J13, genomic survey sequence.//1.1e-18:231:74//AQ239443

30 R-HEMBA1000985//HS\_3184\_A1\_D12\_T7 CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=3184 Col=23 Row=G, genomic survey sequence.//6.3e-52:286:95//AQ150008

R-HEMBA1000991

35 R-HEMBA1000996//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//1.4e-42:343:81//AC002368

R-HEMBA1001004

R-HEMBA1001008//CITBI-E1-2504L23. TF CITBI-E1 Homo sapiens genomic clone 2504L23, genomic survey sequence.//3.1e-57:317:94//AQ262056

R-HEMBA1001011//HS\_3017\_B1\_G03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3017 Col=5 Row=N, genomic survey sequence.//7.3e-34:237:86//AQ101944

40 R-HEMBA1001014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//2.4e-49:417:80//AL031662

R-HEMBA1001020//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//7.6e-41:303:76//AC002549

R-HEMBA1001024//Homo sapiens (subclone 2\_g5 from P1 H16) DNA sequence.//7.4e-48:341:85//L48475

45 R-HEMBA1001037//Homo sapiens 22q11 BAC Clone 489D1 In MDR Region, complete sequence.//2.0e-50:416:82//AC005527

R-HEMBA1001047//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//8.4e-22:288:71//AC004699

R-HEMBA1001051//H. sapiens mRNA for FAN protein.//7.1e-18:114:98//X96586

50 R-HEMBA1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.1e-94:520:93//AC006014

R-HEMBA1001058//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//1.1e-56:242:82//AC004187

55 R-HEMBA1001060//Human Tigger1 transposable element, complete consensus sequence.//4.2e-66:323:81//U49973

R-HEMBA1001063//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 523G1, WORKING DRAFT SEQUENCE.//4.0e-114:556:98//AL034375

R-HEMBA1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.8e-105:512:97//AF034803

- R-HEM BB1001096//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//2.4e-13:225:69//Z76735
- 5 R-HEM BB1001102//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.4e-35:295:80//AL022577
- R-HEM BB1001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462O23, WORKING DRAFT SEQUENCE.//7.9e-46:380:80//AL031431
- 10 R-HEM BB1001114//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (Intestinal protein OCI-5) (GTR2-2), 5'UTR. ESTs, STSs.//1.1e-38:306:84//Z99570
- R-HEM BB1001117//RPCI11-3518.TK RPCI-11 Homo sapiens genomic clone RPCI-11-3518, genomic survey sequence.//1.5e-08:67:100//AQ047113
- R-HEM BB1001119//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//9.0e-26:481:67//AC003071
- 15 R-HEM BB1001126//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.045:127:69//Z99495
- R-HEM BB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds.//5.0e-23:285:73//M25077
- 20 R-HEM BB1001137//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-09, complete sequence.//2.5e-07:334:62//AL010222
- R-HEM BB1001142//Human BAC clone RG164L14 from 7q21-q22, complete sequence.//2.5e-46:412:79//AC002564
- R-HEM BB1001151//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904
- 25 R-HEM BB1001153//RPCI11-10L7.TP RPCI-11 Homo sapiens genomic clone RPCI-11-10L7, genomic survey sequence.//2.3e-34:213:82//B71766
- R-HEM BB1001169//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//0.040:465:56//AC003070
- R-nnnnnnnnnnn//Sequence 1 from patent US 5618695.//2.8e-15:176:80//I40055
- 30 R-HEM BB1001177
- R-HEM BB1001182//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//1.9e-05:174:70//AL010226
- R-HEM BB1001199
- R-HEM BB1001208
- 35 R-HEM BB1001209//RPCI11-41E13.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41E13, genomic survey sequence.//1.1e-95:473:97//AQ029098
- R-HEM BB1001210//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//6.2e-08:412:61//AC005199
- R-HEM BB1001218//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//1.0e-46:498:74//B75158
- 40 R-HEM BB1001254//Methanococcus jannaschii section 3 of 150 of the complete genome.//0.96:203:61//U67461
- R-HEM BB1001267//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.8e-39:320:80//Z98046
- R-HEM BB1001271//Homo sapiens chromosome 17, clone hRPK.349\_A\_8, complete sequence.//3.9e-47:494:75//AC005544
- 45 R-HEM BB1001282//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING DRAFT SEQUENCE.//0.0011:97:79//AL031428
- R-HEM BB1001288
- R-HEM BB1001289//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//2.0e-



- 31:301:78//AC005601  
R-HEM BB1001294//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//0.053:283.60//AC003083  
R-HEM BB1001302
- 5 R-HEM BB1001304//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//6.3e-15:396.64//AL033397  
R-HEM BB1001314//Homo sapiens genomic DNA, 21q region, clone: f30F8SpN6, genomic survey sequence.//3.4e-42:293.86//AG013777
- 10 R-HEM BB1001315//Human NFE genomic fragment.//7.5e-30:243.78//M98511  
R-HEM BB1001317//Homo sapiens chromosome 17, clone hRPC.1028\_K\_7, complete sequence.//2.3e-39:301:82//AC004585
- 15 R-HEM BB1001326//HS\_3054\_A1\_F12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=23 Row=K, genomic survey sequence.//0.90:117.63//AQ106096  
R-HEM BB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain: BALB/c.//0.037:103.77//D63850  
R-HEM BB1001335//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//9.1e-19:229.77//AC003037  
R-HEM BB1001337
- 20 R-HEM BB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//2.9e-45:551.72//U85056  
R-HEM BB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.7e-59:292.99//AF097441  
R-HEM BB1001348//Homo sapiens clone DJ069F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//9.1e-41:326.82//AC004859
- 25 R-HEM BB1001356//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//1.8e-11:213.67//Z82207  
R-HEM BB1001364//HS\_3050\_A2\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=10 Row=K, genomic survey sequence.//1.8e-21:158.91//AQ133940  
R-HEM BB1001366//Homo sapiens chromosome 10 clone CIT987SK-118815 map 10p11.2-10p12.1, complete sequence.//4.1e-37:419.73//AC005876
- 30 R-HEM BB1001367//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//9.5e-15:201:75//U91326  
R-HEM BB1001369//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 477J10, WORKING DRAFT SEQUENCE.//1.8e-28:224.83//AL021686  
R-HEM BB1001380//HS\_2267\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2267 Col=21 Row=C, genomic survey sequence.//4.0e-14:100.95//AQ084896
- 35 R-HEM BB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.6e-55:312.81//AF071314  
R-HEM BB1001387//Homo sapiens chromosome 9, P1 clone 8660 (LBNL H105), complete sequence.//1.0:166:63//AC003953
- 40 R-HEM BB1001394//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence.//1.4e-55:494:76//AC005549  
R-HEM BB1001410//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.011:208:63//AC006204  
R-HEM BB1001424//Homo sapiens, WORKING DRAFT SEQUENCE, 76 unordered pieces.//1.5e-22:325.69//AC002370
- 45 R-HEM BB1001426//Homo sapiens 12q24 PAC RPC13-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-46:328.84//AC002350  
R-HEM BB1001429//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.6e-105:550.95//AC006160
- 50 R-HEM BB1001436  
R-HEM BB1001443//HS\_2228\_A1\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=9 Row=C, genomic survey sequence.//0.37:173.62//AQ066934  
R-HEM BB1001449//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.7e-23:339.69//AC005522
- 55 R-HEM BB1001454//Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60), complete sequence.//1.1e-39:299.84//AC005355  
R-HEM BB1001458//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//6.0e-05:486.59//AE001430

- R-HEMBB1001463//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//1.2e-50:317.89//AC005154
- R-HEMBB1001464//CIT-HSP-2370C10.TF CIT-HSP Homo sapiens genomic clone 2370C10, genomic survey sequence.//0.20:95.71//AQ107941
- 5 R-HEMBB1001482//Mus musculus clone OST20235, genomic survey sequence.//4.3e-09:192.70//AF046762
- R-HEMBB1001500//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu<sup>++</sup>-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.9e-21:253.70//Z94801
- R-HEMBB1001521//Mus musculus clone OST1209, genomic survey sequence.//7.5e-30:332.75//AF046642
- 10 R-HEMBB1001527//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.5e-55:483.76//AC005000
- R-HEMBB1001531//Human BAC clone 7E17 from 12q, complete sequence.//1.3e-08:159.71//AC002070
- R-HEMBB1001535//Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.//4.0e-30:286.79//Z74581
- 15 R-HEMBB1001536//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.6e-39:342.80//U73169
- R-HEMBB1001537//Genomic sequence from Human 9q34, complete sequence.//3.7e-41:361.77//AC000394
- R-HEMBB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10, complete sequence.//0.34:212.61//AC003049
- 20 R-HEMBB1001562//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//8.0e-40:267.88//AC002301
- R-HEMBB1001564//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.1e-30:286.76//AC005225
- R-HEMBB1001565//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.5e-15:194.75//AC004840
- 25 R-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//2.6e-33:234.79//AL031677
- R-HEMBB1001586//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-30:371.74//AC005236
- 30 R-HEMBB1001588//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//8.0e-32:323.73//AC003106
- R-HEMBB1001603//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-59, complete sequence.//0.034:302.59//AL010235
- R-HEMBB1001618//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and OpG island.//7.1e-31:503.68//Z93023
- 35 R-HEMBB1001619//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.7e-50:539.72//AC002368
- R-HEMBB1001630//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.3e-27:228.82//Z86062
- 40 R-HEMBB1001635//Homo Sapiens Chromosome X clone bWXD90, complete sequence.//1.5e-23:407.69//AC004075
- R-HEMBB1001637//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-54:519.74//AC002368
- 45 R-HEMBB1001641//Human DNA sequence from clone 133H11 on chromosome 6p24. Contains STSs, GSSs and genomic marker D6S410, complete sequence.//1.9e-08:464.60//AL024506
- R-HEMBB1001653//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.8e-39:318.82//AC002344
- R-HEMBB1001665//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.8e-47:283.90//U14572
- 50 R-HEMBB1001668
- R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//1.8e-115:573.97//AB014546
- R-HEMBB1001684//Sequence 1 from patent US 5700927.//1.9e-40:343.77//I86429
- R-HEMBB1001685//Homo sapiens chromosome 17, clone hRPK.721\_K\_1, complete sequence.//2.6e-43:31.83//AC005411
- 55 R-HEMBB1001695
- R-HEMBB1001704//CIT-HSP-2324C15.TR CIT-HSP Homo sapiens genomic clone 2324C15, genomic survey sequence.//0.0074:259.58//AQ028704
- R-HEMBB1001706//Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.1e-34:296.80//AC004851

- R-HEM BB1001707//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.7e-32:241:76//AC004020
- R-HEM BB1001717//CIT-HSP-2378C19.TF CIT-HSP Homo sapiens genomic clone 2378C19, genomic survey sequence.//4.8e-35:228:89//AQ108992
- 5 R-HEM BB1001735//Homo sapiens chromosome 5, BAC clone 114k9 (LBNL H94), complete sequence.//1.8e-10:80:90//AC005613
- R-HEM BB1001736//CIT-HSP-2369K6.TF CIT-HSP Homo sapiens genomic clone 2369K6, genomic survey sequence.//9.9e-38:242:90//AQ105221
- 10 R-HEM BB1001747//Homo sapiens cosmids Qc14E2, Qc12H12, Qc1F19, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//3.3e-60:366:80//U82671
- R-HEM BB1001749//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//1.4e-60:242:92//AC005829
- R-HEM BB1001753//RPC111-59J22.TK RPC111 Homo sapiens genomic clone R-59J22, genomic survey sequence.//6.2e-08:281:64//AQ200046
- 15 R-HEM BB1001756//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//3.1e-18:395:67//AC004130
- R-HEM BB1001760//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//9.9e-18:416:64//AP000050
- 20 R-HEM BB1001762//Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Iaalpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like (NG10), hypothetical protein (NG8), and butyrophilin-like (NG11) genes, partial cds; NG12 pseudogene, partial sequence; and hypothetical butyrophilin-like protein (NG13) gene, partial cds.//0.21:521:57//AF050157
- R-HEM BB1001785//Torulopsis glabrata mitochondrial intergenic region ATPase 6 -ATPase 9 genes.//0.00073:189:65//X02170
- 25 R-HEM BB1001797//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0049:322:62//AC005140
- R-HEM BB1001802//Human desmin gene, complete cds.//8.1e-95:510:93//M63391
- R-HEM BB1001812//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.3e-71:368:96//Z98882
- 30 R-HEM BB1001816//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//8.4e-21:164:76//AJ006996
- R-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//1.7e-104:498:98//AF056209
- R-HEM BB1001836//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.2e-44:388:71//AC005328
- 35 R-HEM BB1001839
- R-HEM BB1001850//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence.//0.00093:488:60//AB005241
- 40 R-HEM BB1001863//Human poly(ADP-ribose) polymerase gene, 5' end.//1.2e-16:458:65//M60436
- R-HEM BB1001867//Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.//5.0e-31:399:74//Z68327
- R-HEM BB1001868//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.26:303:59//AB020754
- 45 R-HEM BB1001869//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//7.0e-37:285:85//AC002553
- R-HEM BB1001872//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y44F5, WORKING DRAFT SEQUENCE.//0.093:367:58//AL009027
- R-HEM BB1001874
- 50 R-HEM BB1001875//Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmid sequence.//0.037:406:60//AE001272
- R-HEM BB1001880//Homo sapiens chromosome 17, clone hRPK.235\_1\_10, complete sequence.//1.3e-49:461:77//AC005922
- R-HEM BB1001899//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y116A8, WORKING DRAFT SEQUENCE.//0.56:295:60//Z98858
- 55 R-HEM BB1001905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//1.9e-28:181:75//AL022345
- R-HEM BB1001906
- R-HEM BB1001908//Genomic sequence from Human 17, complete sequence.//2.9e-36:274:76//AC001231

- R-HEM BB1001910//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//3.5e-41:408:76//AC003070
- R-HEM BB1001911//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* ,WORKING DRAFT SEQUENCE.//6.1e-64:310:89//AJ011929
- 5 R-HEM BB1001915//Mouse mRNA for arylhydrocarbon receptor, complete cds.//2.0e-20:220:78//D38417
- R-HEM BB1001921//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1141E15, WORKING DRAFT SEQUENCE.//1.9e-47:410:80//AL034422
- R-HEM BB1001922//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//6.2e-32:378:74//AC004099
- 10 R-HEM BB1001925//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.2e-41:304:84//AC000406
- R-HEM BB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11.//8.3e-12:202:69//AB020867
- 15 R-HEM BB1001944//P.falciparum gene for beta subunit RNA polymerase.//0.00090:264:62//X75544
- R-HEM BB1001945//Swietenia humilis DNA for simple tandem repeat (242bp).//0.056:224:62//AJ000408
- R-HEM BB1001947//RPC111-60L13.TJ RPC111 Homo sapiens genomic clone R-60L13, genomic survey sequence.//7.4e-23:146:94//AQ202335
- 20 R-HEM BB1001950//Human DNA sequence from clone 415G2 on chromosome 22 Contains synapsin IIIa exon 1, EST and GSS, complete sequence.//0.57:115:68//Z83846
- R-HEM BB1001952//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-36:283:84//AC004676
- 25 R-HEM BB1001953//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.9e-60:334:82//AC005037
- R-HEM BB1001957//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.9e-56:518:77//AC005077
- 30 R-HEM BB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.//3.2e-19:157:86//AC005736
- R-HEM BB1001967//Homo sapiens DNA for amyloid precursor protein, complete cds.//5.7e-68:314:89//D87675
- R-HEM BB1001973//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC E7.1 / cosmid 40M1, WORKING DRAFT SEQUENCE.//1.4e-37:484:70//AJ009617
- 35 R-HEM BB1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//2.1e-28:286:75//AL034417
- R-HEM BB1001988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//6.9e-29:203:88//AL034420
- 40 R-HEM BB1001990//Homo sapiens full-length insert cDNA clone ZC33G03.//7.6e-95:456:99//AF086192
- R-HEM BB1001996
- R-HEM BB1001997//Homo sapiens clone RG050N15, WORKING DRAFT SEQUENCE, 26 unordered pieces.//6.4e-26:162:83//AC005055
- 45 R-HEM BB1002002//Human DNA sequence from PAC 2A2 on chromosome X contains ESTs.//8.2e-83:362:93//Z84816
- R-HEM BB1002005//Homo sapiens chromosome 3p clone RPC15-1034C16, WORKING DRAFT SEQUENCE, 45 unordered pieces.//8.5e-36:291:83//AC005903
- R-HEM BB1002009//Homo sapiens clone DJ0828F13, complete sequence.//5.6e-08:307:65//AC004904
- 50 R-HEM BB1002015//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.9e-05:375:62//B36336
- R-HEM BB1002042//CIT-HSP-2313E13.TF CIT-HSP Homo sapiens genomic clone 2313E13, genomic survey sequence.//0.34:241:62//AQ028389
- 55 R-HEM BB1002043//Homo sapiens chromosome 21, P1 clone LBL#8 (LBNL H8), complete sequence.//7.4e-35:297:82//AC005612
- R-HEM BB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.8e-96:582:90//AC005740
- R-HEM BB1002045//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.7e-63:575:77//AC005778
- R-HEM BB1002049//Human Chromosome X clone bWXD187, complete sequence.//1.9e-21:384:64//AC004383
- 60 R-HEM BB1002050//Homo sapiens chromosome 17, clone hRPK.112\_j\_9, complete sequence.//2.5e-37:368:76//AC005553
- R-HEM BB1002068//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//0.30:167:65//AC004782

- R-HEM BB1002069//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.3e-73:449:84//AC004799
- R-HEM BB1002092//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//3.8e-45:307:87//AC005828
- 5 R-HEM BB1002094//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.1e-47:457:76//AC005943
- R-HEM BB1002115//HS\_2223\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2223 Col=19 Row=N, genomic survey sequence.//3.0e-58:295:98//AQ152279
- 10 R-HEM BB1002139//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.//6.6e-49:283:93//U14573
- R-HEM BB1002142//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-45:451:76//AC006006
- R-HEM BB1002152//Homo sapiens chromosome 10 clone CIT987SK-1079E16 map 10q25, complete sequence.//1.3e-57:359:81//AC005881
- 15 R-HEM BB1002189//Human Chromosome 11 pac pDJ392a17, complete sequence.//4.5e-43:420:77//AC000385
- R-HEM BB1002190//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//8.2e-33:340:64//AC004913
- R-HEM BB1002193//Sequence 5 from patent US 5709858.//3.2e-23:154:92//I80846
- R-HEM BB1002217//Homo sapiens clone HS19.2 Alu-Ya5 sequence.//2.6e-52:415:81//AF015148
- R-HEM BB1002218//, complete sequence.//3.4e-17:178:82//AC005300
- 20 R-HEM BB1002232//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0052122; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-55:292:88//AC004599
- R-HEM BB1002247//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//2.9e-13:227:70//AC005829
- R-HEM BB1002249//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//1.1e-06:284:64//AL031733
- 25 R-HEM BB1002254//Human Chromosome X, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.3e-104:593:91//AC002415
- R-HEM BB1002255//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//2.1e-40:284:85//Z93930
- 30 R-HEM BB1002266//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//1.3e-09:371:63//AL010216
- R-HEM BB1002280//Homo sapiens PAC clone DJ0545C24 from 7q21-q22, complete sequence.//1.3e-39:247:86//AC004534
- R-HEM BB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//4.1e-84:549:86//U73642
- 35 R-HEM BB1002306//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.5e-10:164:71//AC004129
- R-HEM BB1002327//Homo sapiens BAC clone GS539F22 from 7p12-p14, complete sequence.//0.39:365:59//AC005028
- R-HEM BB1002329//HS-1049-B1-D05-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=9 Row=W, genomic survey sequence.//0.96:180:58//B39313
- 40 R-HEM BB1002340//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//7.9e-17:258:73//AC004849
- R-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//6.9e-96:479:97//AJ010841
- R-HEM BB1002358//Human Xp22 BAC CT-28515 (from CalTech/Research Genetics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-53:309:83//AC002366
- 45 R-HEM BB1002359//Homo sapiens clone NH0486122, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.9e-27:350:74//AC005038
- R-HEM BB1002364//Homo sapiens Xp22 PAC RPC11-108M6 (Roswell Park Cancer Center PAC library) complete sequence.//8.6e-53:302:79//AC003036
- 50 R-HEM BB1002371//Human gene for catalase (EC 1.11.1.6) exon 11 mapping to chromosome 11, band p13.//3.2e-38:199:100//X04094
- R-HEM BB1002381//Homo sapiens (JH8) mRNA, partial cds.//3.2e-07:120:78//AF072467
- R-HEM BB1002383//Human DNA sequence from cosmid U19H10 on chromosome X. Contains ESTs and CA repeat.//0.98:351:58//AL021182
- 55 R-HEM BB1002387//HS-1052-B2-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=20 Row=N, genomic survey sequence.//2.0e-07:276:67//B41091
- R-HEM BB1002415//Homo sapiens chromosome 17, clone hRPK.209\_D\_14, complete sequence.//1.4e-25:202:

- 79//AC005730  
R-HEM BB1002425//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//3.6e-60:401:87//AC004799
- 5 R-HEM BB1002442//Homo sapiens clone UWGC:r9a from 6p21, complete sequence.//3.1e-51:358:81//AC006046  
R-HEM BB1002453//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 86D1, WORKING DRAFT SEQUENCE.//1.4e-115:557:98//AL034349  
R-HEM BB1002457//Human DNA sequence from clone 364122 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//6.3e-37:338:80//AL031012
- 10 R-HEM BB1002458//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//9.7e-09:314:64//AE000659  
R-HEM BB1002477//Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAI project).//0.42:110:74//AL021635  
R-HEM BB1002489//Salvelinus fontinalis microsatellite sequence SFO-12.//6.6e-06:167:71//U50302
- 15 R-HEM BB1002492//RPC111-74F21.TK RPC111 Homo sapiens genomic clone R-74F21, genomic survey sequence.//3.1e-14:410:63//AQ238960  
R-HEM BB1002495//HS\_3220\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=14 Row=K, genomic survey sequence.//1.3e-24:137:100//AQ180762  
R-HEM BB1002502//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//9.6e-81:538:86//AC006120
- 20 R-HEM BB1002509//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.0061:482:57//AL031313  
R-HEM BB1002510//HS\_2179\_A1\_F03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=5 Row=K, genomic survey sequence.//6.9e-35:423:72//AQ298309
- 25 R-HEM BB1002520//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//2.0e-62:201:85//AL033397  
R-HEM BB1002522//Homo sapiens chromosome 5, Pac clone 61c2 (LBNL H139), complete sequence.//0.99:323:58//AC004225  
R-HEM BB1002531
- 30 R-HEM BB1002534//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.0e-61:380:79//AP000009  
R-HEM BB1002545//RPC111-2F3.TVB RPC111 Homo sapiens genomic clone RPC11-2F3, genomic survey sequence.//3.5e-12:414:63//B63283  
R-HEM BB1002550
- 35 R-HEM BB1002556//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.6e-62:299:85//AC006160  
R-HEM BB1002579//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1141E15, WORKING DRAFT SEQUENCE.//1.7e-42:286:88//AL034422  
R-HEM BB1002582//Homo sapiens clone DJ1119N05, complete sequence.//3.0e-14:426:60//AC004968
- 40 R-HEM BB1002590//Homo sapiens clone RG132J19, complete sequence.//1.1e-30:392:74//AC005163  
R-HEM BB1002596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508115, WORKING DRAFT SEQUENCE.//8.5e-44:335:83//AL021707  
R-HEM BB1002600//Homo sapiens 12p13.3 PAC RPC15-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-105:470:96//AC005865
- 45 R-HEM BB1002601//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//1.3e-44:445:77//AC004223  
R-HEM BB1002603//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//7.0e-40:321:82//AC006162  
R-HEM BB1002607//CIT-HSP-2347D7.TF CIT-HSP Homo sapiens genomic clone 2347D7, genomic survey sequence.//1.1e-44:234:98//AQ060197
- 50 R-HEM BB1002610//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//7.0e-22:455:65//U91321  
R-HEM BB1002613//Homo sapiens 12p13.3 BAC RPC111-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.0e-72:302:85//AC005908  
R-HEM BB1002614//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.8e-10:512:60//AC004801
- 55 R-HEM BB1002617//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-24:486:63//AC005520

- R-HEMBB1002623//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.4e-41:326:83//AC004953
- R-HEMBB1002635//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//2.6e-42:360:80//AC005910
- 5 R-HEMBB1002664//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//9.1e-51:335:87//AF042090
- R-HEMBB1002677//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), C8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//0.0011:399:59//AF030694
- 10 R-HEMBB1002683//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//4.1e-55:515:76//AF042090
- R-HEMBB1002684//Human BAC clone RG066D11 from 7q22, complete sequence.//1.7e-18:504:62//AC002430
- R-HEMBB1002686//Homo sapiens full-length insert cDNA clone ZC65D06.//7.0e-85:413:99//AF086217
- 15 R-HEMBB1002692//Homo sapiens 12p13.3 BAC RPC111-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.8e-69:505:82//AC006206
- R-HEMBB1002697//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.26:390:58//AC004153
- R-HEMBB1002699//Human NFE genomic fragment.//8.0e-32:226:79//M98511
- 20 R-HEMBB1002702//CIT-HSP-344K23.TVC CIT-HSP Homo sapiens gene clone 344K23, genomic survey sequence.//8.6e-43:351:8011859764
- R-HEMBB1002705//Plasmodium yoelii hroptro protein, complete cds.//0.0064:454:59//L27838
- R-HEMBB1002712//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//9.6e-09:187:67//Z98052
- 25 R-MAMMA1000009//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.1e-21:201:80//AC005037
- R-MAMMA1000019//Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence.//4.2e-48:306:82//AF015720
- 30 R-MAMMA1000020//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//1.4e-41:306:86//AL022163
- R-MAMMA1000025//Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence.//6.1e-36:281:83//AL031058
- 40 R-MAMMA1000043//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence.//1.3e-67:321:88//AC000090
- 35 R-MAMMA1000045//Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.//6.7e-86:559:86//AC004054
- R-MAMMA1000055//Branta canadensis CA dinucleotide repeat locus Bcamicro1.//0.79:63:77//AF025889
- R-MAMMA1000057//Homo sapiens DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in an intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the human homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS, complete sequence.//1.6e-53:397:83//AL021366
- 45 R-MAMMA1000069//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.0e-37:295:83//AC005057
- R-MAMMA1000084//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//7.1e-45:296:88//AC005867
- 50 R-MAMMA1000085
- R-MAMMA1000092//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING DRAFT SEQUENCE.//8.2e-34:539:69//AL034410
- R-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//3.4e-39:297:85//AC003976
- 55 R-MAMMA1000117//Homo sapiens p47-phox (NCF1) pseudogene, clone P38, exon 5.//2.6e-07:162:67//U69641
- R-MAMMA1000129//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.1e-13:141:80//AC004882
- R-MAMMA1000133

- R-MAMMA1000134//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.7e-18:171:80//AC005328
- R-MAMMA1000139//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-49:366:75//AC005000
- 5 R-MAMMA1000143//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC D9.2, WORKING DRAFT SEQUENCE.//3.9e-56:318:89//AJ009615
- R-MAMMA1000155//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and puta-
- 10 R-MAMMA1000163//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.3e-06:408:58//AC005089
- R-MAMMA1000171//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.5e-42:173:89//AQ037381
- 15 R-MAMMA1000173
- R-MAMMA1000175//H.sapiens CpG island DNA genomic MseI fragment, clone 186c5, reverse read cpq186c5.r1b.//0.072:90:72//Z57594
- R-MAMMA1000183//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//1.5e-44:445:75//AC004552
- 20 R-MAMMA1000198//Homo sapiens clone c102D0968, complete sequence.//1.9e-23:135:85//AF038667
- R-MAMMA1000221//HS\_3242\_B2\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=4 Row=P, genomic survey sequence.//0.031:167:67//AQ220385
- R-MAMMA1000227//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING DRAFT SEQUENCE.//4.5e-36:487:71//AL031728
- 25 R-MAMMA1000241//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideremia protein, Tapetochochoidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//6.2e-07:445:59//AL022401
- R-MAMMA1000251//Homo sapiens chromosome 19, cosmid F23465, complete sequence.//1.6e-25:390:69//AC005266
- 30 R-MAMMA1000254//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//1.1e-37:327:80//AL008715
- R-MAMMA1000257//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//1.3e-22:281:74//AL034549
- 35 R-MAMMA1000264//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//1.7e-29:337:67//AC003656
- 40 R-MAMMA1000266//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 681N20, WORKING DRAFT SEQUENCE.//7.7e-37:339:80//AL031670
- R-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.2e-40:283:86//AF001549
- R-MAMMA1000277//CIT-HSP-516K6.TP CIT-HSP Homo sapiens genomic clone 516K6, genomic survey sequence.//3.0e-29:265:80//B49900
- 45 R-MAMMA1000278//Sequence 25 from patent US 5708157.//2.6e-39:282:82//180056
- R-MAMMA1000279//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494
- R-MAMMA1000284//CITBI-E1-2522B20.TF CITBI-E1 Homo sapiens genomic clone 2522B20, genomic survey sequence.//1.8e-11:288:61//AQ028722
- 50 R-MAMMA1000287
- R-MAMMA1000302//Homo sapiens chromosome 17, clone hRPC.112\_J\_9, complete sequence.//4.1e-16:169:77//AC005553
- R-MAMMA1000307//RPC111-89L1.TV RPC111 Homo sapiens genomic clone R-89L1, genomic survey sequence.//1.3e-86:429:97//AQ284795
- 55 R-MAMMA1000309//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.0020:384:60//AF029779
- R-MAMMA1000312//chneutes sp. 16S ribosomal RNA gene, partial sequence.//0.0026:310:60//AF003518



R-MAMMA1000313//Human cosmid Xq28\_1A649, complete sequence.//1.5e-26:317:67//U82694  
 R-MAMMA1000331//Homo sapiens clone DJ1007F24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//  
 3.1e-39:277:86//AC004947  
 R-MAMMA1000339//Homo sapiens clone HS19.1 Alu-Ya5 sequence.//3.2e-44:180:89//AF015147  
 5 R-MAMMA1000340//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence.//0.97:  
 293:64//AE001388  
 R-MAMMA1000348//Homo sapiens BAC129, complete sequence.//4.4e-27:365:72//U85195  
 R-MAMMA1000356//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.73:  
 332:61//AC002493  
 10 R-MAMMA1000360//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//4.6e-80:279:89//  
 AC005189  
 R-MAMMA1000361//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 753D4, WORKING  
 DRAFT SEQUENCE.//7.8e-18:346:63//AL031676  
 R-MAMMA1000372//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORK-  
 15 ING DRAFT SEQUENCE.//5.3e-40:299:83//AL022344  
 R-MAMMA1000385//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 310013, WORKING  
 DRAFT SEQUENCE.//1.0e-28:225:84//AL031658  
 R-MAMMA1000388//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey se-  
 quence.//4.7e-60:298:99//AQ038102  
 20 R-MAMMA1000395  
 R-MAMMA1000402//Homo sapiens PAC clone DJ1107K12 from 7p12-p14, complete sequence.//1.4e-84:276:88//  
 AC004692  
 R-MAMMA1000410//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//6.7e-35:360:  
 76//AC002394  
 25 R-MAMMA1000413//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//3.1e-69:327:  
 79//AC004662  
 R-MAMMA1000414//Homo sapiens DNA sequence from PAC 164L12 on chromosome Xq13.1-Xq21.2. Contains  
 GSS (BAC end sequence).STS.//3.6e-41:180:87//AL009028  
 R-MAMMA1000416//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//  
 3.1e-59:478:77//AC005377  
 30 R-MAMMA1000421//Human coxVib gene, last exon and flanking sequence.//5.3e-53:294:82//X58139  
 R-MAMMA1000422//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 8B22, WORKING  
 DRAFT SEQUENCE.//1.0:252:59//AL031737  
 R-MAMMA1000423//Homo sapiens clone DA0065G23, complete sequence.//2.0e-50:491:76//AC004816  
 35 R-MAMMA1000424//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribos-  
 omal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//3.5e-40:340:80//Z98950  
 R-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//0.0019:87:79//AF062484  
 R-MAMMA1000431//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//  
 2.0e-58:564:77//AC004821  
 40 R-MAMMA1000444//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//3.0e-43:328:83//  
 AC002067  
 R-MAMMA1000446//Human chromosome X clone Qc15B1, complete sequence.//0.95:209:65//U82672  
 R-MAMMA1000458//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence.//  
 0.99:182:61//AB019236  
 45 R-MAMMA1000468  
 R-MAMMA1000472//Homo sapiens genomic DNA, 21q region, clone: 655M9N34, genomic survey sequence.//  
 1.0e-38:142:88//AG010148  
 R-MAMMA1000478//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING  
 DRAFT SEQUENCE.//1.3e-37:286:83//Z93015  
 50 R-MAMMA1000483//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey se-  
 quence.//4.3e-34:158:86//B54637  
 R-MAMMA1000490//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//4.2e-98:569:90//  
 AC006130  
 R-MAMMA1000500//Human BRCA1, Rho7 and vat1 genes, complete cds, and ipf35 gene, partial cds.//1.2e-41:  
 334:79//L78833  
 55 R-MAMMA1000501//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 153G14, WORK-  
 ING DRAFT SEQUENCE.//1.4e-38:250:84//AL031118  
 R-MAMMA1000516//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING

DRAFT SEQUENCE.//1.3e-43:318:83/Z82207  
 R-MAMMA1000522//Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequence.//4.4e-13:202:73//AL031289  
 R-MAMMA1000559//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING DRAFT SEQUENCE.//2.2e-30:245:83/Z93015  
 R-MAMMA1000565//Homo sapiens chromosome 10 clone LA10NC01\_183\_B\_7 map 10q24, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.6e-39:281:80//U82205  
 R-MAMMA1000567//Rattus norvegicus nonmuscle caldesmon mRNA, complete cds.//9.2e-19:216:76//U18419  
 R-MAMMA1000576  
 R-MAMMA1000583//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//5.4e-53:297:85//AC005666  
 R-MAMMA1000585//Homo sapiens clone DJ1015P16, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-35:450:71//AC006018  
 R-MAMMA1000594//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from cosmid 5L5, WORKING DRAFT SEQUENCE.//4.3e-26:293:75//AJ009613  
 R-MAMMA1000597//CIT-HSP-2341F4.TF CIT-HSP Homo sapiens genomic clone 2341F4, genomic survey sequence.//0.83:110:70//AQ057131  
 R-MAMMA1000605//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.6e-50:290:86//AC004956  
 R-MAMMA1000612//CIT-HSP-2334J18.TF CIT-HSP Homo sapiens genomic clone 2334J18, genomic survey sequence.//0.76:132:65//AQ038364  
 R-MAMMA1000616//Ibalia leucospoides mitochondrion 16S rRNA gene, partial sequence.//6.8e-06:431:59//U06970  
 R-MAMMA1000621//Human NBR2 mRNA, complete cds.//5.3e-27:258:80//U88573  
 R-MAMMA1000623  
 R-MAMMA1000625//Homo sapiens chromosome 19, cosmid R31665, complete sequence.//3.3e-07:325:63//AC005498  
 R-MAMMA1000643//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39B17, WORKING DRAFT SEQUENCE.//1.4e-06:236:68//AL023656  
 R-MAMMA1000664//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0326F06; HTGS phase 1, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-40:338:81//AC004555  
 R-MAMMA1000669//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//1.2e-46:327:86//AL021578  
 R-MAMMA1000670  
 R-MAMMA1000672//Human DNA sequence from clone 478D8 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.2e-29:328:76//AL031785  
 R-MAMMA1000684//Mus musculus frizzled-1 mRNA, complete cds.//0.21:247:63//AF054623  
 R-MAMMA1000696//Human Chromosome X clone bVXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.7e-46:464:71//AC004387  
 R-MAMMA1000707//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-09:244:66//AC005075  
 R-MAMMA1000713//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-51:439:74//AC005478  
 R-MAMMA1000714//Homo sapiens BAC clone RG152H24 from 7p15-p21, complete sequence.//2.8e-29:288:75//AC004694  
 R-MAMMA1000718//Human Xp22 BAC CT-285115 (from CalTech/Research Genetics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//3.9e-37:231:91//AC002366  
 R-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//1.4e-35:299:81//AC005781  
 R-MAMMA1000723//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//3.9e-59:409:79//AL022163  
 R-MAMMA1000731//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.4e-29:560:66//AC005077  
 R-MAMMA1000732//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.4e-14:309:68//AC004832

- R-MAMMA1000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//4.1e-29:377:71//AL008722
- R-MAMMA1000734//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191J18, WORKING DRAFT SEQUENCE.//2.0e-108:420:99//AL024507
- 5 R-MAMMA1000738//Human V beta T-cell receptor (TCRBV) gene locus.//6.6e-41:347:82//U03115
- R-MAMMA1000744//T2708-T7 TAMU Arabidopsis thaliana genomic clone T2708, genomic survey sequence.//0.095:367:60//B20150
- R-MAMMA1000746//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//7.4e-95:569:87//AC004661
- 10 R-MAMMA1000752//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.3e-48:295:84//AC003071
- R-MAMMA1000760//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//5.7e-45:347:82//Z82178
- R-MAMMA1000761//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.1e-32:292:80//U73169
- 15 R-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.5e-50:467:79//AC005412
- R-MAMMA1000776//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//1.0e-63:429:79//AC002454
- 20 R-MAMMA1000778//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.//3.5e-25:234:81//Z95704
- R-MAMMA1000782//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//0.0021:119:74//AL031120
- R-MAMMA1000798//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3.//6.3e-08:269:64//AJ229042
- 25 R-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//1.1e-36:261:80//AC005339
- R-MAMMA1000831//CIT-HSP-2387 J3.TF.1 CIT-HSP Homo sapiens genomic clone 2387J3, genomic survey sequence.//0.68:156:65//AQ240607
- 30 R-MAMMA1000839//Homo sapiens chromosome 17, clone hRPK.726\_O\_12, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.6e-50:335:86//AC005517
- R-MAMMA1000841//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//1.3e-40:322:77//U91323
- R-MAMMA1000842//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//4.1e-44:471:74//Z97985
- 35 R-MAMMA1000843//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.85:394:80//AC004815
- R-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.54:303:63//AL031744
- 40 R-MAMMA1000851//Homo sapiens chromosome X, MeCP2 locus, complete sequence.//1.7e-10:115:83//AF030876
- R-MAMMA1000855//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//5.0e-44:352:83//AC004263
- R-MAMMA1000856//Homo sapiens chromosome 19, cosmid F24200, complete sequence.//1.8e-10:149:74//AC00461
- 45 R-MAMMA1000862//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #16.//8.1e-05:205:66//AF009075
- R-MAMMA1000863//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//2.9e-49:421:80//AC002364
- 50 R-MAMMA1000865//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//9.1e-41:302:83//AC002301
- R-MAMMA1000867//Human BRCA1, Rho7 and vat1 genes, complete cds, and ipf35 gene, partial cds.//1.9e-17:500:61//L78833
- R-MAMMA1000875//Homo sapiens chromosome 16, cosmid clone RT99 (LANL), complete sequenced.//1.2e-17:211:74//AC004653
- 55 R-MAMMA1000876//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//4.7e-09:160:85//AC003658
- R-MAMMA1000877//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains

ESTs STS and CpG island.//3.2e-34:354:75//Z93023

R-MAMMA1000880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.4e-41:411:74//AC002425

R-MAMMA1000883

R-MAMMA1000897

R-MAMMA1000905//Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence.//1.3e-73:304:91//AC004506

R-MAMMA1000906//Human DNA from chromosome 19-specific cosmid F14150, genomic sequence, complete sequence.//8.4e-23:194:83//AC003110

R-MAMMA1000908//Human Chromosome 15q26.1 PAC clone pDJ416i6, complete sequence.//1.5e-09:170:71//AC003024

R-MAMMA1000914//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//8.3e-13:323:67//AC005247

R-MAMMA1000921//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//6.8e-28:333:72//AL034379

R-MAMMA1000931//HS\_3227\_B1\_B03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=5 Row=D, genomic survey sequence.//1.4e-55:443:79//AQ191777

R-MAMMA1000940//Homo sapiens clone RG013F03, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:340:84//AC005046

R-MAMMA1000941//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.8e-53:330:84//AC002347

R-MAMMA1000942//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:391:74//AC004383

R-MAMMA1000943//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.6e-75:566:81//AC002477

R-MAMMA1000956//Plasmodium falciparum MAL3P7, complete sequence.//0.013:285:59//AL034559

R-MAMMA1000957//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.2e-45:288:90//AC005096

R-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-108:561:98//AC006001

R-MAMMA1000968//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.9e-41:287:87//AC004263

R-MAMMA1000975//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-65:542:79//Z95152

R-MAMMA1000979//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//3.2e-34:296:80//AJ011930

R-MAMMA1000987//Homo sapiens CC chemokine gene cluster, complete sequence.//1.7e-40:255:87//AF088219

R-MAMMA1000998//Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence.//2.5e-39:315:73//AC005190

R-MAMMA1001003//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//2.4e-52:296:84//AC006101

R-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//7.9e-88:432:98//AJ011929

R-MAMMA1001021//Homo sapiens PAC clone DJ0859M06 from 7q11, complete sequence.//3.8e-39:286:87//AC004910

R-MAMMA1001024//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-31:274:80//AC004913

R-MAMMA1001030//Homo sapiens full-length insert cDNA clone ZD96C01.//3.2e-99:469:99//AF088074

R-MAMMA1001035//RPC1-1-46G8Sp6 RPC1-1 Homo sapiens genomic clone RPC1-1-46G8Sp6, genomic survey sequence.//3.5e-49:270:90//AQ275285

R-MAMMA1001038//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//1.1e-41:285:87//AF042089

R-nnnnnnnnnnn

R-MAMMA1001050//Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SEQUENCE.//1.3e-55:334:91//D84394

R-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//1.7e-51:481:77//L25125

R-MAMMA1001067//CIT-HSP-2371K20.TF CIT-HSP Homo sapiens genomic clone 2371K20, genomic survey sequence.//7.2e-65:946:95//AQ111326

R-MAMMA1001073

5 R-MAMMA1001074//Homo sapiens BAC clone NH0400010 from Y, complete sequence.//8.6e-33:457:69//AC006040

R-MAMMA1001075//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.15:325:62//AC004605

R-MAMMA1001078//Homo sapiens chromosome 5, BAC clone 203c13 (LBNL H155), complete sequence.//1.6e-45:344:84//AC005609

10 R-MAMMA1001082//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//8.5e-15:413:64//Z93403

R-MAMMA1001091//Sequence 7 from patent US 5468610.//0.0027:159:64//115499

R-MAMMA1001092//Homo sapiens chromosome 17, clone hRPK.372\_K\_20, complete sequence.//2.0e-51:267:82//AC005951

15 R-MAMMA1001105//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), 5'UTR. ESTs, STS.//6.9e-22:178:85//Z99570

R-MAMMA1001110//Homo sapiens chromosome 17, clone HRPCC1169K15, complete sequence.//3.0e-19:141:81//AC003963

20 R-MAMMA1001126//Human DNA from overlapping chromosome 7 PAC and P1 clones containing the XRCC2 gene, genomic sequence, complete sequence.//2.2e-46:462:75//AC003109

R-MAMMA1001133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING DRAFT SEQUENCE.//1.8e-68:455:86//AL031847

R-MAMMA1001139//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//7.1e-09:100:84//AL022345

25 R-MAMMA1001143//Papio hamadryas lipoprotein lipase (LPL) gene, intron 7.//1.9e-49:362:85//U73684

R-MAMMA1001145//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.//9.5e-49:512:74//AC005922

R-MAMMA1001154//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-88D1 ~complete genomic sequence, complete sequence.//1.5e-29:305:76//AC002289

30 R-MAMMA1001161//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//1.1e-64:339:90//AL031286

R-MAMMA1001162//Human DNA from cosmid DNA MMD8 (f10080) and MMD8 (f13544) from chromosome 19q13.3 (obtained by automated sequence analysis).//3.4e-09:243:64//M89651

R-MAMMA1001181//Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.7e-29:351:74//AC004387

35 R-MAMMA1001186//Homo sapiens chromosome 19, cosmid R28778, complete sequence.//2.2e-25:415:68//AC006125

R-MAMMA1001191//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.99:243:61//AE000662

40 R-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//8.0e-57:223:86//U29156

R-MAMMA1001202//Mus musculus clone OST13722, genomic survey sequence.//1.0e-30:220:85//AF046748

R-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.9e-61:567:78//AC005412

45 R-MAMMA1001206//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//4.6e-08:442:61//AC004763

R-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//1.3e-117:564:97//AC005393

R-MAMMA1001220//HS-1023-A1-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=19 Row=M, genomic survey sequence.//6.0e-16:276:68//B33708

50 R-MAMMA1001222//F17E12TFB IGF Arabidopsis thaliana genomic clone F17E12, genomic survey sequence.//0.041:277:61//B97762

R-MAMMA1001243

R-MAMMA1001244//HS-1058-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=2 Row=M, genomic survey sequence.//3.5e-05:104:74//B43862

55 R-MAMMA1001249//H.sapiens DNA for matrix attachment region.//0.0013:95:75//Z54221

R-MAMMA1001256//Human BAC clone GS188P18, complete sequence.//3.4e-32:356:74//AC000115

R-MAMMA1001259

R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//6.3e-20:226:75//AB014561

- R-MAMMA1001268//Human DNA sequence from PAC 225D2 on chromosome Xq21. Contains ESTs, CA repeat.//1.1e-47:352:85//Z95124
- R-MAMMA1001271
- 5 R-MAMMA1001274//H.sapiens DNA for trapped exon (ID HMC07C06), genomic survey sequence.//3.1e-40:232:93//X88457
- R-MAMMA1001280//Homo sapiens full-length insert cDNA clone YW26C09.//1.9e-112:574:95//AF087976
- R-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//2.9e-114:582:96//AL022314
- 10 R-MAMMA1001296//Human DNA sequence from PAC 487J7 on chromosome 6q21-22.1. Contains an unknown gene coding for three alternative mRNAs. Contains ESTs, STSs, a BAC end-sequence (GSS) and a CA repeat polymorphism.//1.9e-64:268:88//AL008730
- 15 R-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//1.5e-38:306:83//AC005703
- R-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat.//1.5e-37:306:82//Z83838
- 20 R-MAMMA1001322//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3-.41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//2.4e-15:260:71//AL022398
- R-MAMMA1001324//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//4.0e-06:90:83//AC005614
- 25 R-MAMMA1001330//Human BAC clone RG066D11 from 7q22, complete sequence.//1.4e-45:439:74//AC002430
- R-MAMMA1001341//Human DNA sequence from PAC 211D12 on chromosome 20q12-13.2. Contains Krs-2, K+ channel protein, stress responsive.//1.3e-24:137:81//Z93016
- R-MAMMA1001343//Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.//5.4e-51:197:89//AC002041
- 30 R-MAMMA1001346//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//0.99:182:64//AC004685
- R-MAMMA1001383//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-42:303:86//AC004815
- R-MAMMA1001388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508I15, WORKING DRAFT SEQUENCE.//1.5e-44:324:83//AL021707
- 35 R-MAMMA1001397//Homo sapiens genomic DNA, chromosome 21q11.1, segment 15/28, WORKING DRAFT SEQUENCE.//2.0e-39:254:89//AP000044
- R-MAMMA1001408//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.4e-36:251:88//AC005805
- 40 R-MAMMA1001411//T15F1-T7.1 TAMU Arabidopsis thaliana genomic clone T15F1, genomic survey sequence.//1.0:98:71//AQ248928
- R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds.//4.8e-18:117:96//AF038957
- 45 R-MAMMA1001420//Homo sapiens chromosome 5, P1 clone 104F10 (LBNL H88), complete sequence.//2.8e-09:377:63//AC005179
- R-MAMMA1001435//S. pombe chromosome I cosmid c26H5.//1.0:356:59//Z99126
- R-MAMMA1001442//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//3.4e-17:259:72//AC004047
- 50 R-MAMMA1001446//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.9e-17:231:71//AC004491
- R-MAMMA1001452//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//6.1e-50:558:73//AL024493
- 55 R-MAMMA1001465//cSRL-2F3-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-2F3, genomic survey sequence.//3.0e-23:141:96//B04295
- R-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//3.4e-09:309:64//L31783
- R-MAMMA1001487//Homo sapiens chromosome 17, clone hRPC.1108\_L\_11, complete sequence.//5.1e-30:286:79//AC005206

R-MAMMA1001501  
 R-MAMMA1001502//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B7, WORKING  
 DRAFT SEQUENCE.//4.3e-19:349:64//AL031714  
 R-MAMMA1001510  
 5 R-MAMMA1001522//Homo sapiens chromosome 5, BAC clone 24h24 (LBNL H194), complete sequence.//1.5e-09:136:75//AC005352  
 R-MAMMA1001547//Human Chromosome X, complete sequence.//3.5e-40:300:84//AC002418  
 R-MAMMA1001551//Human DNA sequence from PAC 42616 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-57:282:89//AL020997  
 10 R-MAMMA1001575  
 R-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.6e-60:530:78//M61764  
 R-MAMMA1001590//Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds.//1.3e-29:161:86//U78027  
 15 R-MAMMA1001600//Homo sapiens 12q24 PAC RPC1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.1e-18:390:66//AC004216  
 R-MAMMA1001604//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island. complete sequence.//1.0:227:62//AL022238  
 20 R-MAMMA1001606//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.3e-17:219:69//AL031985  
 R-MAMMA1001620//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//2.1e-51:298:84//AL031650  
 R-MAMMA1001627//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//7.8e-45:328:85//Z86090  
 25 R-MAMMA1001630//, complete sequence.//2.5e-08:170:72//AC005399  
 R-MAMMA1001633//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.2e-21:241:70//AC005386  
 R-MAMMA1001635//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//1.1e-32:346:74//Z84466  
 30 R-MAMMA1001649  
 R-MAMMA1001663//Homo sapiens clone 162B15, complete sequence.//9.4e-68:267:89//AC004811  
 R-MAMMA1001670//Human DNA sequence from PAC 75N13 on chromosome Xq21.1. Contains ZNF6 like gene, ESTs, STSs and CpG islands.//1.7e-49:322:88//Z82216  
 35 R-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//2.4e-114:575:96//AC005614  
 R-MAMMA1001679//CIT-HSP-2335N4.TF CIT-HSP Homo sapiens genomic clone 2335N4, genomic survey sequence.//2.4e-82:400:99//AQ037393  
 40 R-MAMMA1001683//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.7e-47:533:72//AC004166  
 R-MAMMA1001686//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.6e-12:194:72//AC005261  
 R-MAMMA1001692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y73BF9, WORKING DRAFT SEQUENCE.//9.6e-44:414:77//AL022345  
 45 R-MAMMA1001711//Homo sapiens clone BAC 9H13 chromosome 8 map 8q21, complete sequence.//3.1e-31:436:70//AF110324  
 R-MAMMA1001715//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 73E16, WORKING DRAFT SEQUENCE.//8.8e-76:524:84//Z95330  
 R-MAMMA1001730  
 50 R-MAMMA1001735//Cricetulus griseus (chinese hamster) mRNA for beta tubulin (clone B9T), partial.//2.7e-13:382:63//X60786  
 R-MAMMA1001740//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//3.9e-47:318:87//AP000050  
 R-MAMMA1001743//Homo sapiens clone DJ0981007, complete sequence.//4.0e-108:566:95//AC006017  
 55 R-MAMMA1001744  
 R-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//3.5e-113:564:97//AF070718  
 R-MAMMA1001751//Homo sapiens chromosome 19, cosmid R27328, complete sequence.//3.6e-30:312:75//

AC005625

R-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//4.7e-34:320:77//AF041338

R-MAMMA1001757//Homo sapiens chromosome 17, clone hRPC.4\_G\_17, complete sequence.//14.7e-10:244:67//AC003688

R-MAMMA1001760//RPC111-38L16.TV RPC1-11 Homo sapiens genomic clone RPC1-11-38L16, genomic survey sequence.//1.3e-10:236:64//AQ029432

R-MAMMA1001764//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//10.74:361:60//AC005140

R-MAMMA1001768//Homo sapiens chromosome 17, clone hRPC.147\_L\_13, complete sequence.//1.6e-42:416:76//AC005332

R-MAMMA1001769//Homo sapiens chromosome 17, clone hRPC.1073\_F\_15, complete sequence.//1.4e-13:129:83//AC004686

R-MAMMA1001771//M.musculus mRNA for semaphorin B.//1.1e-34:530:69//X85991

R-MAMMA1001783//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.1e-42:282:85//AC000360

R-MAMMA1001785//Human chromosome 16p13.11 BAC clone CIT987SK-98H8 complete sequence.//3.0e-49:282:86//U91319

R-MAMMA1001788

R-MAMMA1001790//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//9.8e-43:530:71//AC004913

R-MAMMA1001806//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.8e-43:324:79//AC004020

R-MAMMA1001812//Plasmodium falciparum chromosome 2, section 69 of 73 of the complete sequence.//0.65:183:63//AE001432

R-MAMMA1001815//Homo sapiens clone GS223D04, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:417:62//AC005018

R-MAMMA1001817//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.//2.6e-40:313:84//AC005859

R-MAMMA1001818

R-MAMMA1001820//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//12.2e-45:340:82//AC004086

R-MAMMA1001824//Homo sapiens clone DJ1107K15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9e-53:291:85//AC004966

R-MAMMA1001836//HS\_3164\_B1\_A02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=E, genomic survey sequence.//6.5e-08:79:89//AQ185484

R-MAMMA1001837//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//8.4e-55:309:85//AC003682

R-MAMMA1001848//Homo sapiens PAC clone DJ0296G17 from Xq23, complete sequence.//1.6e-16:125:90//AC006144

R-MAMMA1001851//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:516:74//AC002099

R-MAMMA1001854//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.7e-38:308:82//AC002425

R-MAMMA1001856//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, complete sequence.//6.5e-50:283:86//U80460

R-MAMMA1001864//Human Chromosome 15q26.1 PAC clone pDJ398g19, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.4e-36:224:86//AC005143

R-nnnnnnnnnnn//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//1.4e-11:495:63//AE001417

R-MAMMA1001874//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.2e-42:446:76//AC003117

R-MAMMA1001878//Human DNA sequence from PAC 431A14 on chromosome 6p21. Contains CYCLOPHILIN (PEPTIDYLPROLYL ISOMERASE) like and CIP1 (WAF1, CDKN1A, CDKN1, MDA-6, SDI1, PIC1, CAP20) genes. Contains probable GTPase and receptor genes and ESTs, STSs and CpG islands.//6.9e-44:391:78//Z85996

R-MAMMA1001880//Human DNA sequence from fosmid F77D12 on chromosome 22q12-qter contains ESTs, tRNA.//1.3e-15:181:76//Z82097

R-MAMMA1001890//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-670B5 ~complete genomic se-



quence, complete sequence.//1.7e-43:283.86//AC002303  
 R-MAMMA1001907//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 385E7, WORKING DRAFT SEQUENCE.//1.4e-48:422:79//AL031720  
 R-nnnnnnnnnnn//Saccharomyces cerevisiae chromosome IV cosmid 9481.//2.9e-14:505.60//U28373  
 5 R-MAMMA1001931//Homo sapiens NACP/alpha-synuclein gene, allele A0, intron 4, partial sequence.//0.51:162:63//AF041008  
 R-MAMMA1001958//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50O24, WORKING DRAFT SEQUENCE.//1.4e-51:422:79//AL034380  
 R-MAMMA1001963//Homo sapiens clone HS19.3 Alu-Ya5 sequence.//1.9e-31:163.91//AF015149  
 10 R-MAMMA1001969//Human DNA from chromosome 19 cosmid F19410, genomic sequence, complete sequence.//8.7e-10:186:76//AC002128  
 R-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.0e-62:298:86//AC003071  
 R-MAMMA1001992//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-44:525.72//AC004581  
 15 R-MAMMA1002009//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 109G6, WORKING DRAFT SEQUENCE.//1.4e-43:282:79//AL023879  
 R-MAMMA1002011  
 R-MAMMA1002032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//1.1e-39:310:84//AL031284  
 20 R-MAMMA1002033//Homo sapiens chromosome 5, Pac clone 162o17 (LBNL H147), complete sequence.//2.5e-17:170.81//AC003954  
 R-MAMMA1002041//Homo sapiens PAC clone DJ0728D04, complete sequence.//8.7e-79:296:85//AC004865  
 R-MAMMA1002042//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//8.8e-46:386:80//U91318  
 25 R-MAMMA1002047//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//1.9e-32:326:75//U91318  
 R-MAMMA1002056//Homo sapiens chromosome 17, clone hRPK.506\_H\_21, complete sequence.//6.6e-48:367:82//AC005962  
 30 R-MAMMA1002058//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.25:139:69//AC005052  
 R-MAMMA1002068//Homo Sapiens Chromosome X clone bWXd171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-45:406:78//AC004676  
 R-MAMMA1002078//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//2.3e-22:357:64//AC005291  
 35 R-MAMMA1002082//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//2.5e-38:304:82//AC004263  
 R-MAMMA1002084//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1174N9, WORKING DRAFT SEQUENCE.//8.9e-41:319:83//AL031602  
 40 R-MAMMA1002093//CIT-HSP-2060J9.TF CIT-HSP Homo sapiens genomic clone 2060J9, genomic survey sequence.//9.7e-17:129:88//B69983  
 R-MAMMA1002108  
 R-MAMMA1002118//Human DNA sequence from cosmid E116C6, on chromosome 22 Contains ESTs, complete sequence.//0.94:168:64//Z73495  
 45 R-MAMMA1002125//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//4.8e-40:313:83//AC005670  
 R-MAMMA1002132//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.0e-70:461:83//AC004953  
 R-MAMMA1002140//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu<sup>++</sup>-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.1e-32:477:73//Z94801  
 50 R-MAMMA1002143//Homo sapiens platelet-activating factor acetylhydrolase gene, promoter region and exon 1.//6.6e-06:130:73//AF027357  
 R-MAMMA1002145//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//6.0e-19:242:73//AL031447  
 R-MAMMA1002153//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0281M17; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.1e-51:291:75//AC006052  
 55 R-MAMMA1002155//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 608E8, WORKING DRAFT SEQUENCE.//1.2e-53:461:79//AL022343

R-MAMMA1002156//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//5.1e-37:305:82//AC004997

R-MAMMA1002158//Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLUCOSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.//8.1e-34:296:81//AL034418

R-MAMMA1002170//Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.33. Contains the 3' part of a gene for the ortholog of mouse transmembrane receptor Celsr1, a novel gene for a protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylate)-Methyltransferases, and the 3' part of a novel gene for a protein similar to mouse B99. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.9e-39:332:82//AL031588

R-MAMMA1002174//Homo sapiens chromosome 10 clone C19877SK-1109P11, complete sequence.//4.4e-12:189:72//AC005871

R-MAMMA1002198//Homo sapiens clone DJ0800G07, complete sequence.//1.1e-48:338:81//AC004890

R-MAMMA1002209//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//1.2e-23:269:74//AC005821

R-MAMMA1002215//Homo sapiens clone GS250N06, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:243:68//AC005158

R-MAMMA1002219//Homo sapiens 12p13.3 RPC14-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.3e-45:295:88//AC004802

R-MAMMA1002230//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//7.3e-41:385:78//AL034379

R-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//7.3e-45:363:79//U38253

R-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//2.8e-119:582:98//AC005666

R-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//4.7e-42:319:84//AC005600

R-MAMMA1002267//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//1.5e-33:571:67//AC006120

R-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//2.3e-35:462:70//AF068749

R-MAMMA1002269//345117.TV CIT978SKA1 Homo sapiens genomic clone A-345117, genomic survey sequence.//4.7e-05:153:69//B15590

R-MAMMA1002282//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 112K5, WORKING DRAFT SEQUENCE.//8.5e-37:467:71//Z85987

R-MAMMA1002292//Hordeum vulgare lipoxygenase 2 (LoxC) mRNA, complete cds.//0.074:178:61//L37358

R-MAMMA1002293//Homo sapiens chromosome 16, cosmid clone RT167 (LANL), complete sequence.//5.8e-26:355:71//AC005568

R-MAMMA1002294//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//1.2e-35:281:82//AC004231

R-MAMMA1002297//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//6.7e-48:381:80//Z69375

R-MAMMA1002298//Homo sapiens BAC clone RG208H19 from 7q11.23, complete sequence.//8e-17:296:70//AC005074

R-MAMMA1002299//HS\_3116\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=14 Row=K, genomic survey sequence.//4.1e-60:354:91//AQ140526

R-MAMMA1002308

R-MAMMA1002310//Human DNA sequence from cosmid B10B1 on chromosome 22 Contains ESTs, CA repeat and STS, complete sequence.//9.9e-35:283:83//Z73979

R-MAMMA1002311//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.3e-86:503:90//AC006210

R-MAMMA1002312//H. sapiens gene encoding La autoantigen.//1.3e-23:382:67//X97869

R-MAMMA1002317//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//1.3e-59:323:87//AL031054

R-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//2.2e-106:522:98//AC005756

R-MAMMA1002322//Homo sapiens genomic DNA, chromosome 21q11.1, segment 13/28, WORKING DRAFT SEQUENCE.//2.3e-48:452:76//AP000042

R-MAMMA1002329//M.musculus mRNA for semaphorin B.//2.0e-12:210.73//X85991  
 R-MAMMA1002332//Homo sapiens PAC clone DJ1139101 from Xq23, complete sequence.//3.4e-46:393.71//AC004973  
 R-MAMMA1002333//HS\_3245\_A1\_B04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=7 Row=C, genomic survey sequence.//3.1e-21:146.92//AQ205759  
 5 R-MAMMA1002339//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//9.7e-39:310.79//AF001549  
 R-MAMMA1002347//Homo sapiens 12q24.1 PAC RPCI3-305120 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-46:443.76//AC006088  
 10 R-MAMMA1002351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1059H15, WORKING DRAFT SEQUENCE.//1.1e-90:553.89//AL022100  
 R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2.//8.8e-81:388.92//Y15228  
 R-MAMMA1002353//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//5.5e-35:302.80//AC002996  
 15 R-MAMMA1002355//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 222E13, WORKING DRAFT SEQUENCE.//5.4e-52:361.76//Z93241  
 R-MAMMA1002356//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//8.3e-28:187.91//AC004662  
 R-MAMMA1002359//Human DNA sequence from cosmid L118D5, Huntington's Disease Region, chromosome 4p16.3 contains CpG islands.//6.3e-47:297.85//268869  
 20 R-MAMMA1002360//HS\_2163\_B2\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=16 Row=F, genomic survey sequence.//1.5e-20:374.66//AQ125213  
 R-MAMMA1002361//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//2.2e-35:264.85//AL033520  
 25 R-MAMMA1002362//H. sapiens PEX gene.//1.8e-40:243.86//Y10196  
 R-MAMMA1002360//RPCI11-73J4.TJ RPCI11 Homo sapiens genomic clone R-73J4, genomic survey sequence.//1.7e-38:295.77//AQ268168  
 R-MAMMA1002384//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-37:311.81//AC004801  
 30 R-MAMMA1002385  
 R-MAMMA1002392//Human BAC clone RG066D11 from 7q22, complete sequence.//2.0e-37:365.77//AC002430  
 R-MAMMA1002411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING DRAFT SEQUENCE.//9.4e-22:496.65//AL031668  
 R-MAMMA1002413//Homo sapiens 12q24.2 PAC RPCI1-157K6 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.3e-15:153.77//AC005146  
 35 R-MAMMA1002417//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.8e-23:508.62//AL020997  
 R-MAMMA1002427//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.5e-37:288.84//U91321  
 40 R-MAMMA1002428//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//6.0e-05:130.75//AL034423  
 R-MAMMA1002434//Homo sapiens DNA sequence from PAC 380E11 on chromosome 6p22.3-p24. Contains HB15 gene, ESTs, CA repeat, STS and GSS.//4.8e-18:205.78//AL022396  
 R-MAMMA1002446//CIT-HSP-2021L14.TR CIT-HSP Homo sapiens genomic clone 2021L14, genomic survey sequence.//4.6e-41:387.72//B65379  
 45 R-MAMMA1002454//Homo sapiens chromosome 19, cosmid F23259, complete sequence.//1.2e-67:491.82//AC005512  
 R-MAMMA1002461//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//1.4e-28:188.85//AC003982  
 R-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//6.3e-09:280.61//U10556  
 50 R-MAMMA1002475//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//1.5e-25:310.74//Z83822  
 R-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-98:533.93//AC005077  
 R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.7e-114:560.97//AF055460  
 55 R-MAMMA1002494//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//2.1e-46:329.84//Z69375  
 R-MAMMA1002498//Rat mRNA.//0.0068:223.64//M59859  
 R-MAMMA1002524//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING

DRAFT SEQUENCE, 5 unordered pieces.//0.012:460:60//AC005139  
 R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.2e-101:529:95//AF065214  
 R-MAMMA1002545//Homo sapiens ribosomal protein s4 Y isoform gene, complete cds.//6.6e-50:471:77//AF041427  
 R-MAMMA1002554//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//5.7e-38:279:84//AC004056  
 R-MAMMA1002556//Homo sapiens chromosome 10 clone CIT-HSP-1255F20 map 10p11.2-10p12.1, complete sequence.//9.6e-13:237:67//AC005878  
 R-MAMMA1002566//CITBI-E1-2509P21.TR CITBI-E1 Homo sapiens genomic clone 2509P21, genomic survey sequence.//9.7e-14:216:73//AQ261427  
 R-MAMMA1002571//CITBI-E1-2516L21.TF CITBI-E1 Homo sapiens genomic clone 2516L21, genomic survey sequence.//4.6e-25:142:99//AQ279542  
 R-MAMMA1002573//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 811H13, WORKING DRAFT SEQUENCE.//1.1e-30:250:82//AL023805  
 R-MAMMA1002585//Rabbit angiotensin-converting enzyme (ACE) gene, 5' end.//1.0:196:61//M58580  
 R-MAMMA1002590//H. sapiens CpG island DNA genomic MseI fragment, clone 8d5, forward read cpg8d5.f1g.//1.0:114:64//Z63758  
 R-MAMMA1002597//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1103G7, WORKING DRAFT SEQUENCE.//9.0e-96:459:98//AL034548  
 R-MAMMA1002598//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING DRAFT SEQUENCE.//0.79:362:58//AL031847  
 R-MAMMA1002603//Homo sapiens chromosome 17, clone hRPC.214\_C\_8, complete sequence.//1.3e-46:333:80//AC005803  
 R-MAMMA1002612//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 269M15, WORKING DRAFT SEQUENCE.//7.4e-41:283:86//AL021395  
 R-MAMMA1002617//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 591N18, WORKING DRAFT SEQUENCE.//1.7e-20:308:71//AL031594  
 R-MAMMA1002618//Homo sapiens clone RG122E10, complete sequence.//1.2e-31:230:76//AC005067  
 R-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.0e-113:551:98//AJ010598  
 R-MAMMA1002622//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.8e-43:324:83//AC004050  
 R-MAMMA1002623//Homo sapiens chromosome 17, clone hRPC.1171\_I\_10, complete sequence.//2.7e-80:344:84//AC004687  
 R-MAMMA1002625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1056L3, WORKING DRAFT SEQUENCE.//2.6e-34:391:72//AL031727  
 R-MAMMA1002629//Human DNA from overlapping chromosome 19-specific cosmids R32543, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//5.5e-58:346:81//AC003006  
 R-MAMMA1002636//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-52:285:92//AC004895  
 R-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//2.1e-13:359:64//AF055666  
 R-MAMMA1002646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 394I7, WORKING DRAFT SEQUENCE.//2.5e-24:285:68//AL023585  
 R-MAMMA1002650//Human IGF-II gene exon 2 for insulin-like growth factor II located on chromosome 11.//0.64:237:61//X03424  
 R-MAMMA1002655//Homo sapiens mini satellite ceb1 repeat region.//0.18:152:65//AF048727  
 R-MAMMA1002662//Homo sapiens clone DJ0739M23, complete sequence.//2.5e-46:370:82//AC004870  
 R-MAMMA1002665//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//7.4e-55:298:92//Z92844  
 R-MAMMA1002671//RPC111-45M10.TK RPC111 Homo sapiens genomic clone R45M10, genomic survey sequence.//0.99:151:66//AQ194411  
 R-MAMMA1002673//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//3.1e-38:410:76//AL022162  
 R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.4e-107:544:96//D86987  
 R-MAMMA1002685//HS\_2052\_A1\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=3 Row=O, genomic survey sequence.//1.2e-23:255:75//AQ231087  
 R-MAMMA1002698//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)

- complete sequence.//1.1e-38:299:83//AC004673  
 R-MAMMA1002699//Mus musculus intersectin-EH binding protein lbp1 mRNA, partial cds.//3.3e-05:61.93//AF057285
- 5 R-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//3.5e-39:37.181//AB011399  
 R-MAMMA1002708//Homo sapiens 12p13.3 PAC RPCI5-977L1 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.26:365:62//AC005293  
 R-MAMMA1002711//Homo sapiens chromosome 21 PAC LLNLP704F18108Q13.//2.5e-31:304:77//AJ006995  
 R-MAMMA1002721//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING DRAFT SEQUENCE.//2.3e-40:279:87//Z83826
- 10 R-MAMMA1002727//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.45:183:64//AC004710  
 R-MAMMA1002728//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.1e-42:410:74//AC002037  
 R-MAMMA1002744//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.6e-19:473.63//U96629
- 15 R-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//2.2e-108:544:97//AC005856  
 R-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-106:551:95//AC006055  
 R-MAMMA1002754//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-34:305:79//AC005020
- 20 R-MAMMA1002758//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.00014:130:74//U95626  
 R-MAMMA1002764//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//8.7e-10:118:81//AC005781
- 25 R-MAMMA1002765//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//1.2e-31:290:78//AC006128  
 R-MAMMA1002769//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//0.94:260:62//Z82975
- 30 R-MAMMA1002780//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//2.6e-21:529:62//AL031667  
 R-MAMMA1002782//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 199H16, WORKING DRAFT SEQUENCE.//2.8e-30:234:72//AL022320  
 R-MAMMA1002796//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 237J2, WORKING DRAFT SEQUENCE.//1.0:155:66//AL021394
- 35 R-MAMMA1002807//Human DNA sequence from BAC 941F9 on chromosome 22q11.2-qter. Contains ESTs, STSs and 3' part of FIBULIN-1 D PRECURSOR like gene, part of a Brain Protein E46 like gene and a CpG island, complete sequence.//5.0e-42:443:75//Z95331  
 R-MAMMA1002820//345M16.TVB CIT978SKA1 Homo sapiens genomic clone A-345M16, genomic survey sequence.//1.3e-14:95:87//B17487
- 40 R-MAMMA1002830//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//4.1 e-20:223:74//AC002073  
 R-MAMMA1002833//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.8e-37:295:84//AC005295
- 45 R-MAMMA1002835  
 R-MAMMA1002838//Human gene hY3 encoding a cytoplasmic Ro RNA.//4.4e-14:108:92//V00585  
 R-MAMMA1002842//CIT-HSP-2017022.TRB CIT-HSP Homo sapiens genomic clone 2017022, genomic survey sequence.//5.2e-43:168:85//B67141
- 50 R-MAMMA1002843//Homo sapiens clone GS051M12, complete sequence.//8.7e-44:525:71//AC005007  
 R-MAMMA1002844  
 R-MAMMA1002858//H. sapiens ERF-1 mRNA 3' end.//2.8e-99:361:91//X79067
- 55 R-MAMMA1002868//Homo sapiens clone DJ0852O24, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.6e-39:288:81//AC004906  
 R-MAMMA1002871//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//0.0022:490:57//AC006044  
 R-MAMMA1002880//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//1.3e-09:143:76//AC005296  
 R-MAMMA1002881//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial

cds for thymopoietin beta //5.1e-41:264:87//U18271

R-MAMMA1002886//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//4.7e-32:216:90//AL0202069

R-MAMMA1002887

R-MAMMA1002890

3.4e-49:376:81//AG006257

R-MAMMA1002892//Homo sapiens PAC clone DJ0765G07 from 7q11, complete sequence.//6.0e-60:344:79//

AC004881

R-MAMMA1002895//RPC111-90K13.TV RPC111 Homo sapiens genomic clone R-90K13, genomic survey se-

quence.//2.1e-34:300:77//AQ283502

R-MAMMA1002908//Human Chromosome X, complete sequence.//4.2e-39:297:85//AC004070

R-MAMMA1002909//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0442P12;

HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-23:344:74//AC005798

R-MAMMA1002930//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//5.2e-39:261:88//

AC006019

R-MAMMA1002938//C.pasteurianum gap gene.//1.0:343:59//X72219

R-MAMMA1002941//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//6.3e-88:556:

87//AC006120

R-MAMMA1002947

0.48:156:69//AC005469

R-MAMMA1002964//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like

gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.2e-39:473:73//AL020997

R-MAMMA1002970//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//4.7e-47:

420:77//AC005200

R-MAMMA1002972//alpha 1 syntrophin [human, mRNA Partial, 1771 nt] //0.97:305:62//S81737

R-MAMMA1002973//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chro-

mosome X.//2.6e-35:256:85//Z70280

R-MAMMA1002982 1.0e-27:110:85//AG005524

R-MAMMA1002987//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.4e-28:527:66//AC004460

R-MAMMA1003003//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING

DRAFT SEQUENCE, 1 ordered pieces.//7.9e-48:418:78//AC006109

R-MAMMA1003004//, complete sequence.//2.0e-12:442:61//AC005406

R-MAMMA1003007//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING

DRAFT SEQUENCE, 1 ordered pieces.//1.7e-48:293:91//AC006109

R-MAMMA1003011//A-306G8.TP C1T978SK Homo sapiens genomic clone A-306G8, genomic survey sequence.//

0.45:168:64//B18092

R-MAMMA1003015//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.9e-

44:399:77//AC005740

R-MAMMA1003019//RPC111-9J9.TV RPC111 Homo sapiens genomic clone RPC111-9J9, genomic survey se-

quence.//2.7e-14:294:68//B71583

R-MAMMA1003026//HS\_2166\_B2\_C12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomc clone Plate=2166 Col=24 Row=F, genomic survey sequence.//0.021:189:64//AQ125639

R-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//1.8e-

98:525:95//AC005214

R-MAMMA1003035//Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore LL12NC01 or LL12NC02 hu-

man cosmid libraries) complete sequence.//6.7e-06:297:63//AC004550

R-MAMMA1003039//RPC111-56J17.TJ RPC111 Homo sapiens genomic clone R-56J17, genomic survey se-

quence.//0.21:375:59//AQ081889

R-MAMMA1003040//Human DNA sequence from cosmid L108F12, Huntington's Disease Region, chromosome

4p16.3.//2.7e-29:298:67//Z49235

R-MAMMA1003044//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//2.9e-14:113:91//

AC004560

R-MAMMA1003047

R-MAMMA1003049

R-MAMMA1003055//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 377F16, WORKING

DRAFT SEQUENCE.//2.3e-45:317:86//Z93783

R-MAMMA1003056//Homo sapiens chromosome 19, cosmid R34275, complete sequence.//1.0:229:63//

AC005305

R-MAMMA1003057//M.domesticus MD6 mRNA.//6.2e-42:326:82//X54352  
 R-MAMMA1003066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING  
 DRAFT SEQUENCE.//3.1e-49:299:87//Z83826  
 R-MAMMA1003089//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//2.7e-30:520:67//  
 5 AC005084  
 R-MAMMA1003099//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey se-  
 quence.//4.2e-44:338:82//B71494  
 R-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//3.4e-48:  
 423:79//U72634  
 10 R-MAMMA1003113//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE,  
 100 unordered pieces.//4.8e-114:567:97//AC006087  
 R-MAMMA1003127//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING  
 DRAFT SEQUENCE.//1.4e-34:283:83//Z99716  
 R-MAMMA1003135//P.knowlesi Mbn-cutting sites in lambda KBS50.//0.010:243:62//M38776  
 15 R-MAMMA1003140//Homo sapiens chromosome 17, clone HCIT87G17, complete sequence.//6.7e-34:288:81//  
 AC003663  
 R-MAMMA1003146//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, com-  
 plete cds.//4.8e-08:438:59//M97514  
 R-nnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING  
 20 DRAFT SEQUENCE.//1.7e-63:149:94//AL021579  
 R-MAMMA1003166//HS\_3128\_A1\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3128 Col=1 Row=C, genomic survey sequence.//3.0e-17:261:70//AQ140766  
 R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence.//2.6e-111:593:94//AF070640  
 R-NT2RM4000024  
 25 R-NT2RM4000027//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//0.026:476:56//  
 AC004993  
 R-NT2RM4000030//Mus musculus sex determining protein (Sry) gene, complete cds.//0.00044:378:59//  
 U70653  
 R-NT2RM4000046//M.mulatta MHC DR beta 6 gene encoding major histocompatibility complex.//0.27:130:64//  
 30 Z26239  
 R-NT2RM4000061  
 R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds.//7.2e-112:550:97//AF070639  
 R-NT2RM4000086//RPCI11-6J23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6J23, genomic survey se-  
 quence.//7.2e-18:277:71//B49463  
 35 R-NT2RM4000104//F.rubripes GSS sequence, clone 063K10aG5, genomic survey sequence.//3.6e-08:287:61//  
 Z88817  
 R-NT2RM4000139//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//9.4e-08:  
 336:65//AC005199  
 R-NT2RM4000155  
 40 R-NT2RM4000156//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, complete sequence.//3.4e-23:335:  
 72//AC005856  
 R-nnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//1.6e-87:551:87//  
 D12846  
 R-NT2RM4000169//Human ribosomal protein L37a mRNA sequence.//5.9e-14:122:88//L22154  
 45 R-NT2RM4000191  
 R-NT2RM4000197//HS\_3241\_A2\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3241 Col=10 Row=O, genomic survey sequence.//2.8e-86:430:97//AQ206812  
 R-NT2RM4000199//Mus musculus Yp BAC GSMB-368G7 (Genome Systems Mouse BAC Library) complete se-  
 quence.//0.0047:193:63//AC006056  
 50 R-NT2RM4000200  
 R-NT2RM4000202//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//2.1e-40:  
 334:76//AC004035  
 R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//5.2e-102:546:94//AB018255  
 R-NT2RM4000215  
 55 R-nnnnnnnnnnn//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//  
 2.1e-55:303:86//AC005383  
 R-NT2RM4000233//Struthio camelus microsatellite sequence OSM 7.//1.2e-07:198:67//AF003735  
 R-NT2RM4000244//Homo sapiens chromosome 19, BAC CIT-B-393I15 (BC301323), complete sequence.//1.7e-

- 49:322:88//AC006116  
 R-NT2RM4000251//Homo sapiens Chromosome 22q11.2 BAC Clone 72f8 in DGCR Region, complete sequence.//  
 0.97:184:66//AC000085  
 R-NT2RM4000265//Human PAC clone DJ073F11 from Xq23, complete sequence.//6.2e-66:552:78//AC000055  
 5 R-NT2RM4000290//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39417, WORKING  
 DRAFT SEQUENCE.//1.4e-05:229:65//AL023585  
 R-NT2RM4000324  
 R-NT2RM4000327//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 75N14, WORKING  
 DRAFT SEQUENCE.//3.3e-42:443:75//IZ97199  
 10 R-NT2RM4000344//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//  
 6.4e-64:433:84//AC004826  
 R-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds.//7.7e-11:210:69//D13630  
 R-NT2RM4000354//Caenorhabditis elegans cosmid T14A8.//0.084:257:60//U50066  
 R-NT2RM4000356  
 15 R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//8.7e-112:577:95//AB014542  
 R-NT2RM4000368  
 1.6e-48:348:85//AG006257  
 R-NT2RM4000386//Rat mRNA for growth potentiating factor, complete cds.//4.4e-35:141:87//D42148  
 R-NT2RM4000395//RPC111-8N9, TP RPC111 Homo sapiens genomic clone RPC111-8N9, genomic survey se-  
 20 quence.//1.4e-25:207:75//B71494  
 R-NT2RM4000414//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING  
 DRAFT SEQUENCE.//7.1e-17:492:64//AL031985  
 R-NT2RM4000421//RPC111-66B1, TK RPC111 Homo sapiens genomic clone R-66B1, genomic survey sequence.//  
 1.8e-40:311:82//AQ241167  
 25 R-NT2RM4000425//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SE-  
 QUENCE, 35 unordered pieces.//2.5e-47:316:87//AC005867  
 R-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//1.6e-17:133:  
 78//AF062476  
 R-NT2RM4000457  
 30 R-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//4.6e-113:559:96//AJ010952  
 R-NT2RM4000486//Homo sapiens mRNA, complete cds, clone: RES4-22C.//0.00015:170:67//AB000461  
 R-NT2RM4000496  
 R-NT2RM4000511//Rat troponin T cardiac isoform gene, complete cds.//0.21:290:58//M80829  
 R-NT2RM4000514//CIT-HSP-2169K4, TR CIT-HSP Homo sapiens genomic clone 2169K4, genomic survey se-  
 35 quence.//1.5e-20:150:89//B95717  
 R-nnnnnnnnnnn//HS-1024-B2-G01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone  
 Plate=CT 803 Col=2 Row=N, genomic survey sequence.//6.3e-10:74:98//B34556  
 R-NT2RM4000520//Caenorhabditis elegans cosmid F36H12.//0.15:406:61//AF078790  
 R-NT2RM4000531  
 40 R-NT2RM4000532//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//1.0:119:  
 66//AE001391  
 R-NT2RM4000534//paramecium species 4.51er mt dna dimer: replication init. region, clone 2.//9.8e-05:326:60//  
 K00909  
 R-NT2RM4000585//HS\_3252\_A2\_G08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 45 nomic clone Plate=3252 Col=16 Row=M, genomic survey sequence.//1.9e-69:376:93//AQ219890  
 R-NT2RM4000590//CIT-HSP-539O24, TV CIT-HSP Homo sapiens genomic clone 539O24, genomic survey se-  
 quence.//1.7e-38:226:93//B50657  
 R-NT2RM4000595//Human Chromosome X clone bWDX342, complete sequence.//1.0:239:61//AC004072  
 R-NT2RM4000603//RPC111-49P13, TK RPC111 Homo sapiens genomic clone R-49P13, genomic survey se-  
 50 quence.//0.77:139:64//AQ051950  
 R-nnnnnnnnnnn  
 R-NT2RM4000616//HS\_3107\_A2\_B03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3107 Col=6 Row=C, genomic survey sequence.//1.3e-54:272:99//AQ210034  
 R-NT2RM4000674  
 55 R-NT2RM4000689//Mus musculus pericentrin mRNA, complete cds.//3.5e-70:551:80//U05823  
 R-NT2RM4000698  
 R-nnnnnnnnnnn  
 R-NT2RM4000712//Homo sapiens clone NH0512E16, complete sequence.//0.54:294:58//AC005039



R-NT2RM4000717//Plasmodium falciparum MAL3P8, complete sequence //0.050:387:58//AL034560  
 R-NT2RM4000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
 DRAFT SEQUENCE //1.0e-107:566:95//AL034379  
 R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds. //1.1e-103:536:95//AB018303  
 5 R-NT2RM4000741//CIT-HSP-2294N4.TR CIT-HSP Homo sapiens genomic clone 2294N4, genomic survey se-  
 quence //5.2e-41:244:93//AQ006361  
 R-NT2RM4000751//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING  
 DRAFT SEQUENCE //2.7e-28:416:67//AL034405  
 10 R-NT2RM4000764//Human HepG2 3' region Mbol cDNA, (clone hmd3g01m3. //2.1e-33:199:96//D17217  
 R-NT2RM4000778//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//  
 0.00060:241:62//AC002980  
 R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds. //2.9e-104:546:94//AB007920  
 R-NT2RM4000787//Homo sapiens, clone hRPK\_3\_A\_1, complete sequence //5.3e-32:321:77//AC006198  
 15 R-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence //1.9e-111:552:97//  
 AC005306  
 R-NT2RM4000795//Homo sapiens Chromosome 17p13 Cosmid Clone cos39, complete sequence. //0.74:364:57//  
 U58675  
 R-NT2RM4000796//Homo sapiens full-length insert cDNA clone ZD62D10 //2.7e-105:510:98//AF086348  
 R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end. //7.7e-27:158:96//M21868  
 20 R-NT2RM4000813  
 R-NT2RM4000820//, complete sequence. //2.0e-104:432:97//AC005406  
 R-NT2RM4000833//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX122, complete sequence.//  
 2.0e-07:166:68//AB012248  
 R-NT2RM4000848//Rabies virus matrix (M) protein mRNA, complete cds. //0.073:70:84//M22013  
 25 R-NT2RM4000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING  
 DRAFT SEQUENCE, 3 unordered pieces. //1.0:237:62//AC004709  
 R-NT2RM4000855  
 R-nnnnnnnnnnn//HS\_3189\_B2\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genom-  
 ic clone Plate=3189 Col=16 Row=D, genomic survey sequence. //2.1e-06:114:73//AQ300597  
 30 R-NT2RM4000895//Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence. //3.8e-  
 46:207:91//AF077058  
 R-NT2RM4000950//Human BAC clone RG341D10 from 7p15-p21, complete sequence. //1.0:336:60//AC002530  
 R-NT2RM4000971//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12,  
 U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete se-  
 35 quence. //7.1e-09:259:64//AF011889  
 R-NT2RM4000979  
 R-NT2RM4000996//HS\_3164\_A1\_E02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3164 Col=3 Row=I, genomic survey sequence. //2.0e-82:443:94//AQ141622  
 40 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds. //1.2e-112:545:97//AB018272  
 R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds. //7.9e-113:556:97//AB014539  
 R-NT2RM4001032//Homo sapiens Surf-5 and Surf-6 genes. //1.2e-10:120:82//AJ224639  
 R-NT2RM4001047//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 163G9, WORKING  
 DRAFT SEQUENCE. //1.0:158:67//AL008733  
 45 R-NT2RM4001054//CIT-HSP-2292N8.TR CIT-HSP Homo sapiens genomic clone 2292N8, genomic survey se-  
 quence. //5.8e-19:118:97//AQ004096  
 R-nnnnnnnnnnn//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2. //1.0e-05:271:64//  
 M10296  
 R-NT2RM4001092//CITBI-E1-2524J20.TR CITBI-E1 Homo sapiens genomic clone 2524J20, genomic survey se-  
 quence. //1.0:186:63//AQ277294  
 50 R-NT2RM4001116  
 R-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence. //3.6e-79:468:90//  
 AC004593  
 R-NT2RM4001151//HS\_2270\_B1\_E05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2270 Col=9 Row=J, genomic survey sequence. //5.5e-62:312:98//AQ163739  
 55 R-NT2RM4001155//Homo sapiens chromosome 12p13.3 clone RPC14-816N1, WORKING DRAFT SEQUENCE,  
 31 unordered pieces. //1.4e-107:536:97//AC005841  
 R-NT2RM4001160//HS\_3015\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3015 Col=19 Row=P, genomic survey sequence. //7.1e-35:201:95//AQ118712

- R-NT2RM4001187//X.laevus xUBFbeta2 mRNA for upstream binding factor 1.//0.019:177:63//X57201
- R-NT2RM4001191//HS\_3002\_A1\_F05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=9 Row=K, genomic survey sequence.//3.9e-33:230:75//AQ088791
- R-NT2RM4001200//Homo sapiens full-length insert cDNA clone YL35H03.//7.5e-69:335:99//AF085857
- 5 R-NT2RM4001203  
R-NT2RM4001204  
R-NT2RM4001217  
R-NT2RM4001256  
R-NT2RM4001258
- 10 R-NT2RM4001309  
R-NT2RM4001313//Homo sapiens 12q24.1 PAC RPC11-71H24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.00055:183:63//AC004551  
R-NT2RM4001316//Homo sapiens chromosome 17, clone hCIT.117\_K\_16, complete sequence.//4.5e-21:212:79//AC004757
- 15 R-NT2RM4001320//CIT-HSP-2303E22.TR CIT-HSP Homo sapiens genomic clone 2303E22, genomic survey sequence.//3.8e-30:86:89//AQ021084  
R-NT2RM4001340  
0.0027:493:60//AC005133  
R-NT2RM4001344
- 20 R-NT2RM4001347//CITBI-E1-2506I20.TR CITBI-E1 Homo sapiens genomic clone 2506I20, genomic survey sequence.//8.5e-16:1.01:99//AQ262797  
R-NT2RM4001371//CITBI-E1-2503G21.TR CITBI-E1 Homo sapiens genomic clone 2503G21, genomic survey sequence.//0.063:140:65//AQ265776  
R-NT2RM4001382//HS\_3044\_A1\_F02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=3 Row=K, genomic survey sequence.//0.96:103:66//AQ098668
- 25 R-NT2RM4001384//R.norvegicus mRNA for dendrin.//8.5e-07:120:75//Y09000  
R-NT2RM4001410//Bovine cytochrome P450-scc mRNA fragment.//2.3e-15:199:75//M25920  
R-NT2RM4001411//Rattus norvegicus FcεRI gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds.//1.7e-55:235:83//U57391
- 30 R-NT2RM4001412  
R-NT2RM4001414//Homo sapiens Xp22 Cosmids U98B4 and U24F2 (Lawrence Livermore human cosmid library) complete sequence.//1.7e-80:489:89//U69730  
R-NT2RM4001437//RPC111-56D2.TJ RPC111 Homo sapiens genomic clone R-56D2, genomic survey sequence.//3.8e-43:250:93//AQ081969
- 35 R-NT2RM4001444//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//0.0034:224:63//AC005926  
R-NT2RM4001454//Homo Sapiens Chromosome X clone bWXD90, complete sequence.//2.4e-33:360:68//AC004075  
R-NT2RM4001455//HS\_3229\_B1\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=7 Row=J, genomic survey sequence.//1.0:183:61//AQ191289
- 40 R-NT2RM4001483//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.2e-51:451:79//AC005822  
R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.2e-102:547:93//AB014585  
R-NT2RM4001519//HS\_2208\_A1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=13 Row=K, genomic survey sequence.//0.25:214:63//AQ091836
- 45 R-NT2RM4001522//H.sapiens gene for Cu/Zn-superoxide dismutase.//3.6e-13:246:70//Z29336  
R-NT2RM4001557//Plasmodium falciparum MAL3P4, complete sequence.//0.055:320:58//AL008970  
R-NT2RM4001565//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//3.9e-26:329:72//AC005910
- 50 R-NT2RM4001568//Human trophinin mRNA, complete cds.//6.3e-38:296:86//U04811  
R-NT2RM4001569//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudogenes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//2.0e-35:213:89//AL031663
- 55

R-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//5.4e-60:558:77//AF071317

R-nnnnnnnnnnn//M.musculus mRNA of enhancer-trap-locus 1./4.8e-86:565:85//X69942

R-NT2RM4001594//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.083:283:61//U31120

5 R-NT2RM4001597//HS\_2059\_A1\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2059 Col=21 Row=M, genomic survey sequence.//4.4e-09:105:83//AQ245136

R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//6.7e-111:565:95//AB018334

R-NT2RM4001611//Homo sapiens ryanodine receptor (RyR) mRNA, partial cds.//1.0:364:61//AF051936

10 R-NT2RM4001629//RPI11-54G14.TJ RPI11 Homo sapiens genomic clone R-54G14, genomic survey sequence.//0.0018:347:61//AQ083173

R-NT2RM4001650

R-NT2RM4001662//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//0.75:212:62//AL022575

15 R-NT2RM4001666//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//2.6e-26:461:65//AC004685

R-NT2RM4001682//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//1.5e-107:544:96//AL031775

20 R-NT2RM4001710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//1.8e-110:580:95//AL031447

R-NT2RM4001714//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.1e-10:543:59//AC004153

25 R-nnnnnnnnnnn//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//8.7e-111:577:94//AL034430

R-NT2RM4001731//Ovis aries dinucleotide repeat polymorphism at MAF92 locus.//0.017:93:73//M80527

R-NT2RM4001741//Mouse mRNA for talin.//2.4e-34:273:83//X56123

R-NT2RM4001746//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316G12, WORKING DRAFT SEQUENCE.//1.7e-112:567:96//AL031709

30 R-NT2RM4001754//Homo sapiens PAC clone 248O15 from 13q12-q13, complete sequence.//1.4e-64:475:83//AC002483

R-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//1.9e-18:202:78//ZB3868

R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.0e-22:236:80//AB018270

R-NT2RM4001783//Homo sapiens clone DJ0981O07, complete sequence.//4.4e-106:551:95//AC006017

35 R-NT2RM4001810//T28D3TF TAMU Arabidopsis thaliana genomic clone T28D3, genomic survey sequence.//0.76:279:60//B27099

R-NT2RM4001813

R-NT2RM4001823

R-NT2RM4001828//HS\_3073\_A2\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=2 Row=L, genomic survey sequence.//1.6e-46:255:96//AQ121030

40 R-NT2RM4001836//Sus scrofa microsatellite S0398 sequence.//9.4e-06:141:69//U78024

R-NT2RM4001841//Salmo salar microsatellite Ssa65 DNA.//1.5e-06:175:65//AF019184

R-NT2RM4001842//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-07:332:61//AC005077

45 R-NT2RM4001856//Mus musculus clone OST16642, genomic survey sequence.//4.8e-30:235:85//AF046633

R-nnnnnnnnnnn//HS\_3244\_B1\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=19 Row=L, genomic survey sequence.//3.0e-40:263:89//AQ252798

R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//5.0e-119:592:97//Y17711

50 R-NT2RM4001876//Megastigmus wachtili dinucleotide microsatellite, clone MWA47CT.//0.13:134:64//AJ001069

R-NT2RM4001880

R-NT2RM4001905//HS\_2016\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=21 Row=P, genomic survey sequence.//0.0066:264:59//AQ226877

55 R-NT2RM4001922//HS\_2228\_B2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=14 Row=D, genomic survey sequence.//2.5e-35:205:96//AQ065498

R-NT2RM4001930//Homo sapiens chromosome 17, clone hRPC.34\_M\_24, complete sequence.//0.26:325:63//AC004562

R-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//2.9e-85:421:

98//AC005207

R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//6.2e-109:556:95//AF098162

R-NT2RM4001953//Homo sapiens DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING DRAFT SEQUENCE.//1.3e-08:175:70//Z83826

5 R-NT2RM4001965//CIT-HSP-385N14.TR CIT-HSP Homo sapiens genomic clone 385N14, genomic survey sequence.//5.7e-69:532:81//B55044

R-nnnnnnnnnnn//R.norvegicus mRNA for IP63 protein.//1.9e-61:352:83//X99330

R-NT2RM4001979//Homo sapiens full-length insert cDNA clone ZD29F04.//1.1e-98:465:100//AF086241

10 R-NT2RM4001984//Borrelia burgdorferi (section 47 of 70) of the complete genome.//0.14:461:60//AE001161

R-NT2RM4001987

R-NT2RM4002013

R-NT2RM4002018

R-NT2RM4002034//Homo sapiens chromosome 5, BAC clone 24p24 (LBNL H195), complete sequence.//3.6e-42:277:89//AC005353

15 R-NT2RM4002044//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.83:476:57//AC006204

R-NT2RM4002054

R-NT2RM4002062//Human microsomal epoxide hydrolase gene, exons 5 and 6.//0.11:136:67//U06659

20 R-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//2.9e-99:503:96//U82267

R-nnnnnnnnnnn//Homo sapiens CAGH45 mRNA, complete cds.//9.6e-41:554:68//U80742

R-NT2RM4002067//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329A5, WORKING DRAFT SEQUENCE.//7.7e-64:476:81//Z97832

R-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//1.1e-33:238:85//AF072758

25 R-NT2RM4002075//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0031:403:57//AC005504

R-NT2RM4002093//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//9.4e-07:322:62//AC000383

30 R-nnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.6e-44:432:74//D12646

R-NT2RM4002128//Human HepG2 partial cDNA, clone hmd21e2m5.//2.0e-26:186:90//D17000

R-NT2RM4002140

R-NT2RM4002145//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-15:193:76//AF086247

R-NT2RM4002146//Human ABL gene, intron 1b, partial sequence.//0.66:170:63//U07562

35 R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds.//4.5e-110:560:96//AF084535

R-NT2RM4002174//Homo sapiens chromosome 17, clone hRPK 74\_E\_22, complete sequence.//8.0e-43:302:85//AC005696

R-NT2RM4002189

R-NT2RM4002194//Human Cosmid g5129g129 from 7q31.3, complete sequence.//0.29:382:60//AC003960

40 R-NT2RM4002205//Spiroplasma virus (SpV1-R8A2 B) complete genome.//3.5e-05:432:56//X51344

R-NT2RM4002213

R-NT2RM4002226//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.94:198:61//AC004448

R-NT2RM4002251

45 R-NT2RM4002256//Homo sapiens PAC clone DJ0570D02 from 7p13-p14, complete sequence.//2.3e-58:299:85//AC004837

R-NT2RM4002266//H.sapiens CpG island DNA genomic MseI fragment, clone 179f11, forward read cpg179f11.ft1a.//0.72:97:69//Z57487

50 R-NT2RM4002278//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//7.5e-49:405:84//AC005069

R-NT2RM4002281//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//1.7e-13:168:77//AL033531

R-NT2RM4002287

55 R-NT2RM4002294//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.98:208:65//AC004676

R-NT2RM4002301//HS\_2028\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2028 Col=19 Row=I, genomic survey sequence.//0.94:321:57//AQ233262

R-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudo-

- gene similar to GPISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//1.9e-35:265.84//AL032822
- R-nnnnnnnnnnn/ Human mRNA for KIAA0319 gene, complete cds.//2.4e-42:569.68//AB002317
- 5 R-NT2RM4002344//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:391:59//AC004709
- R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//8.6e-121:593:97//AB014549
- R-NT2RM4002374//Human DNA sequence from cosmid U131B10, between markers DXS366 and DXS87 on chromosome X contains XK membrane transport protein, ESTs and STS.//3.8e-44:258.86//Z73417
- 10 R-NT2RM4002383//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//0.0084:345.60//AC005316
- R-NT2RM4002390
- R-NT2RM4002409//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411
- 15 R-NT2RM4002438
- R-NT2RM4002446//Human DNA sequence from clone 360A4 on chromosome 16. Contains ESTs, complete sequence.//2.8e-103:533:95//AL031008
- R-NT2RM4002452
- R-NT2RM4002457//Homo sapiens chromosome 16, cosmid clone 321D4 (LANL), complete sequence.//0.99:171:64//AC004034
- 20 R-NT2RM4002460//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//0.96:94:71//Z92545
- R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.9e-102:508:97//AF083255
- 25 R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//7.0e-31:172:98//AB014591
- R-NT2RM4002493//CIT-HSP-2296C24.TF CIT-HSP Homo sapiens genomic clone 2296C24, genomic survey sequence.//0.46:182:62//AQ006882
- R-NT2RM4002499//Human v-fos transformation effector protein (Fte-1), mRNA complete cds.//7.3e-24:134:99//M84711
- 30 R-NT2RM4002504//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 geneexons 1,2, and 3, complete sequence.//3.9e-11:334:63//AC002368
- R-nnnnnnnnnnn
- R-NT2RM4002532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//3.4e-17:171:79//Z97985
- 35 R-NT2RM4002534
- R-NT2RM4002567//Homo sapiens chromosome 7 clone UWGC:g1564a040 from 7p14-15, complete sequence.//2.2e-26:181:76//AC005271
- R-NT2RM4002571
- 40 R-NT2RM4002593//CIT-HSP-2303L15.TF CIT-HSP Homo sapiens genomic clone 2303L15, genomic survey sequence.//0.034:73:82//AQ015579
- R-NT2RM4002623//Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence.//0.0014:670:55//AC005862
- R-NT2RP2000001//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.00087:251:59//AE001422
- 45 R-NT2RP2000006//Human DNA sequence from PAC 155D22 on chromosome 6q27. Contains EST, STSs and a GSS.//2.7e-37:259:86//Z97205
- R-NT2RP2000008//RPCI11-41G16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41G16, genomic survey sequence.//4.1e-25:365:70//AQ029090
- R-NT2RP2000027//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//6.0e-05:307:62//AC004098
- 50 R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//8.4e-41:223:96//AB018290
- R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//5.8e-63:325:96//AF061749
- R-NT2RP2000054//Human tyrosinase gene, 5'-flanking region (containing enhancer element responsible for pigment cell-specific transcription).//0.88:210:60//D26163
- 55 R-NT2RP2000056//Mus musculus epsilon tyrosine phosphatase cytoplasmic isoform (Ptpre) mRNA, complete cds.//4.7e-38:377:78//U36758
- R-NT2RP2000067//Rat mRNA for growth potentiating factor, complete cds.//6.0e-10:137:79//D42148

- R-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//3.1e-76:381:98//AC005754
- R-NT2RP2000076//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.3e-06:380:60//AE001372
- 5 R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//3.5e-77:379:97++F050079
- R-NT2RP2000079//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//6.5e-32:314:78//AL034549
- 10 R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//5.6e-74:378:96//AB018338
- R-NT2RP2000091//Homo sapiens clone RG015P03, complete sequence.//9.3e-21:226:76//AC005048
- R-NT2RP2000097//Human DNA sequence from cosmid U209G1 on chromosome X.//9.2e-40:278:81//Z68873
- R-NT2RP2000098//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.34:132:65//AC004015
- R-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//3.1e-09:259:67//AC003973
- 15 R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//1.8e-74:386:95//AB018356
- R-NT2RP2000120//CITBI-E1-2503M8.TR CITBI-E1 Homo sapiens genomic clone 2503M8, genomic survey sequence.//5.1e-05:87:77//AQ263909
- R-nnnnnnnnnnn
- 20 R-nnnnnnnnnnn/Homo sapiens PAC clone DJ04L15 from Xq23, complete sequence.//4.9e-11:153:69//AC004827
- R-NT2RP2000147
- R-NT2RP2000153//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.0058:261:57//U95626
- R-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-119:603:96//AC005924
- 25 R-NT2RP2000161//CIT-HSP-2045P7.TR CIT-HSP Homo sapiens genomic clone 2045P7, genomic survey sequence.//0.89:173:63//B79728
- R-NT2RP2000175
- R-NT2RP2000183
- 30 R-NT2RP2000195//Homo sapiens chromosome 17, clone hRPC.60\_A\_24, complete sequence.//4.3e-39:306:83//AC005325
- R-NT2RP2000205//Human DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155
- R-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//7.3e-55:306:94//AC004382
- 35 R-NT2RP2000232
- R-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//17.6e-13:144:75//U88401
- R-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//9.6e-63:410:86//AC004066
- 40 R-NT2RP2000248//Caenorhabditis elegans cosmid T01C8.//1.0:282:58//U58726
- R-NT2RP2000257//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.5e-11:163:72//AC004894
- R-NT2RP2000258//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.58:442:58//AC004077
- 45 R-NT2RP2000270//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//1.1e-39:292:84//AL009179
- 50 R-NT2RP2000274//CIT-HSP-237901.TR CIT-HSP Homo sapiens genomic clone 237901, genomic survey sequence.//6.9e-10:121:81//AQ109409
- R-NT2RP2000288
- R-NT2RP2000289
- R-NT2RP2000297//Homo sapiens full-length insert cDNA clone ZB81C03.//7.7e-109:519:99//AF086165
- 55 R-NT2RP2000298
- R-NT2RP2000310//Homo sapiens p53 induced protein mRNA, partial cds.//1.5e-38:224:93//AF010310
- R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE

pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//4.3e-113:580:96//AL022398

R-NT2RP2000329//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.4e-47:367:77//AC006039

R-NT2RP2000337//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//4.9e-08:494:58//L04272

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//3.4e-46:262:94//U83981

R-NT2RP2000369//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.0e-07:334:61//AC002993

R-NT2RP2000414//Mouse DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone BAC394, WORKING DRAFT SEQUENCE.//7.0e-08:98:83//AJ004828

R-NT2RP2000420//Homo sapiens chromosome 17, clone hRPK.640\_1\_15, complete sequence.//0.99:150:62//AC005324

R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//4.6e-19:142:90//AF102265

R-NT2RP2000438//RPC111-62113.TK RPC111 Homo sapiens genomic clone R-62113, genomic survey sequence.//3.1e-06:103:79//AQ199572

R-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//2.0e-22:276:73//AC004691

R-NT2RP2000459//CIT-HSP-2013N9.TR CIT-HSP Homo sapiens genomic clone 2013N9, genomic survey sequence.//5.5e-27:205:87//853940

R-NT2RP2000498//Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence.//6.0e-12:119:84//AC001234

R-NT2RP2000503//Human CYP11B2 gene for steroid 18-hydroxylase (P-450 C18), 5'-flanking region and exon 1.//0.48-201:64//D10170

R-NT2RP2000510//Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence.//3.6e-07:472:59//AF033929

R-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//2.3e-61:317:97//AL022318

R-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.6e-29:167:97//AB005543

R-NT2RP2000617  
R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//2.5e-64:335:96//AB014514

R-NT2RP2000644//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.8e-28:383:70//Z92545

R-NT2RP2000656//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.0093:110:70//AL021997

R-NT2RP2000658//Bacillus thuringiensis chitinase (chi) gene, complete cds.//0.73:301:60//U89796

R-NT2RP2000668  
R-NT2RP2000678//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 8/15, WORKING DRAFT SEQUENCE.//2.8e-11:256:66//AP000015

R-NT2RP2000710//Genomic sequence from Human 17, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.036:176:69//AC002346

R-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//2.7e-110:555:96//AC004540

R-NT2RP2000731//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//2.6e-18:319:68//AL023775

R-NT2RP2000758//CIT-HSP-507A14.TP CIT-HSP Homo sapiens genomic clone 507A14, genomic survey sequence.//1.0:189:60//B50590

R-NT2RP2000764  
R-NT2RP2000809//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-24:215:81//AC004002

R-NT2RP2000812//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey se-

quence.//9.5e-32:176:97//B99575

R-nnnnnnnnnnnn//paramecium species 5,87 mt dna dimer: replication init. region.//0.0077:418.57//K00916

R-NT2RP2000816//F.rubripes GSS sequence, clone 011H02aA6, genomic survey sequence.//0.61:52:73//AL011013

R-NT2RP2000819

R-NT2RP2000841//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 43408, WORKING DRAFT SEQUENCE.//0.00012:181:70//AL033504

R-NT2RP2000842//Mus musculus (C57BL/10 X C3H)F2 clone 4.9 novel mRNA from reninexpressing kidney tumor cell line, partial sequence.//3.7e-27:388:72//U13370

R-NT2RP2000845//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//0.0022:200:68//AC005703

R-NT2RP2000863

R-NT2RP2000880//Homo sapiens mRNA for putative GTP-binding protein, partial.//2.3e-43:279:89//AJ006412

R-NT2RP2000892//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7//10.//0.0028:221:62//AB020875

R-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//2.2e-55:290:96//AB018266

R-NT2RP2000938//Homo sapiens full-length insert cDNA clone ZD55G12.//2.1e-37:215:93//AF086336

R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//3.0e-96:494:96//AB018298

R-NT2RP2000965

R-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//4.5e-87:440:97//AL021393

R-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//5.4e-93:484:95//AC005277

R-NT2RP2000987//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.1e-06:318:62//AE001372

R-NT2RP2001036//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410i8, WORKING DRAFT SEQUENCE.//2.0e-24:273:73//AL031732

R-NT2RP2001044//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.3e-07:365:65//AC005140

R-NT2RP2001065//Caenorhabditis elegans cosmid F10G7.//9.2e-06:273:59//U40029

R-NT2RP2001070//CITBI-E1-2503F4.TF CITBI-E1 Homo sapiens genomic clone 2503F4, genomic survey sequence.//0.13:97:72//AQ265973

R-NT2RP2001094//Mycoplasma mycoides mycoides SC immunodominant protein P72 (p72) gene, complete cds, mannitol-1-phosphate dehydrogenase (mt1D) gene, partial cds and insertion sequence IS1296, complete sequence.//0.018:373:57//U61140

R-NT2RP2001119

R-NT2RP2001127//Homo sapiens HRIHFB2060 mRNA, partial cds.//4.5e-55:304:94//AB015348

R-NT2RP2001137//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase

Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-I, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//0.69:129:65//AL022394

R-NT2RP2001149//Sequence 5 from Patent US 4798885.//8.5e-28:322:77//01838

R-NT2RP2001168

R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//4.8e-95:490:96//AB 007949

R-NT2RP2001174//CIT-HSP-2170B18.TR CIT-HSP Homo sapiens genomic clone 2170B18, genomic survey sequence.//1.3e-33:204:93//B89680

R-NT2RP2001196//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-65, complete sequence.//1.7e-06:413:61//AL010134

R-NT2RP2001218//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//8.5e-15:278:68//AL022153

R-NT2RP2001226//Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SNRNP associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.//0.0020:462:57//AL030995

R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP Homo sapiens genomic clone 2356P23, genomic survey sequence.//8.0e-108:547:96//AQ081110

R-NT2RP2001245//Spodoptera frugiperda 16S rRNA gene, Val-tRNA, and Leu-tRNA genes, and ND-1 protein gene, 5' end.//0.0052:350:58//M76713



- R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//4.6e-111:544:97//AB018353  
 R-NT2RP2001277//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y59A8, WORKING DRAFT SEQUENCE.//0.0058:327:59//Z98870
- 5 R-NT2RP2001290//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:187:65//AC004709  
 R-NT2RP2001295//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//0.59:218:62//AC006041  
 R-NT2RP2001312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//0.12:117:64//AL033520
- 10 R-NT2RP2001327//Caenorhabditis elegans cosmid R04D3, complete sequence.//0.31:119:66//Z70212  
 R-NT2RP2001328//HS\_2213\_A1\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=13 Row=G, genomic survey sequence.//1.7e-22:200:83//AQ136874  
 R-NT2RP2001347//Plasmodium falciparum MAL3P8, complete sequence.//0.81:509:56//AL034560  
 R-NT2RP2001378//H.sapiens DNA sequence.//0.94:147:63//Z22404
- 15 R-NT2RP2001381//Homo sapiens cyclin E2 mRNA, complete cds.//3.2e-09:75:97//AF091433  
 R-NT2RP2001392//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//0.079:178:62//L19301  
 R-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//3.4e-60:351:90//Z93242
- 20 R-NT2RP2001397//Hamster mRNA for cyclinB2, complete cds.//5.4e-55:320:83//D17294  
 R-NT2RP2001420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108D11, WORKING DRAFT SEQUENCE.//1.0e-44:246:85//AL034419  
 R-NT2RP2001423//Human DNA sequence from clone 726F20 on chromosome 1p36 11-36.23. Contains ESTs and a GSS, complete sequence.//3.7e-05:417:61//AL031273 R-NT2RP2001427//Human Chromosome 11 Cosmid cSRL34e5, complete sequence.//0.94:287:59//U73643
- 25 R-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//5.2e-31:299:77//AF046702  
 R-NT2RP2001440//Rattus norvegicus mRNA for 14-3-3 protein gamma-subtype, complete cds.//7.8e-75:548:83//D17447  
 R-NT2RP2001445//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-06:452:59//AC004801
- 30 R-NT2RP2001449//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.1e-08:218:67//AC004846  
 R-NT2RP2001450  
 R-NT2RP2001467//Human BAC clone RG343P13 from 7q31, complete sequence.//3.8e-31:254:83//AC002465
- 35 R-NT2RP2001506//C. parvum p-47, nttn, bonT genes.//1.2e-06:415:60//Y12091  
 R-NT2RP2001511//Plasmodium falciparum MAL3P7, complete sequence.//0.11:155:63//AL034559  
 R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//2.1e-104:545:95//Y14494  
 R-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//7.0e-16:283:68//AC004596
- 40 R-NT2RP2001536//Human DNA from chromosome 14-specific cosmid containing XRCC3 DNA repair gene, genomic sequence, complete sequence.//7.7e-16:108:96//AF037222  
 R-NT2RP2001560//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//0.052:112:66//B73597  
 R-NT2RP2001569//CIT-HSP-2335F8.TF CIT-HSP Homo sapiens genomic clone 2335F8, genomic survey sequence.//6.0e-78:383:98//AQ042029
- 45 R-NT2RP2001576//Homo sapiens sulfonyleurea receptor (SUR2) gene, exon 37.//0.33:135:66//AF013222  
 R-NT2RP2001581//Homo sapiens (clone MFD220) PCR primer.//2.7e-07:240:63//L15407  
 R-NT2RP2001597//HS\_3016\_B2\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3016 Col=12 Row=L, genomic survey sequence.//5.3e-45:310:87//AQ118854
- 50 R-NT2RP2001601//Homo sapiens chromosome 17, clone hRPK.855\_D\_21, complete sequence.//0.015:445:58//AC006079  
 R-NT2RP2001613//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.5e-16:413:63//AF009326  
 R-NT2RP2001628//Phytomonas serpens kinetoplast maxicircle ribosomal protein S12 (G6) edited mRNA, complete cds.//0.11:190:63//AF034626
- 55 R-NT2RP2001663//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//3.0e-26:157:81//AC004125  
 R-NT2RP2001677//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.0e-58:305:96//

AC004472

R-NT2RP2001678//Human BAC clone RG222A16 from 7q31, complete sequence.//0.95:107.66//AC002385

R-NT2RP2001699//Mus musculus erythroid ankyrin and two alternatively spliced erythroid ankyrins (Ank1) gene, putative exon 41 and partial cds.//8.8e-05:211.63//U76758

5 R-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.7e-68:352.97//AC004079

R-NT2RP2001721//HS-1052-B1-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=11 Row=N, genomic survey sequence.//7.7e-05:346.59//B40914

10 R-NT2RP2001740//HS\_3213\_A2\_D02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//1.1e-16:162.82//AQ175104

R-NT2RP2001748//Human gene for L-histidine decarboxylase, complete cds.//2.0e-33:312.77//D16583

R-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//2.3e-100:435.97//AC004783

15 R-NT2RP2001813//Human leukocyte common antigen T200 (CD45, LCA) gene, exon 9.//0.031:261.60//M23468

R-NT2RP2001861

R-NT2RP2001869//Sequence 5 from patent US 5595900.//4.2e-21:194.77//134189

R-NT2RP2001876

20 R-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//5.0e-111:485.97//AL031864

R-NT2RP2001900

R-NT2RP2001907//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//5.4e-42:382.77//U07563

25 R-NT2RP2001926//HS\_3180\_B2\_F02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=L, genomic survey sequence.//2.8e-25:138.80//AQ185415

R-NT2RP2001936//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320.60//AC005504

R-NT2RP2001943//Dictyostellium discoideum PkgA (pkgA) gene, partial cds.//1.4e-08:378.59//AF020280

30 R-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.6e-85:409.100//AC005033

R-NT2RP2001947//Human mRNA for KIAA0390 gene, complete cds.//0.85:140.64//AB002388

R-NT2RP2001969

R-NT2RP2001976//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence.//2.0e-60:307.98//B99575

35 R-NT2RP2001985//Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAll project).//0.031:282.61//AL022140

R-NT2RP2002025

R-NT2RP2002032//CITBI-E1-2502C19.TF CITBI-E1 Homo sapiens genomic clone 2502C19, genomic survey sequence.//1.2e-52:285.95//AQ264715

40 R-NT2RP2002033//Human (lambda) DNA for immunoglobulin light chain.//1.1e-08:389.61//D68270

R-NT2RP2002041//Homo sapiens 12p13.3 BAC RPC111-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-49:264.97//AC006206

R-NT2RP2002046//Human BAC clone GS119P05 from 7q21, complete sequence.//0.0023:429.61//AC004011

45 R-NT2RP2002047//P.falciparum PK1 gene.//0.00015:239.62//X83707

R-NT2RP2002058//HS\_2183\_A1\_G01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=1 Row=M, genomic survey sequence.//1.2e-21:185.84//AQ022560

R-NT2RP2002066//G.gallus microsatellite DNA (LEI0222 (=T15ivD04)).//0.18:102.70//Z83792

50 R-NT2RP2002070//P.falciparum major merozoite surface antigen (PMMSA) mRNA, complete cds, isolate FC27.//0.95:192.61//M19143

R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//3.8e-25:182.86//AF052183

55 R-NT2RP2002079//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STSs, GSSs, and a putative CpG island, complete sequence.//1.7e-10:97.90//AL009178

R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//4.6e-59:376.89//AJ007509

R-NT2RP2002105

R-NT2RP2002124//RPC111-75J16.TJ RPC111 Homo sapiens genomic clone R-75J16, genomic survey sequence.//0.58:191.64//AQ266779

R-NT2RP2002137//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//0.0065:294.61//AC005913

R-NT2RP2002154

R-NT2RP2002172//RPC111-90C20.TJ RPC111 Homo sapiens genomic clone R-90C20, genomic survey sequence.//0.049:160:65//AQ282591

R-NT2RP2002185//CIT-HSP-2341115.TF CIT-HSP Homo sapiens genomic clone 2341115, genomic survey sequence.//6.0e-36:230.90//AQ053355

R-NT2RP2002192//HS\_2222\_B1\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=15 Row=L, genomic survey sequence.//1.9e-15:249:71//AQ178491

R-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//4.7e-35:438:73//AF032872

R-NT2RP2002208//Hansenua wingei mitochondrial DNA, complete sequence.//0.00057:468:57//D31785

R-NT2RP2002219//HS\_2058\_A1\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=E, genomic survey sequence.//3.4e-55:512:77//AQ234380

R-NT2RP2002231//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-31, complete sequence.//1.5e-06:398:61//Z98557

R-nnnnnnnnnnn//Sequence 11 from patent US 5624818.//3.3e-91:553:87//41141

R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//3.0e14:132:84//AF005418

R-NT2RP2002259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE.//1.6e-96:548:91//AL033527

R-NT2RP2002270//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.1e-06:391:60//AC004605

R-NT2RP2002292//Genomic sequence from Human 13, complete sequence.//0.91:159:64//AC001226

R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.3e-101:527:94//AF069532

R-NT2RP2002316//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//0.00052:389:59//AE001408

R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds.//2.3e-112:567:95//AF093666

R-NT2RP2002333//Rat POU domain factor (Bm-5) mRNA.//1.5e-22:323:73//L23204

R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//3.7e-102:600:89//AF038958

R-NT2RP2002394//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:399:59//AC005308

R-NT2RP2002408//HS\_2212\_A1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=17 Row=L, genomic survey sequence.//9.6e-35:231:88//AQ184632

R-NT2RP2002426//Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complete sequence.//2.8e-39:308:82//AL021877

R-NT2RP2002439//Leishmania tarentolae mitochondrial electron transport chain component mRNA.//0.022:102:71//M74225

R-NT2RP2002457//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.00099:354:59//Z98289

R-NT2RP2002464//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 6/15, WORKING DRAFT SEQUENCE.//0.0015:219:67//AP000013

R-NT2RP2002475

R-nnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//3.1e-113:605:92//AB005289

R-NT2RP2002498//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//0.32:210:64//Z98047

R-NT2RP2002503//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.0e-86:429:98//AC006213

R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//2.7e-105:583:91//AB018334

R-NT2RP2002520//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//0.14:406:58//AJ223323

R-NT2RP2002537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING DRAFT SEQUENCE.//2.8e-16:188:78//AL023583

R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA.//4.7e-108:571:93//AF009314  
 R-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//1.1e-103:422:95//AC005316  
 R-NT2RP2002591//Human DNA binding protein (HPF2) mRNA, complete cds.//1.8e-36:526:67//M27878  
 5 R-NT2RP2002595  
 R-NT2RP2002606//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING DRAFT SEQUENCE.//7.2e-10:211:71//AL033529  
 R-NT2RP2002609  
 R-NT2RP2002618//Plasmodium falciparum MAL3P6, complete sequence.//2.9e-05:566:60//Z98551  
 10 R-NT2RP2002621//Human DNA sequence from PAC 341110 on chromosome 6q22.2-22.33. Contains 60S ribosomal protein L5 like (pseudo)gene, ESTs and STSs.//1.1e-38:348:78//Z97352  
 R-NT2RP2002643//Homo sapiens chromosome 11 clone pTWB15.28 map 11p15.4-p15.5, genomic survey sequence.//1.2e-35:414:66//AF074030  
 R-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//1.3e-77:403:95//AC005384  
 15 R-NT2RP2002701  
 R-NT2RP2002706//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.0e-42:147:90//AC005778  
 R-NT2RP2002710//P.falciparum serine rich protein (SERP I) gene.//0.84:135:67//J03983  
 20 R-NT2RP2002721// complete sequence.//1.0:363:59//AC005815  
 R-NT2RP2002736//Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence.//0.44:267:60//AC004138  
 R-NT2RP2002740//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence.//0.0016:474:60//AC004674  
 25 R-NT2RP2002741//HS\_3051\_B1\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=21 Row=P, genomic survey sequence.//1.1e-38:217:86//AQ106283  
 R-NT2RP2002750//Homo sapiens 12q24.1 PAC RPC11-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.0e-36:430:75//AC002395  
 R-NT2RP2002752//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366L4, WORKING DRAFT SEQUENCE.//8.2e-41:437:76//AL023494  
 30 R-NT2RP2002753//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-100:496:97//AC004882  
 R-NT2RP2002769//paramedecium species 5,311 mt dna dimer: replication init. region.//7.4e-10:404:60//K00917  
 R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence.//1.2e-63:341:94//AF070537  
 35 R-NT2RP2002800//RPC11-37G8.TV RPC1-11 Homo sapiens genomic clone RPC1-11-37G8, genomic survey sequence.//4.9e-60:321:95//AQ029850  
 R-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.9e-100:492:98//AC006078  
 R-NT2RP2002857//HS\_3026\_B2\_H07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=14 Row=P, genomic survey sequence.//8.9e-06:242:62//AQ 128697  
 40 R-NT2RP2002862//RPC11-42115.TJ RPC111 Homo sapiens genomic clone R-42115, genomic survey sequence.//1.5e-44:270:85//AQ052700  
 R-NT2RP2002880//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.0:295:58//AL02318  
 45 R-NT2RP2002891  
 R-NT2RP2002925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 243L18, WORKING DRAFT SEQUENCE.//2.0e-24:395:67//AL034395  
 R-NT2RP2002928//Plasmodium falciparum MAL3P5, complete sequence.//0.044:461:55//AL034556  
 R-NT2RP2002929//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.35:491:56//AC005140  
 50 R-NT2RP2002954//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//1.0:275:61//AC005701  
 R-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//2.7e-61:508:79//U62483  
 55 R-NT2RP2002979//RPC11-20F13.TPK RPC1-11 Homo sapiens genomic clone RPC1-11-20F13, genomic survey sequence.//0.88:110:72//AC008132  
 R-NT2RP2002980//Homo sapiens PAC clone DJ0841B21 from 7q21.1-q31.1, complete sequence.//1.1e-102:433:95//AC004140

- R-NT2RP2002986//Human DNA sequence from clone 1147O16 on chromosome Xp21.1-21.3. Contains 13 exons of the DMD muscular dystrophy gene. Contains an STS and GSSs, complete sequence.//0.31:219:62//AL031542
- R-NT2RP2002987//Homo sapiens chromosome 18, clone hRPK\_24\_A\_23, complete sequence.//1.3e-51:283:88//AC005968
- 5 R-NT2RP2002993//Human DNA sequence from PAC 106B9 on chromosome Xq21://4.3e-11:430:63//AL021307
- R-NT2RP2003000//Saccharomyces cerevisiae mitochondrion transfer RNA- Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn genes.//0.00088:347:62//L36887
- R-NT2RP2003034//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 2//10://3.5e-33:271:82//AB020870
- 10 R-NT2RP2003073
- R-NT2RP2003099//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//1.5e-45:548:69//AC004914
- R-NT2RP2003108
- R-NT2RP2003117//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-51:323:88//AC005378
- 15 R-NT2RP2003121//HS\_2238\_A1\_E08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=15 Row=I, genomic survey sequence.//0.00055:324:61//AQ293058
- R-NT2RP2003125
- R-NT2RP2003129
- R-NT2RP2003137//Human BAC clone RG084D04 from 7q31, complete sequence.//1.1e-46:521:74//AC003084
- 20 R-NT2RP2003161//Homo sapiens chromosome 10 clone CIT-HSP-1287C20, complete sequence.//1.0:368:59//AC005879
- R-NT2RP2003164//Dictyostelium discoideum actin 4 gene, 3' UTR.//1.0:120:64//M25581
- R-NT2RP2003165//Homo sapiens chromosome 17, clone hRPK\_1018\_N\_14, complete sequence.//2.2e-71:467:86//AC005823
- 25 R-NT2RP2003177
- R-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING DRAFT SEQUENCE.//1.1e-95:585:88//AL031597
- R-NT2RP2003206//P.falciparum interspersed repeat antigen (FIRA) gene.//0.039:338:60//M17877
- R-NT2RP2003230//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-11:542:60//Z98551
- 30 R-NT2RP2003237//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence.//1.0:311:60//AB016888
- R-NT2RP2003243//CIT-HSP-2368D12.TR CIT-HSP Homo sapiens genomic clone 2368D12, genomic survey sequence.//0.39:112:66//AQ077738
- R-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//1.3e-38:273:83//L38481
- 35 R-NT2RP2003272//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//4.4e-15:181:66//AC004187
- R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//4.2e-110:565:95//AB014525
- R-NT2RP2003280//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.2e-12:221:70//AC005831
- 40 R-NT2RP2003286//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//0.86:379:60//AC005261
- R-NT2RP2003293//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0e-39:418:74//AC005079
- 45 R-NT2RP2003295//HS\_2053\_B1\_A10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=19 Row=B, genomic survey sequence.//0.0016:346:61//AQ235251
- R-NT2RP2003297//Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence.//0.74:397:56//AC002332
- R-NT2RP2003308//Homo sapiens PAC clone DJ1098B01 from 7q11.23-q21, complete sequence.//0.99:447:60//AC004960
- 50 R-NT2RP2003329//C.reinhardtii psbB 5' flanking region.//0.79:161:59//X59731
- R-NT2RP2003339//RPCI11-Homo sapiens genomic clone R-57H15, genomic survey sequence.//0.13:184:64//AQ116039
- R-NT2RP2003347//RPCI11-15B19.TV RPCI-11 Homo sapiens genomic clone RPCI-11-15B19, genomic survey sequence.//6.4e-31:218:89//B76357
- 55 R-NT2RP2003367//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//9.0e-11:101:84//U91321
- R-NT2RP2003391//HS\_2255\_B2\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

nomic clone Plate=2255 Col=8 Row=D, genomic survey sequence.//1.6e-38:247:90//AQ068937  
 R-NT2RP2003393//RPC11-44AK6.TJ RPC11 Homo sapiens genomic clone R-44K6, genomic survey sequence.//  
 3.9e-31:290:79//AQ0202481  
 R-NT2RP2003394//Yeast mitochondrial *oxi3* gene exon 1 for cytochrome c oxidase subunit I.//5.1e-14:579:61//  
 5 X14910  
 R-NT2RP2003401//Caprine arthritis-encephalitis virus tat protein (tat) and envelope glycoprotein (env) gene, partial  
 cds.//0.32:174:66//U81429  
 R-NT2RP2003433//Ascidian mRNA for HRSec61, complete cds.//1.5e-10:193:69//D25536  
 R-NT2RP2003445//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING  
 10 DRAFT SEQUENCE.//4.4e-99:585:89//AL023808  
 R-NT2RP2003446  
 R-NT2RP2003456//Plasmodium falciparum MAL3P7, complete sequence.//0.98:399:57//AL034559  
 R-NT2RP2003480//Homo sapiens full-length insert cDNA clone ZE09A11.//4.7e-111:540:98//AF086540  
 R-NT2RP2003499  
 15 R-NT2RP2003506  
 R-NT2RP2003511  
 R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//4.1e-107:566:93//D87460  
 R-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//1.5e-60:  
 518:79//M12783  
 R-NT2RP2003522//HS\_2182\_A1\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 20 nomic clone Plate=2182 Col=9 Row=G, genomic survey sequence.//0.053:251:60//AQ024304  
 R-NT2RP2003533//Homo sapiens chromosome 12p13.3 clone RPC14-816N1, WORKING DRAFT SEQUENCE,  
 31 unordered pieces.//1.5e-37:328:80//AC005841  
 R-NT2RP2003543//HS\_3028\_A2\_C12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 25 nomic clone Plate=3028 Col=24 Row=E, genomic survey sequence.//2.0e-39:203:100//AQ094957  
 R-NT2RP2003559//Homo sapiens full-length insert cDNA clone ZD65E09.//2.3e-59:325:95//AF088055  
 R-NT2RP2003564  
 R-NT2RP2003581  
 R-NT2RP2003596//HS\_2163\_B1\_D11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 30 nomic clone Plate=2163 Col=21 Row=H, genomic survey sequence.//0.0011:212:67//AQ125143  
 R-NT2RP2003604//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//5.4e-102:501:97//U97067  
 R-NT2RP2003629//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING  
 DRAFT SEQUENCE, 9 unordered pieces.//0.0012:363:61//AC005507  
 R-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//5.1e-37:561:68//  
 35 AJ006215  
 R-NT2RP2003668//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chro-  
 mosome X contains ESTs.//0.0053:395:58//Z76735  
 R-NT2RP2003687//Human BAC clone RG22A16 from 7q31, complete sequence.//8.0e-10:205:67//AC002385  
 R-NT2RP2003691//HS\_3252\_A2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 40 nomic clone Plate=3252 Col=22 Row=A, genomic survey sequence.//5.3e-05:332:60//AQ219783  
 R-NT2RP2003702//CIT-HSP-2333P5.TF CIT-HSP Homo sapiens genomic clone 2333P5, genomic survey se-  
 quence.//3.9e-43:431:75//AQ035000  
 R-NT2RP2003704  
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-45:265:93//AB011097  
 45 R-NT2RP2003713//Human DNA sequence from PAC 411B6 on chromosome X \*.//0.64:169:67//Z84470  
 R-NT2RP2003714//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.//  
 4.6e-11:152:73//Z95704  
 R-nnnnnnnnnnnn//H.sapiens mRNA for PIBF1 protein, complete.//0.94:443:59//Y09631  
 R-NT2RP2003737//Homo sapiens clone DJ102214, WORKING DRAFT SEQUENCE, 14 unordered pieces.//  
 50 2.2e-109:547:96//AC004951  
 R-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//4.1e-  
 109:545:97//AC004626  
 R-NT2RP2003760//B. taurus mRNA for gamma-COP.//6.3e-28:400:69//X70019  
 R-NT2RP2003764//Mouse preprosomatostatin gene.//0.90:285:62//X51468  
 55 R-NT2RP2003769//Schizosaccharomyces pombe gene for protein involved in sexual development, complete  
 cds.//0.96:446:58//D87956  
 R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds.//1.8e-104:531:96//AF047437  
 R-NT2RP2003777

- R-NT2RP2003781//HS\_3109\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=7 Row=D, genomic survey sequence.//1.3e-60:346:92//AQ186749  
R-NT2RP2003793  
R-NT2RP2003840
- 5 R-NT2RP2003857//HS\_2205\_A2\_H12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=24 Row=O, genomic survey sequence.//8.1e-22:127:99//AQ151299  
R-NT2RP2003859//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-37G8, genomic survey sequence.//8.3e-60:320:95//AQ029850
- 10 R-NT2RP2003871//HS\_3210\_A1\_C08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3210 Col=15 Row=E, genomic survey sequence.//8.6e-09:322:61//AQ175028  
R-NT2RP2003885//RPCI11-7M10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-7M10, genomic survey sequence.//4.7e-67:380:92//B72214  
R-NT2RP2003912//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//1.2e-33:379:75//AL023693
- 15 R-NT2RP2003952  
R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.3e-114:568:97//AB014458  
R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//1.1e-107:540:97//AB007916  
R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//7.7e-114:568:96//AB018347
- 20 R-NT2RP2003984  
R-NT2RP2003986//Human Chromosome 11 pacPDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.6e-99:551:92//AC000382  
R-NT2RP2003988  
R-NT2RP2004014
- 25 R-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//4.9e-114:568:97//AC004780  
R-NT2RP2004042//nbxb0020F03r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020F03r, genomic survey sequence.//0.1:195:64//AQ258389  
R-nnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//7.6e-110:564:95//AL034555
- 30 R-NT2RP2004081//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.012:503:57//AC005308  
R-NT2RP2004098//H.sapiens CpG island DNA genomic MseI fragment, clone 133h3, reverse read cpg133h3.rt1a.//7.9e-25:140:100//Z64530
- 35 R-NT2RP2004124  
R-NT2RP2004142//CIT-HSP-2316F21.TR CIT-HSP Homo sapiens genomic clone 2316F21, genomic survey sequence.//2.8e-83:409:98//AQ034964  
R-NT2RP2004152//HS\_3065\_A2\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776
- 40 R-NT2RP2004165//Anthodiaris crassispina mRNA for dynein beta-heavy chain, complete cds.//3.4e-20:343:65//D01021  
R-NT2RP2004170//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-89:587:86//AC004064  
R-NT2RP2004172//Dicyostellum discoideum LTR-retrotransposon Skipper, partial genomic sequence, 3' end.//0.24:440:60//AF017047
- 45 R-NT2RP2004187//RPCI11-59E12.TK RPCI11 Homo sapiens genomic clone R-59E12, genomic survey sequence.//3.1e-05:175:66//AQ198120  
R-NT2RP2004194  
R-NT2RP2004196//Fugu rubripes GSS sequence, clone 076D01bE2, genomic survey sequence.//1.6e-22:178:71//AL026601
- 50 R-NT2RP2004207//Homo sapiens BAC clone GS421103 from Xq25-q26, complete sequence.//0.19:175:64//AC005023  
R-NT2RP2004226//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//6.1e-17:445:64//AL023808  
R-NT2RP2004232//M.musculus (Balb/c) mRNA for serine/threonine protein kinase.//3.2e-25:326:71//Z34524
- 55 R-NT2RP2004239//Homo sapiens kb mRNA for protein kinase, complete cds.//8.7e-108:563:94//AB015718  
R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds.//1.1e-101:530:93//AF039687

R-NT2RP2004242

R-NT2RP2004245//Homo sapiens DNA sequence from PAC 455H14 on chromosome Xq21.3-22.3. Contains genomic marker DXS1203 with a CA repeat polymorphism, STSs and GSSs, complete sequence.//5.1e-08:236:65//AL023280

R-NT2RP2004270//Lycopersicon esculentum Idh2 gene.//0.98:259:61//Y10603

R-NT2RP2004300//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1068F16, WORKING DRAFT SEQUENCE.//5.0e-14:396:65//AL023913

R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//1.5e-108:544:96//AF000416

R-NT2RP2004321//Caenorhabditis elegans cosmid F47B8, complete sequence.//0.0078:333:61//Z77662

R-NT2RP2004339//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.4e-75:306:86//AC005229

R-NT2RP2004347//RPC111-90N11.TJ RPC111 Homo sapiens genomic clone R-90N11, genomic survey sequence.//2.9e-87:494:92//AQ284548

R-NT2RP2004364//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//4.2e-10:161:76//AL031010

R-NT2RP2004365//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//3.6e-08:483:57//AE001433

R-NT2RP2004366//F.rubripes GSS sequence, clone 013B16aF3, genomic survey sequence.//2.1e-05:128:67//AL000528

R-NT2RP2004373//Homo sapiens 12q24.2 BAC RPC111-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.81:205:62//AC006065

R-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//3.9e-06:82:84//AQ063969

R-NT2RP2004392//Ceratomyces douglasii mitochondrial cytochrome oxidase I (3' end), cytochrome oxidase II (complete cds) and transfer RNA-Leu gene.//2.7e-06:495:58//L39993

R-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//6.4e-111:572:96//AC005164

R-NT2RP2004399//Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence.//0.13:253:64//AC006085

R-NT2RP2004400//HS\_3238\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=22 Row=O, genomic survey sequence.//5.1e-23:162:89//AQ211412

R-NT2RP2004412//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit 1 (COX1) gene, complete cds.//2.6e-09:458:60//M97514

R-NT2RP2004425//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//0.99:481:56//AL022718

R-NT2RP2004476//Rattus norvegicus activity and neurotransmitter-induced early gene 6 (ania-6) mRNA, 3'UTR.//5.3e-99:600:90//AF030091

R-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//3.9e-115:575:97//AC005591

R-NT2RP2004512//Plasmodium falciparum MAL3P3, complete sequence.//0.00034:517:58//Z98547

R-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//1.8e-115:571:97//AC004890

R-NT2RP2004538//Homo sapiens BAC clone RG318C11 from 7p14-p15, complete sequence.//1.7e-47:322:87//AC005091

R-NT2RP2004551//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//0.035:511:58//AC005184

R-NT2RP2004568//TTC20-Sp6 TAMU Arabidopsis thaliana genomic clone T7C20, genomic survey sequence.//0.70:446:54//B08766

R-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 136B1, WORKING DRAFT SEQUENCE.//2.2e-53:397:74//AL031768

R-NT2RP2004587//CIT-HSP-2376P22.TF CIT-HSP Homo sapiens genomic clone 2376P22, genomic survey sequence.//0.0079:223:63//AQ108976

R-NT2RP2004594//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.3e-10:493:62//AC004605

R-NT2RP2004600//Homo sapiens full-length insert cDNA clone ZE04E06.//2.1e-70:343:99//AF086522

R-NT2RP2004602//Homo sapiens full-length insert cDNA clone YW26E09.//2.0e-96:528:93//AF086033



- R-NT2RP2004614  
 R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//7.3e-117:587.96//AJ006291  
 R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.5e-105:520:96//AB007929  
 R-NT2RP2004675//Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds.//3.4e-22:197:79//U63721
- 5 R-NT2RP2004681//Rat notch 2 mRNA.//8.0e-30:276:78//M93661  
 R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.6e-118:600:96//AB014525  
 R-NT2RP2004709//Homo sapiens full-length insert cDNA clone ZD42A08.//3.5e-14:139:86//AF086259  
 R-NT2RP2004710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//6.9e-117:592:96//AL031447
- 10 R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//4.2e-117:594:96//AB007947  
 R-NT2RP2004743//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.53:403:59//AC005505  
 R-NT2RP2004767//Human DNA sequence from PAC 491M17 on chromosome 1p36.2-1p36.3.//2.0e-81:568.84//Z97988
- 15 R-NT2RP2004775//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//4.0e-08:365.62//L04272
- 20 R-NT2RP2004791//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//7.8e-111:541:98//AC005216  
 R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//2.5e-114:564:96//AF058953  
 R-NT2RP2004802
- 25 R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.7e-118:584:97//AF054179  
 R-NT2RP2004841//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//4.0e-46:447:72//AC002089  
 R-NT2RP2004861//Plasmodium falciparum MAL3P5, complete sequence.//0.19:189:66//AL034556  
 R-NT2RP2004897//Human Chromosome X clone bWDX187, complete sequence.//1.1e-08:330:61//AC004383
- 30 R-NT2RP2004936//CIT-HSP-2374L4.TF CIT-HSP Homo sapiens genomic clone 2374L4, genomic survey sequence.//0.99:129:65//AQ110571  
 R-nnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.014:402:61//Z98551  
 R-NT2RP2004961//RPC111-45P2.TK RPC111 Homo sapiens genomic clone R-45P2, genomic survey sequence.//9.3e-90:453:97//AQ02282
- 35 R-NT2RP2004962//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y40H4, WORKING DRAFT SEQUENCE.//0.017:291.61//AL022573  
 R-NT2RP2004967//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.6e-52:496:77//AC005077  
 R-NT2RP2004978//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//0.088:322:63//AC005614
- 40 R-NT2RP2004982//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.025:339:61//AC003071  
 R-NT2RP2004985//T31H24TF TAMU Arabidopsis thaliana genomic clone T31H24, genomic survey sequence.//0.40:111:70//B78148
- 45 R-NT2RP2004999//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//0.23:157:68//AC005682  
 R-NT2RP2005000  
 R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//3.0e-111:577:95//AB014515  
 R-NT2RP2005003//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//2.4e-21:246:77//AC004673
- 50 R-nnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//9.5e-115:568:97//AF100141  
 R-NT2RP2005018//HS\_3108\_B1\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=17 Row=J, genomic survey sequence.//1.9e-31:222:89//AQ104050  
 R-NT2RP2005020//Rattus norvegicus cationic amino acid transporter-1 (CAT-1) mRNA, complete cds.//6.6e-41:566:73//U70476
- 55 R-NT2RP2005031//CIT-HSP-516A2.TV CIT-HSP Homo sapiens genomic clone 516A2, genomic survey sequence.//4.1e-31:357:75//B49897  
 R-NT2RP2005037

R-NT2RP2005038//Sequence 5 from patent US 5552281.//2.e-32:178.98//U25644  
 R-NT2RP2005108//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.7e-23:475.67//AF009326  
 R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//8.4e-104:518.97//AB014564  
 5 R-NT2RP2005126//H. sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//1.4e-67:464.85//X98743  
 R-NT2RP2005139  
 R-NT2RP2005140//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//7.9e-08:460.60//U00101  
 10 R-NT2RP2005144//Homo sapiens chromosome 12p13.3 clone RPC11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//2.5e-103:519.96//AC005911  
 R-NT2RP2005147//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.068:100.75//AC004971  
 15 R-NT2RP2005159//CITBI-E1-2506A8.TF CITBI-E1 Homo sapiens genomic clone 2506A8, genomic survey sequence.//0.90:113.71//AQ262104  
 R-NT2RP2005162//Homo sapiens chromosome 17, clone HCIT307A16, complete sequence.//5.0e-14:183.75//AC003041  
 R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.5e-100:513.95//AJ007509  
 R-NT2RP2005204  
 20 R-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//7.2e-119:583.97//AC005189  
 R-NT2RP2005239//Homo sapiens mRNA for putative tRNA splicing protein, partial.//8.4e-62:312.98//AJ010952  
 R-NT2RP2005254//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//5.7e-09:328.62//Z99297  
 25 R-NT2RP2005270//Plasmodium falciparum MAL3P8, complete sequence.//2.3e-05:355.61//AL034560  
 R-NT2RP2005276//Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence.//0.0014:541.58//AC000107  
 30 R-NT2RP2005287//Cavia porcellus zinc finger protein (zfc1) mRNA, complete cds.//4.4e-69:459.86//L26335  
 R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.4e-124:594.98//AF060219  
 R-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//1.5e-110:545.96//AJ007590  
 R-NT2RP2005293//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//1.1e-12:554.61//U00101  
 35 R-NT2RP2005315//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//9.5e-15:218.77//AL022069  
 R-NT2RP2005325//Rattus norvegicus LIM homeodomain protein (LH-2) mRNA sequence.//2.0e-72:478.88//L06804  
 40 R-NT2RP2005336//\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.3e-33:139.82//U14567  
 R-NT2RP2005344//Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS.//0.094:451.60//297629  
 R-NT2RP2005354//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-11:89.96//AJ010841  
 45 R-NT2RP2005360//Homo sapiens clone RG023115, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.046:266.60//AC005049  
 R-NT2RP2005393//Homo sapiens chromosome 17, clone hRPK\_85\_B\_7, complete sequence.//6.0e-41:226.86//AC005695  
 R-NT2RP2005407  
 R-NT2RP2005436//Polistes annularis (clone pan117AAT) tandem repeat region.//0.039:169.63//L10835  
 50 R-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//3.0e-38:263.88//AQ055548  
 R-NT2RP2005453//CIT-HSP-2367N1.TR CIT-HSP Homo sapiens genomic clone 2367N1, genomic survey sequence.//0.67:409.59//AQ079845  
 R-NT2RP2005457//Homo sapiens partial XPGC gene, exon 2.//2.0e-42:315.82//X71342  
 55 R-NT2RP2005464//CIT-HSP-2359C16.TF CIT-HSP Homo sapiens genomic clone 2359C16, genomic survey sequence.//1.0:251.60//AQ075816  
 R-NT2RP2005465//Drosophila melanogaster, chromosome 2R, region 44D1-44D2, P1 clone DS08616, complete sequence.//01251288.62//AC005457

R-NT2RP2005472//Chlorarachnion CCMP621 small subunit ribosomal RNA, 5.8S ribosomal RNA, large subunit ribosomal RNA, U6 small nuclear RNA, small subunit ribosomal protein S13 (RPS13), pre-mRNA splicing factor PRP 6 homolog, small subunit ribosomal protein 4 (RPS4), small nucleolar ribonucleoprotein E homolog (snRNPE), ATP-dependent clp protease proteolytic subunit homolog (CLPP), putative RNA polymerase II subunit (RNA POLII), and RNA helicase homolog (RNAHEL) genes, complete cds.//1.0:356:59//U58510

5 R-NT2RP2005476//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.00092:421:60//AL031746

R-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.2e-71:187:100//AC006030

10 R-NT2RP2005491//paramedium species 5,311 mt dna dimer: replication init. region.//1.6e-10:403:62//K00917

R-NT2RP2005495//Homo sapiens clone RG037F03, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.3e-25:208:82//AC005051

R-NT2RP2005496//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//1.5e-22:196:84//AL022722

15 R-NT2RP2005498

R-NT2RP2005501//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//7e-29:252:76//AC005828

20 R-NT2RP2005509//CIT-HSP-2060J6.TR CIT-HSP Homo sapiens genomic clone 2060J6, genomic survey sequence.//3.1e-53:402:84//B69979

R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//9.9e-109:570:94//AF092563

25 R-NT2RP2005525//Human clone JkA2 mRNA induced upon T-cell activation, 3' end.//5.1e-32:175:98//U38432

R-NT2RP2005531//Homo sapiens PAC clone DJ0870F17 from Tq33-q36, complete sequence.//0.94:288:61//AC004911

R-NT2RP2005539//Homo sapiens mRNA for NSI-binding protein (NSI-BP).//2.7e-106:560:94//AJ012449

R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.3e-114:583:96//AB007963

30 R-NT2RP2005549//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*. WORKING DRAFT SEQUENCE.//0.91:287:58//AJ011929

R-NT2RP2005555//Homo sapiens 12p13.3 PAC RPCIS-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.6e-05:222:66//AC004804

R-NT2RP2005557//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//8.2e-22:236:76//AC004996

35 R-NT2RP2005581//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.2e-45:286:85//AC006146

R-NT2RP2005600//Human polymorphic microsatellite DNA.//0.043:304:58//M99148

40 R-NT2RP2005605//Human Cosmid g1572c190, complete sequence.//2.4e-17:163:77//AC000126

R-NT2RP2005620

R-NT2RP2005622//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7, genomic survey sequence.//0.010:308:58//B13538

R-NT2RP2005637//Homo sapiens PAC clone DJ0555L14 from 7q34-q36, complete sequence.//2.5e-26:322:72//AC005996

45 R-NT2RP2005640//Mus musculus squamous cell carcinoma antigen 2 (Scca2) gene, complete cds.//0.030:370:60//AF063937

R-NT2RP2005645//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.2e-08:355:62//AE001398

R-NT2RP2005651

50 R-NT2RP2005654//Leishmania major Friedlin cosmid L5769, complete sequence.//0.96:216:66//AL031908

R-NT2RP2005669//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//6.7e-117:594:95//AF069984

R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//1.8e-89:434:98//AF089814

55 R-NT2RP2005683//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7, genomic survey sequence.//0.037:283:58//B13538

R-NT2RP2005690//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:295:83//AC005478

- R-NT2RP2005694//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-106, complete sequence.//0.0026:414:57//AL010210
- R-NT2RP2005701
- 5 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//4.1e-104:503:98//AB018342
- R-NT2RP2005719//Caenorhabditis elegans cosmid LLC1, complete sequence.//0.83:275:61//Z82277
- R-NT2RP2005722//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.2e-21:199:75//AL031985
- R-NT2RP2005723
- 10 R-NT2RP2005726//Homo sapiens clone DJ0609N19, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-64:503:82//AC004842
- R-NT2RP2005741//Human Chromosome 11 pacBpJ393015, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.5e-09:261:64//AC000384
- R-NT2RP2005748//RPC11-64K11.TK RPC11 Homo sapiens genomic clone R-64K11, genomic survey sequence.//0.00039.215.66//AQ239313
- 15 R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//1.3e-40:223:96//AF068868
- R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//3.7e-103:494:98//AF082516
- R-NT2RP2005763//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//9.7e-34:172:86//AL022098
- 20 R-NT2RP2005767//Human clone H3 mRNA.//2.5e-21:179:87//U03672
- R-NT2RP2005773//HS\_2168\_B1\_G12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=N, genomic survey sequence.//0.99:212:63//AQ086414
- R-NT2RP2005775//Rabbit mRNA for endopeptidase, complete cds.//4.8e-98:591:88//D13310
- 25 R-NT2RP2005781//Streptomyces sp. genomic DNA for sarcosine oxidase.//0.019:384:59//D10623
- R-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.8e-102:490:99//AL034423
- R-NT2RP2005804//Homo sapiens chromosome 17, clone hRPK.147\_L\_13, complete sequence.//6.3e-16:481:63//AC005332
- 30 R-NT2RP2005812//Caenorhabditis elegans cosmid F15810.//0.81:147:63//AF036696
- R-NT2RP2005815
- R-NT2RP2005835
- R-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//1.5e-26:512:64//Z68873
- R-NT2RP2005853//Human DNA sequence from clone 1156N12 on chromosome X. Contains an STS and GSSs, complete sequence.//3.7e-16:340:64//AL009047
- 35 R-NT2RP2005857//Human DNA sequence from cosmid U246D9 on chromosome X. Contains a histone H2B like pseudogene.//1.3e-09:331:65//AL021308
- R-NT2RP2005859//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-83, complete sequence.//0.0097:363:59//AL010152
- 40 R-NT2RP2005868//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-18, complete sequence.//1.1e-07:508:60//AL008971
- R-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-31:500:67//AL11316
- R-NT2RP2005901//Homo sapiens T-cell receptor alpha delta locus from bases 752679 to 1000555 (section 4 of 5) of the Complete Nucleotide Sequence.//0.89:276:60//AE000661
- 45 R-NT2RP2005908
- R-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//1.2e-40:285:80//U63840
- R-NT2RP2005942//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.0011:480:58//Z99289
- 50 R-NT2RP2005980//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//8.9e-21:136:78//AC004616
- R-NT2RP2006023//HS\_2176\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=19 Row=F, genomic survey sequence.//2.5e-66:369:95//AQ023148
- 55 R-NT2RP2006038//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.00029:408:58//AE001369
- R-NT2RP2006043//Polistes annularis (clone pan117AAT) tandem repeat region.//0.032:195:62//L10835
- R-NT2RP2006052//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING

DRAFT SEQUENCE, 14 unordered pieces.//0.11:263:61//AC005140

R-NT2RP2006069

R-NT2RP2006071//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00044:333:61//AC004709

R-NT2RP2006098//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-77, complete sequence.//4.1e-09:393:62//AL010151

R-NT2RP2006100//HS\_2020\_A2\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2020 Col=4 Row=O, genomic survey sequence.//8.3e-53:304:92//AQ228761

R-NT2RP2006103//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds.//1.5e-16:199:79//M85300

R-NT2RP2006141

R-NT2RP2006166//Human Chromosome 16 BAC clone CIT987SK-A-589H1, complete sequence.//8.2e-48:329:76//AC002045

R-NT2RP2006184//RPC111-6016.TP RPC1-11 Homo sapiens genomic clone RPC1-11-6016, genomic survey sequence.//0.52:273:61//B49539

R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//1.9e-108:553:95//AB014554

R-NT2RP2006196//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-57, complete sequence.//4.2e-05:420:59//AL008981

R-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPC1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//2.1e-100:409:96//AC006057

R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//3.8e-93:532:90//X96484

R-NT2RP2006237//P.falciparum PK1 gene.//2.9e-08:481:59//X83707

R-NT2RP2006238//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//3.5e-79:405:89//U91318

R-NT2RP2006258//Human PAC clone DJ0899B21 from 7p15-p21, complete sequence.//2.2e-08:283:63//AC004008

R-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.2e-13:234:68//X97630

R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.0e-108:542:97//AF035262

R-NT2RP2006320//347J16.TVB CIT978SKA1 Homo sapiens genomic clone A-347J16, genomic survey sequence.//1.2e-27:215:65//B17768

R-NT2RP2006321//Human karyopherin beta 3 mRNA, complete cds.//1.7e-48:298:90//U2761

R-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//2.8e-104:524:96//AL033531

R-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.9e-33:298:78//AC004893

R-NT2RP2006334

R-NT2RP2006365//RPC111-72115.TK RPC111 Homo sapiens genomic clone R-72115, genomic survey sequence.//2.6e-35:217:92//AQ267043

R-NT2RP2006393//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B13E4; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//8.0e-40:317:81//AC004046

R-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//3.2e-42:184:86//AL022345

R-NT2RP2006441//Plasmodium falciparum microsatellite TA80 sequence.//0.00021:188:68//AF010568

R-NT2RP2006454//Plasmodium falciparum chromosome 2, section 60 of 73 of the complete sequence.//0.30:265:60//AE001423

R-NT2RP2006456//Homo sapiens clone 23566 mRNA sequence.//2.5e-104:532:96//AF052098

R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//6.6e-108:524:97//AJ006266

R-NT2RP2006467//Sequence 50 from patent US 5691147.//8.3e-22:235:74//I76222

R-NT2RP2006472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1172A22, WORKING DRAFT SEQUENCE.//5.4e-12:407:62//AL034386

R-NT2RP2006534//Dictyostellium discoideum actin 8 gene, 3' UTR.//0.44:111:65//M25216

R-NT2RP2006554//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//0.19:392:58//AE001370

R-NT2RP2006565//Sus scrofa SCAMP 1 gene, exon 9.//1.5e-13:292:68//AJ223742

R-NT2RP2006571//Homo sapiens chromosome 19, cosmid F17972, complete sequence.//0.0024:409:58//AC004660

R-nnnnnnnnnnnn//Human BRCA2 region, mRNA sequence CG005.//3.3e-16:334:64//U050532

R-NT2RP2006598//Mus musculus retinoid X receptor interacting protein (RIP110) mRNA, partial cds.//1.6e-19:

448:64//U22015

R-NT2RP3000002//Human DNA sequence from cosmid N104C7 on chromosome 22, complete sequence.//4.4e-14:501:63//Z82246

R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.9e-115:560:97//AJ011972

R-NT2RP3000046//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//3.9e-57:402:83//AC005995

R-NT2RP3000047//Homo sapiens chromosome 17, clone hRPK.138\_P\_22, complete sequence.//1.0:158:66//AC005697

R-NT2RP3000050//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE.//2.7e-32:411:69//AL033522

R-NT2RP3000055//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1000N6, WORKING DRAFT SEQUENCE.//7.9e-17:309:69//AL034378

R-NT2RP3000072//Brassica rapa DNA for S-locus glycoprotein, complete cds.//2.9e-07:516:60//D88192

R-NT2RP3000080//Homo sapiens clone DJ1129D05, complete sequence.//1.7e-27:186:90//AC005630

R-NT2RP3000085//Arabidopsis thaliana acetyl-CoA carboxylase biotin-containing subunit mRNA, nuclear gene encoding chloroplast protein, complete cds.//0.0051:289:59//U-23155

R-NT2RP3000109//HS\_3065\_A2\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776

R-NT2RP3000134//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.027:414:57//AL031746

R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//3.8e-115:578:96//AB011164

R-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//1.3e-67:354:95//AC005746

R-NT2RP3000186

R-NT2RP3000197//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat.//2.5e-31:295:78//Z82899

R-NT2RP3000207//Homo sapiens chromosome 16 BAC clone CIT987SK-A-954B10, complete sequence.//0.016:305:61//AC004514

R-NT2RP3000220//RPCI11-63O7.TJ RPC111 Homo sapiens genomic clone R-63O7, genomic survey sequence.//0.25:118:66//AQ201832

R-NT2RP3000233//Plasmodium falciparum mRNA for major merozoite surface antigen gp195.//3.2e-11:440:59//X15063

R-NT2RP3000235//Mus musculus chromosome 6 clone TB6 subclone TB6pD1//0.81:114:64//U19530

R-NT2RP3000247//Homo sapiens DNA sequence from clone 326L12 on chromosome Xq27.1 27.3. Contains the cancer/testis antigen CT7 (melanoma-associated antigen MAGE-C1) gene, two MAGE family pseudogenes, STSs and a CA repeat polymorphism, complete sequence.//4.8e-73:362:86//AL023279

R-NT2RP3000251//Homo sapiens chromosome 17, clone hRPK.192\_H\_23, complete sequence.//0.025:131:66//AC005726

R-NT2RP3000252

R-NT2RP3000255//HS-1025-B2-F08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=16 Row=L, genomic survey sequence.//0.67:119:66//B34879

R-NT2RP3000267

R-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.//1.2e-23:424:69//D29766

R-NT2RP3000312//Plasmodium falciparum MAL3P4, complete sequence.//0.55:414:59//AL008970

R-NT2RP3000320//HS\_3056\_A1\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=5 Row=E, genomic survey sequence.//4.1e-32:214:89//AQ134064

R-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//1.5e-22:265:75//U78090

R-NT2RP3000333//Plasmodium falciparum MAL3P6, complete sequence.//0.68:460:57//Z98551

R-NT2RP3000341//H.sapiens mRNA for TIM17 preprotein translocase.//1.4e-19:137:90//X97544

R-NT2RP3000348//CITBI-E1-2513C11.TF CITBI-E1 Homo sapiens genomic clone 2513C11, genomic survey sequence.//0.0014:118:72//AQ278177

R-NT2RP3000350

R-NT2RP3000359//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.8e-55:320:75//AC006039

R-NT2RP3000361//Homo sapiens mRNA for KIAA0552 protein, complete cds.//0.18:275:61//AB011124

- R-NT2RP3000366//CIT-HSP-2317H13.TF CIT-HSP Homo sapiens genomic clone 2317H13, genomic survey sequence.//6.7e-42:214:100//AQ041634
- R-NT2RP3000397//HS-1012-B1-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 787 Col=1 Row=L, genomic survey sequence//0.015:184:63//B31814
- 5 R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.3e-109:529:98//AF071185
- R-NT2RP3000418//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510B21, WORKING DRAFT SEQUENCE.//6.2e-15:445:65//AL031885
- R-NT2RP3000433
- R-NT2RP3000439
- 10 R-NT2RP3000441
- R-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.6e-43:300:76//AL031650 R-NT2RP3000451//3'untranslated region of human mRNA for a K<sup>+</sup> channel protein.//0.71:101:66//E13519
- 15 R-NT2RP3000456//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//5.2e-16:376:65//AF011889
- R-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING DRAFT SEQUENCE.//0.61:326:58//AL031847
- 20 R-NT2RP3000487//Sequence 32 from patent US 5476781.//8.6e-08:409:61//16692
- R-NT2RP3000512//RPC111-60F15.TK RPC111 Homo sapiens genomic clone R-60F15, genomic survey sequence.//2.2e-68:379:93//AQ201516
- R-NT2RP3000526//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 377F16, WORKING DRAFT SEQUENCE.//4.1e-07:224:65//Z93783
- 25 R-NT2RP3000527//HS\_3228\_A1\_H07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=13 Row=O, genomic survey sequence.//4.5e-30:184:93//AQ209131
- R-NT2RP3000531//T6M24-Sp6 TAMU Arabidopsis thaliana genomic clone T6M24, genomic survey sequence.//0.67:88:68//AQ248538
- R-NT2RP3000542//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126B4, WORKING DRAFT SEQUENCE.//2.0e-24:145:82//AL022316
- 30 R-NT2RP3000561//Homo sapiens PAC clone DJ094216 from 7q11, complete sequence.//6.1e-107:548:95//AC006012
- R-NT2RP3000562//HS\_2041\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=15 Row=J, genomic survey sequence.//9.6e-55:279:98//AQ230207
- 35 R-NT2RP3000578//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-105, complete sequence.//0.0060:356:58//AL010212
- R-NT2RP3000582//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-29:282:67//AC004666
- R-NT2RP3000584//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//7.4e-44:245:78//AC002377
- 40 R-NT2RP3000590//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.66:341:59//AC004077
- R-NT2RP3000592//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.022:491:56//AC005505
- 45 R-ntnnnnnnnn//HS\_3025\_A1\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.//2.6e-21:161:88//AQ101452
- R-NT2RP3000599//Plasmodium falciparum MAL3P8, complete sequence.//1.3e-09:543:58//AL034560
- R-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//5.6e-115:55:98//AC006128
- 50 R-NT2RP3000622//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 27 unordered pieces.//0.15:233:63//AC005414
- R-NT2RP3000624//CIT-HSP-2022D4.TR CIT-HSP Homo sapiens genomic clone 2022D4, genomic survey sequence.//1.0:166:66//B64262
- R-NT2RP3000628//Human BAC clone GS188P18, complete sequence.//5.3e-56:384:83//AC000115
- 55 R-NT2RP3000632//Human cyclin-selective ubiquitin carrier protein mRNA, complete cds.//4.0e-61:438:85//U73379
- R-NT2RP3000644//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLf, GCDH, CRTc, and RAD23A genes, genomic sequence.//1.0e-43:408:77//AD000092
- R-NT2RP3000661//F.nubripes GSS sequence, clone 148D22bB9, genomic survey sequence.//2.7e-17:234:69//

AL005927

R-NT2RP3000665//Human chromosome 11 46b2 cosmid, complete sequence.//2.1e-42:526:72//U73645

R-NT2RP3000685//HS\_3007\_A2\_F02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=4 Row=K, genomic survey sequence.//1.6e-101:506:97//AQ118425

R-NT2RP3000690//Plasmodium falciparum MAL3P6, complete sequence.//1.3e-13:411:61//Z98551

R-NT2RP3000736

R-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//0.0071:231:65//U16655

R-NT2RP3000753//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.88:366:56//AL021368

R-NT2RP3000759//HS\_2055\_A2\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=18 Row=G, genomic survey sequence.//0.45:251:60//AQ234828

R-NT2RP3000815//Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complete sequence.//2.0e-20:293:72//AC005822

R-NT2RP3000825//Plasmodium falciparum MAL3P6, complete sequence.//0.0044:325:62//Z98551

R-NT2RP3000826//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117715, WORKING DRAFT SEQUENCE.//5.3e-25:375:72//AL022315

R-NT2RP3000836//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//1.3e-19:181:81//AL022344

R-NT2RP3000841//Homo sapiens, clone hRPK.1\_A\_1, complete sequence.//0.20:226:61//AC006196

R-NT2RP3000845//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//6.8e-91:512:92//AC005781

R-NT2RP3000847//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//7.9e-38:179:86//U14572

R-NT2RP3000850//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//4.4e-48:505:76//AC005014

R-NT2RP3000852//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-82:311:98//AL031297

R-NT2RP3000859

R-NT2RP3000865//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//1.2e-15:482:63//AL022153

R-NT2RP3000868//Fruittfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00045:260:59//AB003097

R-NT2RP3000869//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//0.0058:172:64//AL031731

R-NT2RP3000875//H.sapiens/Hepatitis B virus fusion mRNA for mevalonate kinase.//1.4e-99:531:93//X75311

R-NT2RP3000901

R-NT2RP3000904//Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence.//0.32:261:57//AC000348

R-NT2RP3000917//Plasmodium falciparum MAL3P7, complete sequence.//0.00092:456:58//AL034559

R-NT2RP3000919

R-NT2RP3000968//H.sapiens mRNA for ribosomal protein S15a.//4.5e-24:375:71//X84407

R-NT2RP3000980//Homo sapiens chromosome 17, clone hRPK.855\_D\_21, complete sequence.//0.36:186:62//AC006079

R-NT2RP3000994//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.00052:413:60//AC005140

R-NT2RP3001004//Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence.//1.1e-07:330:64//U32857

R-NT2RP3001007//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-82, complete sequence.//0.045:286:61//AL010255

R-NT2RP3001055//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.3e-56:348:91//Z95125

R-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//8.2e-84:531:86//X78927

R-NT2RP3001081//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//1.1e-08:537:60//AL031746

R-NT2RP3001084

R-NT2RP3001096

R-NT2RP3001107



R-nnnnnnnnnnn/ Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//7.4e-62:272:73//AC005316

R-NT2RP3001111

R-NT2RP3001113

5 R-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//7.2e-112:550:97//AC005189

R-NT2RP3001116//CIT-HSP-2282K23.TR CIT-HSP Homo sapiens genomic clone 2282K23, genomic survey sequence.//0.000.13.160:69//AQ002011

10 R-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//5.9e-99:497:96//AL031864

R-NT2RP3001120

R-NT2RP3001126//Plasmodium falciparum MAL3P7, complete sequence.//0.035:266:56//AL034559

R-NT2RP3001133

15 R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//8.1e-114:549:97//AB018305

R-NT2RP3001147//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.69:198:63//AC004448

R-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.4e-108:542:97//AL034379

20 R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//2.9e-116:563:98//AJ006266

R-NT2RP3001176//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.44:227:62//AC004688

R-NT2RP3001214//Borrelia burgdorferi plasmid lp25, complete plasmid sequence.//0.0023:381:61//AE000785

25 R-NT2RP3001216//RPC11-18C15.TPC RPC1-11 Homo sapiens genomic clone RPC1-11-18C15, genomic survey sequence.//7.0e-29:167:97//B88077

R-NT2RP3001221//Homo sapiens clone 14503, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.020:211:63//AC005827

30 R-NT2RP3001232//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.7e-08:390:62//AL021326

R-NT2RP3001236//RPC11-25C17.TKBR RPC1-11 Homo sapiens genomic clone RPC1-11-25C17, genomic survey sequence.//9.5e-41:217:88//AQ014003

R-NT2RP3001239//Human microtubule-associated protein 1B (MAP1B) gene, complete cds.//2.9e-21:438:63//L06237

35 R-NT2RP3001245//Homo sapiens DNA sequence from PAC 964D12 on chromosome 1q24-q25. Contains EST, GSS.//0.00026:439:59//AL021398

R-NT2RP3001253//HS\_3002\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=24 Row=O, genomic survey sequence.//0.98:190:63//AQ251982

R-NT2RP3001260

40 R-NT2RP3001268//Homo sapiens clone DJ0959C21, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.012:509:57//AC004936

R-NT2RP3001272//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//2.2e-22:134:87//AC005589

R-NT2RP3001274//Sequence 11 from Patent WO9517522.//0.0058:133:66//A45341

45 R-NT2RP3001281//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//4.4e-55:558:76//Z96811

R-NT2RP3001307//HS\_2058\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=11 Row=E, genomic survey sequence.//7.2e-33:260:86//AQ305868

50 R-NT2RP3001318//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.27:210:65//AC004848

R-NT2RP3001325

R-NT2RP3001338//Rat tropoelastin gene, intron 17 (partial).//1.0:184:64//M86367

R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds.//1.2e-112:566:96//AB007920

55 R-NT2RP30%1340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//3.2e-86:450:95//AF083105

R-NT2RP3001355

R-NT2RP3001374//HS\_2184\_A2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2184 Col=8 Row=M, genomic survey sequence.//3.7e-10:101:84//AQ024647

R-NT2RP3001383//Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence.//7.4e-07:

- 279:63//AE001397  
R-NT2RP3001384//Homo sapiens chromosome 19, cosmid R33907, complete sequence.//4.4e-75:382:97//AC005785
- 5 R-NT2RP3001392//HS\_3078\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=10 Row=H, genomic survey sequence.//1.0:164:64//AQ140587  
R-NT2RP3001396//RPC11-63N18.TJ RPC11 Homo sapiens genomic clone R-63N18, genomic survey sequence.//0.14:242:61//AQ238544  
R-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.8e-10:193:72//UJ49046  
R-NT2RP3001399
- 10 R-NT2RP3001407//Caenorhabditis elegans cosmid D1046, complete sequence.//0.0011:392:60//Z68160  
R-NT2RP3001420//Human BAC clone GS165I04 from 7q21, complete sequence.//3.7e-29:412:74//AC002379  
R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence.//1.1e-104:550:94//AF052158  
R-NT2RP3001427//Caenorhabditis elegans cosmid K11D5.//0.39:174:64//U53152  
R-nnnnnnnnnnnnn//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//1.4e-94:533:91//U69668
- 15 R-NT2RP3001432//Homo sapiens DNA sequence from PAC 164C20 on chromosome 6q16.1-22.1. Contains ESTs and GSSs (BAC end sequences), complete sequence.//2.5e-12:415:61//AL009029  
R-NT2RP3001447//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.6e-36:358:77//AC004903
- 20 R-NT2RP3001449//Homo sapiens clone 24497 mRNA sequence.//1.5e-100:499:97//AF070630  
R-NT2RP3001453//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-47:295:86//AC004906  
R-NT2RP3001457  
R-NT2RP3001459
- 25 R-NT2RP3001472//Crithidia fasciculata kinetoplast apocytochrome b gRNA-mRNA chimera, clone:24.//0.33:150:66//D13030  
R-NT2RP3001490//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-103, complete sequence.//2.3e-08:483:60//AL010208  
R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//4.4e-60:338:93//U13395
- 30 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRCB (TRCB) mRNA, complete cds.//2.1e-110:549:97//AF064801  
R-NT2RP3001527//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//5.3e-32:310:78//AL034549  
R-NT2RP3001529//Human Chromosome X, complete sequence.//5.5e-67:280:93//AC002420
- 35 R-NT2RP3001538  
R-NT2RP3001554//Human microtubule-associated protein 1a (MAP1A) mRNA, complete cds.//7.8e-16:391:62//U38292  
R-NT2RP3001580//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00026:456:58//AC004688
- 40 R-NT2RP3001587//Homo sapiens HRIHFB2115 mRNA, partial cds.//5.6e-08:86:88//AB015337  
R-NT2RP3001589//Homo sapiens chromosome 17, clone hRPK.1096\_G\_20, complete sequence.//0.066:360:60//AC005410  
R-NT2RP3001607//CIT-HSP-2010M8.TR CIT-HSP Homo sapiens genomic clone 2010M8, genomic survey sequence.//0.041:194:67//B53490
- 45 R-NT2RP3001608//Human DNA sequence from PAC 296K21 on chromosome X contains cytochrome c, delta-aminolevulinic acid synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//0.69:151:64//Z83821  
R-NT2RP3001621//Human DNA sequence from clone 24018 on chromosome 6p21:31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.4e-46:354:83//AL021808
- 50 R-NT2RP3001629//H.sapiens simple DNA sequence region clone wg1a10.//0.99:137:63//X76572  
R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds.//8.5e-108:541:96//AF099149  
R-NT2RP3001642
- 55 R-NT2RP3001646//HS\_3218\_A2\_A01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=2 Row=A, genomic survey sequence.//2.6e-32:215:91//AQ303003  
R-NT2RP3001671//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-88, complete sequence.//0.018:262:61//AL010157  
R-NT2RP3001672

- R-NT2RP3001676//Homo sapiens cosmid Q95D4, chromosome 21 5' of IFNAR2.//2.1e-48:413:77//AF039905  
 R-NT2RP3001678//RPC11-50C17.TK RPC11 Homo sapiens genomic clone R-50C17, genomic survey sequence.//0.15:232:62//AQ116359
- 5 R-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//7.8e-104:549:95//AB020860  
 R-NT2RP3001688//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//6.6e-41:291:86//AC006019  
 R-NT2RP3001690//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//3.1e-07:433:59//AE001415
- 10 R-NT2RP3001708//Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence.//6.0e-06:237:64//AF053523  
 R-NT2RP3001712//CITBI-E1-2516N9.TF CITBI-E1 Homo sapiens genomic clone 2516N9, genomic survey sequence.//1.5e-95:456:99//AQ279562  
 R-NT2RP3001716//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//0.0012:346:58//AC004617
- 15 R-NT2RP3001724//Human HepG2 3' region Mbol cDNA, clone hmd6a06m3.//1.3e-27:163:95//D17273  
 R-NT2RP3001730//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING DRAFT SEQUENCE.//7.6e-43:409:76//Z98200  
 R-NT2RP3001739
- 20 R-NT2RP3001752//Human clone 23774 mRNA sequence.//1.9e-08:104:84//U97279  
 R-NT2RP3001753//CIT-HSP-2379P21.TF CIT-HSP Homo sapiens genomic clone 2379P21, genomic survey sequence.//8.8e-06:102:78//AQ113378  
 R-NT2RP3001764  
 R-NT2RP3001777//Human mRNA for heparan sulfate proteoglycan (glypican).//0.99:166:66//X54232
- 25 R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//1.3e-111:549:97//AB007928  
 R-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.6e-32:266:83//U13262  
 R-NT2RP3001799//H.sapiens mRNA for OX40 homologue.//8.5e-44:374:79//X75962  
 R-NT2RP3001819
- 30 R-NT2RP3001844//Caenorhabditis elegans cosmid C54G7.//0.0042:231:63//U04010  
 R-NT2RP3001854//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//1.0:404:59//AF030694  
 R-NT2RP3001855
- 35 R-NT2RP3001896//CIT978SK-A-686F10.TV CIT978SK Homo sapiens genomic clone A-636F10, genomic survey sequence.//0.0012:68:82//AQ116409  
 R-NT2RP3001898//Homo sapiens Chromosome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene, complete sequence.//0.37:266:65//AC005950  
 R-NT2RP3001915//Human BAC clone RG367O17 from 7p15-p21, complete sequence.//0.018:144:66//AC002486
- 40 R-NT2RP3001926//Human polyadenylate binding protein (TIA-1) mRNA, complete cds.//2.4e-10:77:100//M77142  
 R-NT2RP3001929  
 R-NT2RP3001931//Homo sapiens full-length insert cDNA clone YU73B11.//1.0e-110:562:96//AF087969  
 R-NT2RP3001938//Human DNA sequence from PAC 447B16 on chromosome Xq13.1-Xq13.3.//0.38:386:56//Z95328
- 45 R-NT2RP3001943//Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.//0.87:298:61//AC004500  
 R-NT2RP3001944//Bos taurus clone CSSM056 satellite DNA sequence.//0.0095:76:78//U03836  
 R-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//7.0e-109:552:96//AC005844
- 50 R-NT2RP3001989//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.15:111:68//Z81029  
 R-NT2RP3002002//Plasmodium falciparum 14-3-3 protein gene, partial cds.//0.016:286:60//AF065987  
 R-NT2RP3002004//H.sapiens mRNA for FAST kinase.//5.1e-41:335:82//X86776  
 R-NT2RP3002007
- 55 R-NT2RP3002014//Human DNA sequence from clone 228A9 on chromosome 22q12.3-13.32 Contains 85 KDA CALCIUM-INDEPENDENT PHOSPHOLIPASE A2, EST, GSS, CpG island, complete sequence.//6.6e-41:297:86//AL022322  
 R-NT2RP3002033  
 R-NT2RP3002045//Drosophila melanogaster fat protein (fat) gene, complete cds.//0.77:320:60//M80537

- R-NT2RP3002054//Caenorhabditis elegans cosmid Y69H2, complete sequence.//0.82:362:57//Z98877  
 R-NT2RP3002056//F.ubripes GSS sequence, clone 020E22B7, genomic survey sequence.//0.010:185:63//Z87006  
 R-NT2RP3002057  
 5 R-NT2RP3002062//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-17:164:81//AC004002  
 R-nnnnnnnnnnn  
 R-NT2RP3002081//HS\_3082\_A1\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=17 Row=M, genomic survey sequence.//4.2e-25:344:73//AQ122260  
 10 R-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//2.6e-23:212:80//AC006210  
 R-NT2RP3002102//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//0.43:168:64//AC004746  
 R-NT2RP3002108//CIT-HSP-2346P16.TF CIT-HSP Homo sapiens genomic clone 2346P16, genomic survey sequence.//3.5e-08:110:78//AQ059071  
 15 R-NT2RP3002146//Streptococcus gordonii competence factor (comC) and histidine protein kinase (comD) genes, complete cds, and response regulator (comE) gene, partial cds.//0.11:534:55//U80077  
 R-NT2RP3002147//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329F2, WORKING DRAFT SEQUENCE.//4.1e-108:551:96//AL031710  
 R-NT2RP3002151//Mus musculus mRNA for Guanine Nucleotide Regulatory Protein, complete cds.//6.8e-62:347:80//AB003503  
 20 R-NT2RP3002163//Anolis pulchellus vitellogenin mRNA, partial cds.//0.77:281:63//U46857  
 R-NT2RP3002165  
 R-NT2RP3002166//D.sargus satellite DNA (clone PSE3).//0.81:124:62//Z48711  
 R-NT2RP3002173  
 25 R-NT2RP3002181//HS-1042-A2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 824 Col=2 Row=K, genomic survey sequence.//1.3e-35:305:81//B36980  
 R-NT2RP3002244//Caenorhabditis elegans cosmid R11E3.//0.0024:393:61//AF100669  
 R-NT2RP3002248//Human DNA sequence from PAC 170A21 on chromosome 22q12-qter contains ESTs.//0.30:217:63//Z82189  
 30 R-NT2RP3002255  
 R-NT2RP3002273//Homo sapiens BAC clone 393122 from 8q21, complete sequence.//0.84:463:57//AF070717  
 R-NT2RP3002276//HS\_2260\_A1\_MF\_E07 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2260 Col=13 Row=I, genomic survey sequence.//0.0017:198:63//AQ292491  
 R-NT2RP3002303//Human HMG-17 gene for non-histone chromosomal protein HMG-17.//7.4e-93:510:93//X13546  
 35 R-NT2RP3002304//Human BAC clone GS188P18, complete sequence.//6.3e-09:477:59//AC000115  
 R-NT2RP3002330//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.087:388:58//AC004688  
 R-NT2RP3002343  
 40 R-NT2RP3002351//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//0.20:489:56//AC004617  
 R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene.//2.4e-104:516:94//Y15164  
 R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//4.7e-102:524:95//AB014578  
 R-NT2RP3002484  
 R-NT2RP3002501//Human DNA sequence from PAC 92M18, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 25, 26 and 27 ESTs and STS.//5.2e-17:232:75//Z73359  
 45 R-NT2RP3002512  
 R-NT2RP3002529//CIT-HSP-2340H2.TR CIT-HSP Homo sapiens genomic clone 2340H2, genomic survey sequence.//0.81:266:58//AQ057387  
 R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//3.3e-82:438:94//AB018272  
 50 R-NT2RP3002549//Medicago truncatula ENBP1 gene, exons 1 to 12.//0.95:381:56//AJ002479  
 R-NT2RP3002566//HS\_2036\_A1\_D08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=15 Row=G, genomic survey sequence.//0.18:162:64//AQ230627  
 R-NT2RP3002587//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-15:213:73//AC004956  
 55 R-NT2RP3002590//Arabidopsis thaliana genomic DNA; chromosome 5, P1 clone: MXK3, complete sequence.//0.00010:431:59//AB019236  
 R-NT2RP3002602//Mus musculus stannin gene, complete cds.//1.6e-20:339:70//AF030522  
 R-NT2RP3002603

R-NT2RP3002631//Homo sapiens chromosome 21 PAC  
 RCP1P704A9190Q2//1.0.24:59//AJ006997

R-NT2RP3002659//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds.//6.8e-24:  
 331:76//M85300

5 R-NT2RP3002660//H.sapiens partial gene for progesterone receptor and Alu element DNA.//9.8e-43:273:82//  
 Z49816

R-NT2RP3002663//Lymnaea stagnalis 16S ribosomal RNA gene, mitochondrial gene encoding ribosomal RNA,  
 partial sequence.//0.60:300:59//U82072

R-NT2RP3002671//S.pombe chromosome III cosmid c553.//1.2e-20:399:66//AL023704

10 R-NT2RP3002682//RPCI11-44K6.TJ RPCI11 Homo sapiens genomic clone R-44K6, genomic survey sequence.//  
 4.7e-09:122:77//AQ202481

R-NT2RP3002687//P.falciparum complete gene map of plastid-like DNA ((R-B)).//1.1e-07:494:59//X95276

R-NT2RP3002688//Human 7SL RNA sequence.//2.7e-32:290:79//X01037

R-NT2RP3002701

15 R-NT2RP3002713//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING  
 DRAFT SEQUENCE.//0.95:334:59//AL031427

R-NT2RP3002763//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//3.9e-40:288:85//U14567

R-NT2RP3002770//R.prowazekii genomic DNA fragment (clone A615F).//0.21:174:63//Z82710

R-NT2RP3002785//Homo sapiens PAC clone DJ0170D19 from Xq23, complete sequence.//0.78:354:59//  
 AC004822

20 R-NT2RP3002799//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flank-  
 ing repeat regions.//1.1e-20:161:77//AF003528

R-NT2RP3002810//Caenorhabditis elegans cosmid F10D2.//0.28:441:56//AF022972

R-NT2RP3002818//HS\_3053\_A2\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3053 Col=16 Row=A, genomic survey sequence.//0.19:220:60//AQ135025

25 R-NT2RP3002861//P.falciparum complete gene map of plastid-like DNA ((R-B)).//9.3e-05:414:60//X95276

R-NT2RP3002869//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//0.14:165:64//  
 AC005256

R-NT2RP3002876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING  
 DRAFT SEQUENCE.//2.6e-59:311:96//AL034380

30 R-NT2RP3002877//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human  
 PAC Library) complete sequence.//4.6e-24:422:63//AC003035

R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//4.7e-109:570:95//AB018314

R-NT2RP3002911//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//3.1e-16:471:64//  
 AC005014

35 R-NT2RP3002948//, complete sequence.//4.5e-94:516:93//AC005500

R-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//3.4e-111:  
 566:96//AC005754

R-NT2RP3002955//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//0.19:424:  
 58//AE001391

40 R-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.1e-89:562:88//D30666

R-NT2RP3002972//Stealth virus 5 clone C1311 T7 genomic sequence.//1.0:122:67//AF067482

R-NT2RP3002978//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING  
 DRAFT SEQUENCE.//4.8e-05:249:63//AL031733

45 R-NT2RP3002988//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATI-  
 DYLINISITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STs and a CpG island.//  
 0.0097:246:67//Z97195

R-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP,  
 GTA, NG23, MuTs homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.9e-24:  
 188:78//AF109905

50 R-NT2RP3003032//Arabidopsis thaliana (clone DW1) DNA retrotransposon Ta11-1 integration site.//5.3e-07:376:  
 63//L47211

R-NT2RP3003059//Homo sapiens chromosome 3, clone hRPK.165\_L\_16, complete sequence.//1.4e-13:323:66//  
 AC005669

55 R-NT2RP3003061//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hli-10).//3.8e-42:  
 265:91//Y16708

R-NT2RP3003068//HS\_3214\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3214 Col=18 Row=N, genomic survey sequence.//0.025:207:64//AQ181894

- R-NT2RP3003071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044
- R-NT2RP3003078//T26A1TF TAMU Arabidopsis thaliana genomic clone T26A1, genomic survey sequence.//0.95:219:63//B27013
- 5 R-NT2RP3003101//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-05:285:62//AC004153
- R-NT2RP3003121//Homo sapiens full-length insert cDNA clone ZD62D10.//2.1e-47:242:98//AF086348
- R-NT2RP3003133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.4e-21:199:75//AL031985
- 10 R-NT2RP3003138//Mouse Kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.1e-14:287:68//D12646
- R-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//1.5e-13:122:80//U17995
- R-NT2RP3003150
- 15 R-NT2RP3003157//Homo sapiens 12q15 BAC GSHB-410F4 (Genome Systems Human Bac Library) complete sequence.//5.5e-42:289:74//AC005294
- R-NT2RP3003185//HS\_2058\_A1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=5 Row=O, genomic survey sequence.//0.025:52:94//AQ231298
- R-NT2RP3003193//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//4.8e-40:349:79//AC005701
- 20 R-NT2RP3003197//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING DRAFT SEQUENCE.//5.2e-10:180:71//AL031319
- R-NT2RP3003203//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904
- R-NT2RP3003204//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 892F13, WORKING DRAFT SEQUENCE.//6.6e-41:282:86//AL009183
- 25 R-NT2RP3003212//Homo sapiens full-length insert cDNA clone ZB91B11.//1.7e-68:363:95//AF086173
- R-NT2RP3003230//Caenorhabditis elegans cosmid T12B5.//0.0018:279:64//AF100307
- R-NT2RP3003242//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.0:346:57//AC005272
- 30 R-NT2RP3003251//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//2.5e-10:436:62//AC003083
- R-NT2RP3003264//CIT-HSP-2296M7.TR CIT-HSP Homo sapiens genomic clone 2296M7, genomic survey sequence.//5.8e-05:308:61//AQ005862
- R-NT2RP3003278//Human HepG2 partial cDNA, clone hmd3b11m5.//9.4e-47:302:89//D17022
- 35 R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//7.4e-101:550:93//L36983
- R-NT2RP3003290//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//3.0e-22:228:78//AL031662
- R-NT2RP3003301
- 40 R-NT2RP3003302//CIT-HSP-2319H19.TR CIT-HSP Homo sapiens genomic clone 2319H19, genomic survey sequence.//1.5e-69:367:95//AQ034950
- R-NT2RP3003311//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//5.1e-08:398:64//AC005505
- R-NT2RP3003313//Caenorhabditis elegans cosmid F39B1, complete sequence.//0.00022:436:58//Z69660
- 45 R-NT2RP3003327//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-237H1 ~complete genomic sequence, complete sequence.//1.5e-16:334:70//AC002287
- R-NT2RP3003330//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003344//HS\_3235\_B2\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=18 Row=P, genomic survey sequence.//4.1e-18:197:80//AQ303203
- R-NT2RP3003346
- 50 R-NT2RP3003353//CITBI-E1-2523B18.TR CITBI-E1 Homo sapiens genomic clone 2523B18, genomic survey sequence.//8.3e-06:130:73//AQ278834
- R-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.9e-97:481:94//AC005519
- R-NT2RP3003384//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-10:226:71//AC004820
- 55 R-NT2RP3003385
- R-NT2RP3003403//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type I Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//2.8e-40:496:

72//AL031585

R-NT2RP3003409//Rat POU domain factor (Brn-5) mRNA.//1.5e-20:375:68//L23204

R-NT2RP3003411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 438L4, WORKING DRAFT SEQUENCE.//1.0:180:61//Z97635

R-NT2RP3003427//RPC11-45J23.TJ RPC111 Homo sapiens genomic clone R-45J23, genomic survey sequence.//0.82:162:69//AQ195566

R-NT2RP3003433//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//1.1e-10:379:61//AC006031

R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//1.1e-95:479:96//AF004828

R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.3e-100:527:93//AB018268

R-NT2RP3003491//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-08:495:59//AE001398

R-NT2RP3003500//W.suaueolens mitochondrial ATP9 gene.//0.0074:514:59//X77238

R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n(GTG)n repeat-containing mRNA.//1.3e-31:217:88//U00952

R-NT2RP3003552

R-NT2RP3003555//Dictyostelium discoideum interaptin (abpD) gene, complete cds.//0.98:321:61//AF057019

R-NT2RP3003564

R-NT2RP3003572//Human DNA sequence from BAC 992D9 on chromosome 22q12.1 contains STS.//0.0015:507:59//AL008638

R-NT2RP3003576//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//1.2e-39:359:79//AC003007

R-NT2RP3003589//Plasmodium falciparum MAL3P8, complete sequence.//0.014:539:58//AL034560

R-NT2RP3003625//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the AD-SL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//1.8e-44:448:77//AL022238

R-NT2RP3003656//Homo sapiens chromosome 17, clone hRPK401\_O\_9, complete sequence.//0.34:257:62//AC005291

R-NT2RP3003659//O.fuscipennis 16S rRNA gene, partial.//0.021:145:65//Z93701

R-NT2RP3003665//HS\_3078\_B2\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=18 Row=F, genomic survey sequence.//1.3e-75:397:95//AQ140580

R-NT2RP3003672

R-NT2RP3003686

R-NT2RP3003701//Human BAC clone GS310A05 from 7q21-q22, complete sequence.//6.4e-17:464:62//AC002452

R-NT2RP3003716//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING DRAFT SEQUENCE.//0.00072:425:62//AL034410

R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//1.7e-101:492:97//AB018300

R-NT2RP3003746//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence.//3.7e-07:217:66//AC003009

R-NT2RP3003795//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//8.1e-26:456:68//Z98052

R-NT2RP3003799//cSRL-138g10-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-138g10, genomic survey sequence.//4.9e-09:117:77//B01736

R-NT2RP3003800//Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds.//2.8e-106:551:95//AF077754

R-NT2RP3003805

R-NT2RP3003809//Homo sapiens full-length insert cDNA clone YZ95A01.//3.6e-106:533:97//AF086107

R-NT2RP3003819//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34606, WORKING DRAFT SEQUENCE.//6.0e-44:288:81//Z84487

R-NT2RP3003825//Mus domesticus interleukin 1 receptor antagonist (IL-1RA) mRNA.//0.0014:410:58//M64404

R-NT2RP3003828

R-NT2RP3003831//\*\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//2.3e-41:289:85//U14567

R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.6e-108:541:97//AF070611

R-NT2RP3003842//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//1.5e-46:457:74//AC002980

R-NT2RP3003846//*Plasmodium falciparum* MAL3P3, complete sequence //3.5e-06:356:62//Z98547  
 R-NT2RP3003870//Homo sapiens full-length insert cDNA clone ZD75H11. //8.2e-09:68:98//AF086402  
 R-NT2RP3003876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12. WORK-  
 5 ING DRAFT SEQUENCE. //0.0027:180:66//AL031650  
 R-NT2RP3003914//*Dictyostelium discoideum* DNA for transposable element Tdd-3 tandem array. //0.029:234:62//  
 X53439  
 R-NT2RP3003918  
 R-NT2RP3003932//Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds. //0.00087:164:  
 67//AF029215  
 10 R-NT2RP3003989  
 R-NT2RP3003992//Sequence 1 from patent US 5591825. //0.56:235:59//I33465  
 R-NT2RP3004013//HS\_3018\_A1\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3018 Col=17 Row=M, genomic survey sequence. //0.00026:421:60//AQ119904  
 R-NT2RP3004016//*Drosophila melanogaster* DNA sequence (P1s DS03465 (D149) and DS08544 (D187)), com-  
 15 plete sequence. //4.8e-12:308:62//AC004532  
 R-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING  
 DRAFT SEQUENCE. //0.42:190:64//AL021579  
 R-NT2RP3004051//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence. //3.6e-21:332:69//  
 AC006130  
 20 R-NT2RP3004070//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING  
 DRAFT SEQUENCE, 5 unordered pieces. //2.0e-05:476:57//AC005308  
 R-NT2RP3004078//Homo sapiens chromosome 19, cosmid R30335, complete sequence. //2.0e-86:486:93//  
 AC005784  
 R-NT2RP3004093//Human PAC clone 257C22A from 13q12-q13, complete sequence. //5.3e-11:230:69//  
 AC002525  
 25 R-NT2RP3004095//Homo sapiens clone NH0486122, WORKING DRAFT SEQUENCE, 5 unordered pieces. //7.5e-  
 93:551:92//AC005038  
 R-NT2RP3004110//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library)  
 complete sequence. //1.6e-104:317:100//AC006064  
 30 R-NT2RP3004125//Pongo pygmaeus CT microsatellite, clone #3, from the tandemly repeated genes encoding U2  
 small nuclear RNA (RNU2 locus) //0.73:168:60//U36532  
 R-NT2RP3004145//Homo sapiens full-length insert cDNA clone ZE09H03. //2.3e-89:427:99//AF086542  
 R-NT2RP3004145//*Arabidopsis thaliana* chromosome II BAC T1B8 genomic sequence, complete sequence. //  
 0.013:134:70//U78721  
 35 R-NT2RP3004155//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence. //3.8e-10:101:87//  
 AC004081  
 R-NT2RP3004206//Homo sapiens clone DJ0794K21, complete sequence. //1.5e-06:442:57//AC005533  
 R-NT2RP3004207//Mouse mRNA for seizure-related gene product 6. //1.7e-07:220:69//D29763  
 R-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence. //7.3e-89:504:92//D42052  
 40 R-NT2RP3004215//*Caenorhabditis elegans* cosmid F11A6, complete sequence. //0.018:353:59//Z81498  
 R-NT2RP3004242//*Plasmodium falciparum* chromosome 2, section 52 of 73 of the complete sequence. //4.5e-06:  
 407:60//AE001415  
 R-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence. //  
 2.8e-105:534:97//AC005385  
 45 R-NT2RP3004253//RPCI11-78J12.TJ RPCI11 Homo sapiens genomic clone R-78J12, genomic survey se-  
 quence. //4.0e-84:382:90//AQ281324  
 R-NT2RP3004258//*Rattus norvegicus* Zis mRNA, complete cds. //7.0e-60:417:84//AF013967  
 R-NT2RP3004262//Mus musculus heat shock protein hsp40-3 gene, complete cds. //2.7e-43:528:73//AF092536  
 R-NT2RP3004334//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence. //1.4e-06:435:  
 50 62//AC004231  
 R-NT2RP3004341//CITBI-E1-2503F11.TR CITBI-E1 Homo sapiens genomic clone 2503F11, genomic survey se-  
 quence. //0.0018:210:65//AQ263365  
 R-NT2RP3004348//Homo sapiens chromosome 17, clone hRPC.85\_B\_7, complete sequence. //7.1e-46:340:83//  
 AC005695  
 55 R-NT2RP3004349//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117O3, WORKING  
 DRAFT SEQUENCE. //9.4e-29:263:79//AL020995  
 R-NT2RP3004378//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoam-  
 ine oxidase B (MAOB), ESTs and polymorphic CA repeats. //2.0e-67:422:90//Z95125



R-NT2RP3004399//HS\_3046\_A1\_E02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=3 Row=1, genomic survey sequence.//0.00014:186:67//AQ137619

R-NT2RP3004424//RPC11-59114.TJ RPC11 Homo sapiens genomic clone R-5914, genomic survey sequence.//7.4e-71:370:95//AQ201461

5 R-NT2RP3004428//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y66A7, WORKING DRAFT SEQUENCE.//0.096:205:64//AL022282

R-NT2RP3004451//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//0.0029:396:60//AC005824

10 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//2.9e-106:526:98//AB007917

R-NT2RP3004466

R-NT2RP3004470//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//8.3e-06:229:64//AC005895

R-NT2RP3004472//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.87:442:59//AC005504

15 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.6e-105:521:97//AB007925

R-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//3.9e-38:322:81//U47024

R-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//4.2e-96:527:92//AC003982

R-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.3e-43:342:82//AC006023

20 R-NT2RP3004503//Human cosmid g1572c101, complete sequence.//2.3e-25:392:68//AC000357

R-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.8e-28:387:70//Y08260

R-NT2RP3004507

R-NT2RP3004527//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//0.68:244:62//AC004518

25 R-nnnnnnnnnnnn//Mouse oncogene (ect2) mRNA, complete cds.//2.6e-79:525:84//L11316

R-NT2RP3004544

R-NT2RP3004566

R-NT2RP3004569//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:296:58//AC004709

30 R-NT2RP3004572//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//8.2e-12:457:63//AC005083

R-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//2.4e-97:488:96//AB007946

R-NT2RP3004594//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//1.7e-10:368:61//AC005234

35 R-NT2RP3004617

R-NT2RP3004618//F2H16TF IGF Arabidopsis thaliana genomic clone F2H16, genomic survey sequence.//0.96:212:64//B26414

R-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds.//2.2e-55:291:95//AB014679

40 R-NT2RP4000008//H.sapiens polyA site DNA sequence.//2.5e-25:202:85//Z24749

R-NT2RP4000023//CIT-HSP-2372A9.TF CIT-HSP Homo sapiens genomic clone 2372A9, genomic survey sequence.//3.6e-51:313:89//AQ112388

R-NT2RP4000035//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.3e-69:536:81//AC005015

45 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds.//2.1e-58:289:82//AF016266

R-NT2RP4000051//Homo sapiens Chromosome 22q11.2 Cosmid Clone 20b In DGCR Region, complete sequence.//0.56:462:58//AC000074

R-NT2RP4000078//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00021:460:60//AC005506

50 R-NT2RP4000102//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//1.6e-08:518:58//AC004648

R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//3.5e-106:536:96//AB011538

R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//1.1e-110:554:97//AB007952

R-NT2RP4000147

55 R-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//3.5e-46:395:83//L20681

R-NT2RP4000151

R-NT2RP4000159//Caenorhabditis elegans cosmid R02F11.//0.00011:261:63//AF016439

R-NT2RP4000167//RPC11-59L8.TK RPC11 Homo sapiens genomic clone R-59L8, genomic survey sequence.//

- 6.2e-26:163.93//AQ200049  
R-NT2RP4000185  
R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.6e-99:505.96//AB014600  
R-NT2RP4000212// complete sequence.//1.0e-106:538.96//AC005300
- 5 R-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.2e-39:272:88//AC005261  
R-NT2RP4000218//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//1.6e-09:457:60//AC004081  
R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//9.0e-69:354:96//AJ006470
- 10 R-NT2RP4000246//Mus musculus mRNA for NDPP-1 protein, complete cds.//2.0e-27:344:73//D10727  
R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//9.7e-78:381:99//AF091092  
R-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.26:124:69//AQ043515  
R-ntnnnnnnnnnn//ORF 5' of ECLF2...ECRF3=G protein-coupled receptor homolog [herpesvirus saimiri HVS, host-squirrel monkey, Genomic, 4 genes, 3720 nt].//0.12:326:61//S76368
- 15 R-NT2RP4000312//Human DNA sequence from clone 523E19 on chromosome 6p11.2-12.3 Contains ESTs STS and GSSs, complete sequence.//2.2e-111:538:98//AL033384  
R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence.//1.4e-108:515:99//AF070524  
R-NT2RP4000323//S. cerevisiae telomeric sequence DNA, clone YLP108CA-2-1.//0.048:107:69//M34311
- 20 R-NT2RP4000355//Homo sapiens clone DJ1136A10, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.3e-39:350:79//AC004972  
R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.4e-109:520:99//AB018281  
R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.7e-109:527:98//AF041195
- 25 R-NT2RP4000370//Homo sapiens PAC clone DJ0777Q23 from 7p14-p15, complete sequence.//9.9e-25:348:72//AC005154  
R-NT2RP4000376//Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.//2.2e-69:391:89//U17901  
R-NT2RP4000381//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//0.066:197:63//AC006080
- 30 R-NT2RP4000415//345F19.TV CIT978SKA1 Homo sapiens genomic clone A-345F19, genomic survey sequence.//0.10:79:75//B15527  
R-NT2RP4000417//Homo sapiens full-length insert cDNA clone ZD52B10.//9.6e-96:468:97//AF086313  
R-NT2RP4000424//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25, Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethyl-aniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//1.8e-08:489:59//AL021026
- 35 R-NT2RP4000448//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.3e-07:510:60//AC005505  
R-NT2RP4000449//HS\_2037\_B2\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=18 Row=B, genomic survey sequence.//1.3e-58:375:88//AQ243047  
R-NT2RP4000455//Phocine herpesvirus type 1 glycoprotein D (gD) gene, partial cds.//0.62:133:63//U92271
- 40 R-ntnnnnnnnnnn  
R-NT2RP4000480//cSRL-54b11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-54b11, genomic survey sequence.//2.1e-19:145:88//B05082  
R-ntnnnnnnnnnn  
R-NT2RP4000500  
R-NT2RP4000515//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.4e-05:411:59//AC005140
- 50 R-NT2RP4000517//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//2.7e-21:230:77//AC003007  
R-NT2RP4000518//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//0.0080:461:59//AL021068
- 55 R-NT2RP4000519  
R-NT2RP4000524

- R-NT2RP4000528//Homo sapiens chromosome 17, clone hRPK 138\_P\_22, complete sequence.//0.99:158:66//AC005697
- R-NT2RP4000541//Homo sapiens Chromosome 22q11.2 Cosmid Clone 33e In DGCR Region, complete sequence.//1.0:309:59//AC000078
- 5 R-NT2RP4000556//Rattus norvegicus cell cycle protein p55CDC gene, complete cds.//0.0031:126:72//AF052695
- R-NT2RP4000588//Homo sapiens BAC clone RG208K23 from 7q31, complete sequence.//1.0:186:64//AC004161
- R-NT2RP4000614//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-62, complete sequence.//1.4e-06:526:58//AL009013
- 10 R-NT2RP4000638//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.9e-48:497:75//AC004666
- R-NT2RP4000648//CIT-HSP-231007.TR CIT-HSP Homo sapiens genomic clone 230017, genomic survey sequence.//0.22:110:68//AQ012747
- R-NT2RP4000657//Lycodichthys dearborni type III antifreeze peptide gene, clone 5'LD-1/NotI-EcoRI subclone SphI-XbaI, partial cds.//0.0065:189:63//U20443
- 15 R-NT2RP4000704//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//0.22:334:60//Z83824
- R-NT2RP4000724//Homo sapiens Chromosome 22q11.2 Cosmid Clone 56c In DGCR Region, complete sequence.//2.2e-70:448:88//AC000080
- R-NT2RP4000728//CIT-HSP-2310K14.TF CIT-HSP Homo sapiens genomic clone 2310K14, genomic survey sequence.//0.00013:289:61//AQ019669
- 20 R-NT2RP4000739//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.53:254:61//AC004765
- R-NT2RP4000781//P.cepacia fusaric acid-resistance genes encoding 5 proteins, complete cds.//1.0:392:59//D12503
- 25 R-NT2RP4000817//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//0.59:378:58//AC003037
- R-NT2RP4000833//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//3.4e-53:307:85//AL023808
- R-NT2RP4000837//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//7.0e-50:367:77//AE000660
- 30 R-NT2RP4000855
- R-NT2RP4000865//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//1.5e-78:479:88//AC003098
- R-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//4.5e-09:186:69//AJ001616
- 35 R-NT2RP4000879//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-08:364:60//AC004153
- R-nnnnnnnnnnn//Human S-adenosylmethionine decarboxylase (AMD1) gene, exons 5-9.//3.5e-90:459:96//M88006
- 40 R-nnnnnnnnnnn//H. sapiens ung gene for uracil DNA-glycosylase.//7.6e-09:392:61//X89398
- R-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//5.8e-45:264:92//U42975
- R-nnnnnnnnnnn//epstein-barr virus simple repeat array (ir3).//0.00012:367:61//J02079
- R-NT2RP4000928//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence.//1.0:138:68//AB006698
- 45 R-NT2RP4000929//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//0.45:288:62//Z82197
- R-NT2RP4000955//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 633O19, WORKING DRAFT SEQUENCE.//1.1e-09:322:62//AL022302
- 50 R-NT2RP4000973//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//2.3e-06:326:62//AF003528
- R-NT2RP4000975
- R-NT2RP4000979//HS\_3009\_B1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3009 Col=15 Row=L, genomic survey sequence.//2.3e-14:117:89//AQ090957
- 55 R-NT2RP4000984//Human immunodeficiency virus type 1 envelope glycoprotein (env) gene, C2-V3 region, isolate HIV194UG011TIN.01\_d11PD, partial cds.//0.11:219:62//U44882
- R-NT2RP4000989//Sequence 30 from patent US 5552281.//3.5e-25:154:97//Z5669
- R-NT2RP4000996//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2),

- CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//3.8e-07:421:59//AF030694
- R-NT2RP4000997//Homo sapiens chromosome 17, clone 104H12, complete sequence.//4.2e-37:499:72//AC000003
- 5 R-NT2RP4001004//HS\_3163\_A2\_H02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=4 Row=O, genomic survey sequence.//2.8e-38:241:90//AQ168515
- R-NT2RP4001006//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//7.1e-55:372:73//AC006023
- 10 R-NT2RP4001010//Homo sapiens full-length insert cDNA clone ZD38E12.//3.3e-09:153:74//AF086247
- R-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.1e-34:361:78//U20086
- R-NT2RP4001041//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//9.9e-84:435:96//AC005216
- R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds.//6.2e-50:282:94//AB007859
- R-NT2RP4001064//H.sapiens NOS2 gene, exon 15.//0.71:183:61//X85771
- 15 R-NT2RP4001078//Human D-site binding protein gene, exon 4 and complete cds.//1.9e-114:569:97//U48213
- R-NT2RP4001079//Homo sapiens mRNA for putative Ca<sup>2+</sup>-transporting ATPase, partial.//2.4e-118:574:98//AJ010953
- R-NT2RP4001080//Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence.//0.013:430:58//AE001429
- 20 R-ntnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds.//1.8e-119:548:95//AB011164
- R-NT2RP4001095//Homo sapiens cosmid IM0525, LC1233, Qc3C1, LB1349, Qc12C11 and 220B3 from Xq28, complete sequence.//2.8e-39:312:81//AF003626
- R-NT2RP4001100//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//8.7e-41:389:78//Z78021
- 25 R-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//2.8e-12:292:68//M96629
- R-NT2RP4001122//Caenorhabditis elegans cosmid F44D12, complete sequence.//0.97:129:66//Z68298
- R-NT2RP4001126//HS\_3146\_A1\_805\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=9 Row=C, genomic survey sequence.//0.013:268:63//AQ141093
- 30 R-NT2RP4001143//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING DRAFT SEQUENCE.//1.8e-31:380:68//AL031668
- R-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-83:325:92//AC005095
- R-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//8.1e-32:553:67//D67067
- 35 R-NT2RP4001150//AK011 Genomic DNA Hordeum vulgare genomic clone tel44a similar to barley TAS, genomic survey sequence.//0.91:132:63//AQ248412
- R-NT2RP4001159//Cloning vector pAP3neo DNA, complete sequence.//4.0e-118:437:97//AB003468
- R-NT2RP4001174//Homo sapiens 12q24 BAC RPC11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//1.7e-33:289:82//AC002996
- 40 R-ntnnnnnnnnnn//P.falciparum mRNA for AARP2 protein.//0.93:187:64//Y08924
- R-NT2RP4001207
- R-NT2RP4001210//CIT-HSP-2042D13.TF CIT-HSP Homo sapiens genomic clone 2042D13, genomic survey sequence.//3.8e-06:268:63//B74772
- 45 R-NT2RP4001213//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//4.7e-16:371:66//M99593
- R-NT2RP4001219//HS\_2190\_A1\_A06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=11 Row=A, genomic survey sequence.//2.4e-06:288:61//AQ216635
- R-NT2RP4001228//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.024:357:58//AL031745
- 50 R-NT2RP4001235//HS\_3047\_A1\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=13 Row=L, genomic survey sequence.//0.0033:301:63//AQ126918
- R-NT2RP4001256//HS\_3007\_A2\_B06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=12 Row=C, genomic survey sequence.//1.5e-11:140:80//AQ118389
- 55 R-NT2RP4001260//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//0.0013:486:59//AE001426
- R-NT2RP4001274//RPC11-24O21.TKBF RPC11 Homo sapiens genomic clone RPC11-24O21, genomic survey sequence.//3.9e-25:142:99//AQ013887

- R-nnnnnnnnnnn/Homo sapiens full-length insert cDNA clone ZD55D10.//1.2e-10:90:92//AF086334  
 R-NT2RP4001313//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//1.7e-23:466:66//AF009326  
 R-NT2RP4001315//CIT-HSP-2312C6.TR CIT-HSP Homo sapiens genomic clone 2312C6, genomic survey sequence.//0.98:305:62//AQ018036  
 5 R-NT2RP4001339  
 R-NT2RP4001345  
 R-NT2RP4001351//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00082:260:59//AB003097  
 10 R-NT2RP4001353//RPC111-55N17.TJ RPC111 Homo sapiens genomic clone R-55N17, genomic survey sequence.//0.74:106:66//AQ081821  
 R-NT2RP4001372  
 R-NT2RP4001373//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//1.5e-09:473:60//AC006080  
 15 R-NT2RP4001375  
 R-NT2RP4001379//CIT-HSP-2335A10.TF CIT-HSP Homo sapiens genomic clone 2335A10, genomic survey sequence.//9.4e-41:441:75//AQ040083  
 R-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//2.4e-22:276:73//AC004691  
 20 R-NT2RP4001407//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.49:254:61//AC005140  
 R-NT2RP4001414  
 R-NT2RP4001433//Human prohibitin (PHB) gene, exons 1-7.//6.6e-66:357:90//L14272  
 R-NT2RP4001442//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.11:307:59//AC005308  
 25 R-NT2RP4001447//cSRL-58d2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-58d2, genomic survey sequence.//0.0039:112:71//B05220  
 R-NT2RP4001474  
 R-NT2RP4001483  
 30 R-NT2RP4001498//Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds.//1.2e-07:339:61//L34027  
 R-NT2RP4001502//HS\_2187\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2187 Col=19 Row=F, genomic survey sequence.//1.3e-20:183:81//AQ214108  
 R-NT2RP4001507//Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.15:333:62//AC005916  
 35 R-NT2RP4001524//Genomic sequence from Human 13, complete sequence.//0.96:159:65//AC001226  
 R-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//9.5e-34:337:80//U20086  
 R-NT2RP4001547//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00027:336:63//AC004710  
 40 R-nnnnnnnnnnn//Arabidopsis thaliana BAC T12H20.//1.5e-11:517:60//AF080119  
 R-NT2RP4001555//Human DNA sequence from PAC 481A17 on chromosome X contains ESTs.//0.0069:305:62//Z82212  
 R-NT2RP4001567//RPC111-61A2.TJ RPC111 Homo sapiens genomic clone R-61A2, genomic survey sequence.//0.0072:180:60//AQ200771  
 45 R-NT2RP4001568  
 R-NT2RP4001571//Trypanoplasma borrelli kinetoplast ribosomal protein S12 (RPS12), putative cryptogene (GR11), 12S ribosomal RNA, and apocytochrome b (CYb) genes, primary transcripts, and cytochrome c oxidase subunit III (COIII) gene, complete cds.//1.6e-09:555:58//U14181  
 R-NT2RP4001574//HS\_2247\_B1\_B05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=D, genomic survey sequence.//1.1e-41:254:90//AQ182345  
 50 R-NT2RP4001575//Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and GSSs, complete sequence.//1.1e-118:567:98//AL031228  
 55 R-NT2RP4001592//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING

DRAFT SEQUENCE.//2.5e-09:370:61//AL031650

R-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livmore human cosmid library) complete sequence.//0.99:73:75//AC002364

R-NT2RP4001614

R-NT2RP4001634//Homo sapiens full-length insert cDNA clone YU73B11.//5.8e-101:526:94//AF087969

R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds.//5.4e-115:559:97//AF007151

R-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//6.8e-33:286:79//Y11092

R-NT2RP4001656//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.2e-109:515:99//AC000384

R-NT2RP4001677//Genomic sequence from Human 9q34, complete sequence.//0.19:504:58//AC000397

R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//4.5e-115:583:96//U96629

R-NT2RP4001725//Human Chromosome 3 pac pDJ7011, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.98:301:60//AC000380

R-nnnnnnnnnnn//Caenorhabditis elegans cosmid F48E3.//2.2e-17:328:64//U28735

R-NT2RP4001739//RPC111-74E7.TJ RPC111 Homo sapiens genomic clone R-74E7, genomic survey sequence.//1.1e-08:141:65//AQ268408

R-NT2RP4001753//H.sapiens HZF3 mRNA for zinc finger protein.//1.7e-111:552:96//X78926

R-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//9.3e-27:358:72//L11316

R-NT2RP4001790//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-99:484:98//AC005020

R-NT2RP4001803//HS\_3087\_B2\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3087 Col=10 Row=D, genomic survey sequence.//2.7e-96:471:97//AQ121405

R-NT2RP4001822

R-NT2RP4001823

R-NT2RP4001828//Human DNA sequence from PAC 179115, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//4.1e-14:136:83//Z92540

R-NT2RP4001838//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.5e-06:418:60//AE001372

R-NT2RP4001849//P.falciparum serine rich protein (SERP I) gene.//0.64:135:67//J03983

R-NT2RP4001889//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//4.3e-26:212:82//AC004548

R-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-111:570:96//AC005014

R-NT2RP4001896

R-NT2RP4001901

R-NT2RP4001927//Borrelia burgdorferi (section 32 of 70) of the complete genome.//1.0:242:60//AE001146

R-NT2RP4001938//Human aminopeptidase N gene, exon 1.//3.3e-42:195:85//M55523

R-NT2RP4001946//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.97:371:57//AC004157

R-NT2RP4001950//RPC111-69C18.TJ RPC111 Homo sapiens genomic clone R-69C18, genomic survey sequence.//4.7e-91:552:89//AQ236641

R-NT2RP4001953//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//6.6e-70:325:84//Z93023

R-NT2RP4001966//Rat mRNA for growth potentiating factor, complete cds.//5.5e-37:141:86//D42148

R-NT2RP4001975//Human Newcastle disease virus inducible protein mRNA, partial 3'UTR region.//1.0e-46:242:98//U25276

R-NT2RP4002018//RPC111-76123.TV RPC111 Homo sapiens genomic clone R-76123, genomic survey sequence.//7.9e-89:438:97//AQ268536

R-NT2RP4002047//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//4.1e-07:325:62//AL031297

R-NT2RP4002052//Human DNA sequence from clone 352E11 on chromosome 22q13.1-13.31. Contains GSSs, complete sequence.//0.31:452:57//AL022353

R-NT2RP4002058//RPC111-69O1.TJ RPC111 Homo sapiens genomic clone R-69O1, genomic survey sequence.//0.23:163:64//AQ268418

R-NT2RP4002071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1172A22, WORKING DRAFT SEQUENCE.//1.1e-11:407:62//AL034386

R-NT2RP4002075//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon

of a putative new gene and STSs and GSSs, complete sequence.//0.085:350:61//AL033375  
 R-NT2RP400278//RPCI11-79116.TV RPCI11 Homo sapiens genomic clone R-79116, genomic survey sequence.//3.3e-87:452:95//AQ283131  
 R-nnnnnnnnnnn  
 5 R-NT2RP4002083//Homo sapiens mineralocorticoid receptor (MLR), exon 5.//0.50:256:61//AF068619  
 R-NT2RP4002408//CIT-HSP-2376023.TF CIT-HSP Homo sapiens genomic clone 2376023, genomic survey sequence.//6.8e-62:320:96//AQ111163  
 R-NT2RP4002791//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.022:435:61//AC002476  
 10 R-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//6.0e-56:660:71//AC002383  
 R-NT2RP4002905//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete sequence.//0.0017:533:57//AL008972  
 R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//8.7e-114:605:94//AB007934  
 15 R-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//2.1e-43:326:74//AC005510  
 R-OVARC1000006//HS\_2253\_B1\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=L, genomic survey sequence.//3.7e-35:191:98//AQ069124  
 R-OVARC1000013//HS\_2212\_A2\_G06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=12 Row=M, genomic survey sequence.//0.14:212:63//AQ210584  
 20 R-OVARC1000014//Human DNA sequence from PAC 463A9, on chromosome Xq25 contains STS.//0.0053:356:62//Z80232  
 R-OVARC1000017  
 R-OVARC1000035//RPCI11-65E1.TJ RPCI11 Homo sapiens genomic clone R-65E1, genomic survey sequence.//3.3e-05:236:63//AQ237194  
 25 R-OVARC1000058//Homo sapiens DNA sequence from BAC 390C10 on chromosome 22q11.21-12.1. Contains an Immunoglobulin LIKE gene and a pseudogene similar to Beta Crystallin. Contains ESTs, STSs, GSSs and taga and tat repeat polymorphisms, complete sequence.//2.7e-48:325:82//AL008721  
 R-OVARC1000060//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//5.0e-21:297:70//AL033397  
 30 R-OVARC1000068//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.00038:553:58//X95276  
 R-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 596C15, WORKING DRAFT SEQUENCE.//5.1e-110:599:93//AL031387  
 R-OVARC1000085//DNA encoding component HC5 of human proteasome.//2.7e-65:366:92//E03413  
 35 R-nnnnnnnnnnn//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.80:285:59//B94391  
 R-OVARC1000091  
 R-OVARC1000092//CIT-HSP-2373J20.TR CIT-HSP Homo sapiens genomic clone 2373J20, genomic survey sequence.//1.4e-17:141:85//AQ111520  
 40 R-OVARC 1000106  
 R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18)mRNA, complete cds.//2.6e-100:495:97//AF069250  
 R-OVARC1000114//Homo sapiens partial XPGC gene, exon 2.//9.5e-49:392:80//X71342  
 R-OVARC1000133//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//0.00020:243:65//U95740  
 45 R-OVARC1000145//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//1.8e-16:370:67//AC005385  
 R-OVARC1000148//CIT-HSP-2386P14.TF.1 CIT-HSP Homo sapiens genomic clone 2386P14, genomic survey sequence.//1.1e-05:55:98//AQ240492  
 R-OVARC1000151//M.musculus GEG-154 mRNA.//9.8e-21:192:81//X71642  
 50 R-OVARC1000168//CIT-HSP-2336F6.TR CIT-HSP Homo sapiens genomic clone 2336F6, genomic survey sequence.//0.050:176:62//AQ042932  
 R-OVARC1000191//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.7e-08:534:58//AC005506  
 R-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.2e-111:556:96//AC004604  
 55 R-OVARC1000209//Blacus sp. 16S ribosomal RNA gene, partial sequence.//0.55:165:67//AF003501  
 R-OVARC1000212//Mouse DNA for beta-casein.//0.56:225:63//X13484  
 R-OVARC1000240//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//6.2e-38:193:82//

- AC005670  
R-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-25:312:73//AF060194
- 5 R-OVARC1000288//Human HepG2 3' region Mbol cDNA, clone hmd1d01m3.//5.4e-07:128:70//D17131  
R-OVARC1000302//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//1.7e-10:100:88//AC005971  
R-OVARC1000304//Mouse mRNA from Mov10 locus.//7.9e-66:379:81//X52574  
R-OVARC 1000309
- 10 R-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.5e-83:453:94//AC005236  
R-OVARC1000328//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//5.0e-58:455:81//U19614  
R-OVARC1000335//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0483123; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.034:429:60//AC005690
- 15 R-OVARC1000347//Mus musculus HRS gene, complete cds.//4.6e-06:339:61//AF020308  
R-OVARC1000384//D. discoideum glycoprotein 24 A and B (GP24A and GP24B) genes, complete cds.//0.48:296:62//M27588  
R-OVARC1000408//Homo sapiens DNA from chromosome 19-cosmid R27740 containing MEF2B and RSRFR2 genes, genomic sequence.//9.4e-39:286:87//AD000812
- 20 R-OVARC1000411//CIT-HSP-2303H10.TF CIT-HSP Homo sapiens genomic clone 2303H10, genomic survey sequence.//1.5e-07:94:84//AQ016720  
R-OVARC1000414//Homo sapiens genomic DNA, 21q region, clone: 149C3X10, genomic survey sequence.//1.8e-32:296:75//AG002388  
R-OVARC1000420//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-48:354:77//AC005378
- 25 R-OVARC1000427//D. discoideum vegetative specific gene V18 gene for ribosomal protein.//2.5e-09:370:59//X15382  
R-OVARC1000431//HS\_2199\_A2\_E02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2199 Col=4 Row=1, genomic survey sequence.//1.3e-34:186:98//AQ093722  
R-OVARC1000437//Gallus gallus tensin mRNA, 3' end.//1.3e-15:160:80//L06662
- 30 R-OVARC1000440//Homo sapiens BAC clone NH0538D15 from 7q11.23-q21.1, complete sequence.//0.0054:337:61//AC006043  
R-OVARC1000442//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.0e-45:322:86//AQ037381  
R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.1e-77:418:94//AB014583
- 35 R-OVARC1000461//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//0.62:333:59//AL034417  
R-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEF1) mRNA, complete cds.//1.1e-81:489:91//AF023451  
R-OVARC1000466//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//0.0088:98:72//AC004526
- 40 R-OVARC1000473//Homo sapiens full-length insert cDNA clone Y153C10.//3.2e-92:317:100//AF085851  
R-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//2.7e-70:502:84//D67671  
R-OVARC1000486//Dictyostellum discoideum FusC (fusC) gene, partial cds.//0.52:411:58//AF019984  
R-OVARC1000496
- 45 R-OVARC1000520//Homo sapiens PAC clone DJ412A9 from 22, complete sequence.//3.8e-17:294:71//AC005005  
R-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//4.5e-109:547:96//AC005024  
R-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.0e-46:264:93//AC004510
- 50 R-OVARC1000543//Caenorhabditis elegans cosmid F10C1.//0.00063:417:59//U49831  
R-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.5e-39:144:92//AL022069  
R-OVARC1000557//Homo sapiens chromosome 19, cosmid R32469, complete sequence.//1.5e-81:429:96//AC005197
- 55 R-OVARC1000564//Homo sapiens chromosome 17, clone HRPc837J1, complete sequence.//0.83:301:58//AC004223  
R-OVARC1000573//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na<sup>+</sup>-isocitrate dehydrogenase gamma subunit



(IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28lu1 gene and cytochrome C (CCP) pseudogene.//2.4e-44:300:88//U52111

R-OVARC1000578//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//6.4e-48:436:78//AF001549

R-OVARC1000588//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//2.7e-32:313:78//AC005952

R-OVARC 1000605

R-OVARC1000622//Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence.//6.2e-43:328:83//AC006012

R-OVARC1000640//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.9e-47:514:73//AC005840

R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//1.6e-29:162:100//AB011162

R-OVARC1000678//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.50:270:60//AC005140

R-nnnnnnnnnnn//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.4e-83:549:86//AJ001713

R-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//3.2e-13:160:76//AL034424

R-OVARC1000689//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.90:230:61//U32943

R-OVARC1000700//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//5.1e-15:133:85//AC005754

R-OVARC1000703//Homo sapiens chromosome 22, clone hRPC.130\_H\_16, complete sequence.//6.9e-48:525:73//AC005585

R-OVARC1000730//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00019:198:63//AQ093513

R-OVARC1000746//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:154:65//X95276

R-OVARC1000769//Human coagulation factor XI gene, intron 2, partial, clone pTZ18R.//2.0e-30:187:78//M21185

R-OVARC1000771

R-OVARC1000781//Sequence 5 from Patent WO9722695.//8.4e-47:401:77//A63552

R-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q11.2-qter, complete sequence.//7.8e-111:567:96//AC004542

R-OVARC1000800//Homo sapiens mitochondrial HSP75 mRNA, complete cds.//1.3e-17:119:95//L15189

R-OVARC1000802//Homo sapiens chromosome 5, BAC clone 120c13 (LBNL H171), complete sequence.//2.3e-51:482:78//AC005574

R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//3.6e-105:536:95//Y1771

R-OVARC1000846//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//2.7e-107:538:96//AC004494

R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//3.6e-114:579:96//AF045584

R-OVARC1000862//M. musculus F1f mRNA.//2.3e-20:346:73//X71978

R-OVARC1000876//Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence.//9.1e-08:427:58//AE001416

R-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//5.6e-34:357:78//U20086

R-OVARC1000885//Lycopersicon esculentum alcohol dehydrogenase homolog (GAD3) mRNA, partial cds.//0.47:305:60//U21801

R-OVARC 1000886

R-OVARC1000891//HS\_3082\_A2\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=8 Row=K, genomic survey sequence.//1.1e-16:187:79//AQ122500

R-OVARC1000897//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//7.2e-07:476:60//AL020969

R-OVARC1000912

R-OVARC1000915//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000924//Homo sapiens Chromosome 22q11.2 Cosmid Clone cosk In NF1 Region, complete sequence.//1.6e-77:465:90//AC002471

R-OVARC1000936//HS\_2195\_A2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=24 Row=E, genomic survey sequence.//2.4e-76:463:90//AQ191108

- R-OVARC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SEQUENCE.//0.0028:161.65//Z99716
- R-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//3.5e-62:526.78//AB005549
- 5 R-OVARC1000948//Hypera postica NADH dehydrogenase subunit 1 (ND1) gene, partial cds, tRNA-Leu gene, complete sequence, and 16S ribosomal gene, partial sequence, mitochondrial genes encoding mitochondrial products.//0.018:212.61//U61169
- R-OVARC1000959//CIT-HSP-2371K16.TR CIT-HSP Homo sapiens genomic clone 2371K16, genomic survey sequence.//1.1e-45:303.87//AQ111323
- 10 R-OVARC1000960//Homo sapiens BAC clone GS293C05 from 7q21-q22, complete sequence.//7.5e-44:353.81//AC005021
- R-OVARC1000971//H.sapiens DNA for repeat unit locus D18S51(285 bp).//2.2e-07:223.70//X91255
- R-OVARC1000984
- 15 R-OVARC1000996//Human DNA sequence from clone 272L16 on chromosome 1q32.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Kalinin, BM600) and a novel Rat Ca2+/Calmodulin dependent Protein Kinase LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D1S491 and a ca repeat polymorphism, complete sequence.//1.3e-06:179.70//AL023754
- R-OVARC1000999//Homo sapiens chromosome 17, clone hCIT.457\_L\_16, complete sequence.//5.8e-71:332.87//AC003957
- 20 R-OVARC1001000//HS\_3032\_B1\_G11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=21 Row=N, genomic survey sequence.//5.1e-51:257.99//AQ096695
- R-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//5.6e-92:473.96//AC004190
- R-OVARC1001010//RPCI11-10P1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-10P1, genomic survey sequence.//4.1e-05:201.65//B71813
- 25 R-OVARC1001011//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.9e-18:219.69//AC005520
- R-OVARC1001032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//2.7e-89:464.86//AL022345
- 30 R-OVARC1001034//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//1.4e-18:451.64//AC005220
- R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//1.3e-99:501.96//AF099149
- R-OVARC1001040//Homo sapiens chromosome 17, clone hRPK.1096\_G\_20, complete sequence.//9.7e-17:180:78//AC005410
- 35 R-OVARC1001044
- R-OVARC1001051//H.sapiens mRNA for homologue to yeast ribosomal protein L41.//3.7e-15:124.88//Z12962
- R-OVARC1001055//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//2.0e-30:292.76//AC006213
- R-OVARC1001062//Sequence 65 from patent US 5691147.//2.6e-54:312.92//I76237
- 40 R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.3e-95:463.98//AF082657
- R-OVARC1001072//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.92:272.59//U47276
- R-OVARC1001074//HS\_2205\_A1\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=13 Row=G, genomic survey sequence.//1.3e-35:205.94//AQ184530
- R-OVARC1001085
- 45 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.5e-95:325.98//AJ005897
- R-OVARC1001113//Homo sapiens diaphanous 1 (HDI1) mRNA, complete cds.//1.0e-73:386.95//AF051782
- R-OVARC1001117//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//6.1e-37:314.81//AC005272
- 50 R-OVARC1001118//Homo sapiens chromosome 5, P1 clone 1195e2 (LBNL H73), complete sequence.//1.5e-44:390.77//AC005372
- R-OVARC1001129//Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.//0.81:461.57//AJ235270
- R-OVARC1001161//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 850H21, WORKING DRAFT SEQUENCE.//4.6e-08:342.64//AL031680
- 55 R-OVARC1001162//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//5.9e-48:347.85//B89781
- R-OVARC1001167//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//

- 1.3e-28:427:70//AC004963  
 R-OVARC1001169//RPC111-36P6.TV RPC1-11 Homo sapiens genomic clone RPC1-11-36P6, genomic survey sequence.//0.56:113:72//AQ045859
- 5 R-OVARC1001170//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//8.8e-39:301:85//AC002549  
 R-OVARC1001173//Human clone HS2.30 Alu-Ya5 sequence.//2.4e-35:183:83//U67213  
 R-OVARC1001180//Homo sapiens 12q24.1 NOVECTOR P443K8 () complete sequence.//9.1e-41:516:72//AC005907
- 10 R-OVARC1001188//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.2e-14:134:85//AC004796  
 R-OVARC1001200//ALS=85 kda insulin-like growth factor binding protein-3 complex acid-labile subunit [baboons, liver, mRNA Partial, 1818 nt].//0.12:345:60//S83462  
 R-OVARC1001232//Bovine tyrosine hydroxylase mRNA, complete cds.//0.66:257:59//M36794  
 R-OVARC1001240//Homo sapiens chromosome 17, clone hCIT.124\_H\_2, complete sequence.//1.4e-41:284:87//AC006071
- 15 R-OVARC1001243//HS\_2055\_B2\_C01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=2 Row=F, genomic survey sequence.//0.59:83:75//AQ243142  
 R-OVARC1001261//Crocodilus porosus mRNA for transthyretin.//0.93:121:66//AJ223148  
 R-OVARC1001268
- 20 R-OVARC1001270//Plasmodium falciparum MAL3P6, complete sequence.//0.0031:295:62//Z98551  
 R-OVARC1001271//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-107:544:97//AC004494  
 R-OVARC1001282//Homo sapiens Xp22-39-47 PAC RPC1-199J3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.025:402:59//AC006062
- 25 R-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.1e-05:319:62//U97018  
 R-nnnnnnnnnnnn/Sequence 13 from patent US 5624818.//5.4e-85:577:84//I41142  
 R-OVARC1001329//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30G7, WORKING DRAFT SEQUENCE.//4.2e-71:282:88//AL034402
- 30 R-OVARC1001330//Homo sapiens PAC clone DJ0697H17 from 7q11.23-q21.1, complete sequence.//0.19:256:59//AC004862  
 R-OVARC1001339//Homo sapiens 12q13 PAC RPC1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.5e-49:366:83//AC004242  
 R-OVARC1001341//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695O20, WORKING DRAFT SEQUENCE.//4.8e-26:447:69//AL032818
- 35 R-OVARC1001342//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//5.5e-86:569:86//AC005874  
 R-OVARC1001344//Homo sapiens chromosome 5, BAC clone 261J17 (LBNL H190), complete sequence.//2.8e-46:424:78//AC005350
- 40 R-OVARC1001357//Sequence 1 from patent US 5597707.//3.0e-42:250:93//I34297  
 R-OVARC1001360//Homo sapiens chromosome 17, clone hRPK.786\_O\_4, complete sequence.//0.20:335:60//AC005863  
 R-OVARC 1001369  
 R-OVARC1001372//S.scrofa DNA for myogenin 3'flanking region (285 bp).//6.9e-29:249:83//X89210
- 45 R-OVARC1001419//CIT-HSP-2362F16.TR CIT-HSP Homo sapiens genomic clone 2362F16, genomic survey sequence.//7.6e-47:242:98//AQ074668  
 R-OVARC1001425//Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete sequence.//2.3e-20:211:66//AC005157
- 55 R-OVARC1001436//Human DNA flanking 3' end of transposon L1.1.//0.18:148:66//M80341  
 R-OVARC1001442  
 R-OVARC1001453//Human PAC clone DJ525N14 from Xq23, complete sequence.//2.3e-19:181:81//AC002086

- R-OVARC1001476//CITBI-E1-2517B6.TR CITBI-E1 Homo sapiens genomic clone 2517B6, genomic survey sequence.//0.24:308.59//AQ278655
- R-OVARC1001480//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 753D4, WORKING DRAFT SEQUENCE.//0.99:294.62//AL031676
- 5 R-OVARC1001489//E.caballus microsatellite DNA marker (clone ASB32).//0.87:81:71//X93546
- R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//9.3e-116:585:96//AF016507
- R-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence, complete sequence.//2.6e-40:285.86//AC002039
- 10 R-OVARC1001525//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:59//AC006036
- R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds.//5.0e-110:566:95//AB016488
- R-OVARC1001547
- R-OVARC1001577//Homo sapiens SRP46 splicing factor transcribed retropseudogene.//5.9e-33:216:92//AF031165
- 15 R-OVARC1001600//Human Chromosome X, complete sequence.//3.0e-22:157:89//AC002418
- R-OVARC1001610//HS\_3070\_A2\_A06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070 Col=12 Row=A, genomic survey sequence.//0.47:107:66//AQ103523
- R-OVARC1001611//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//0.17:236:63//AL034423
- 20 R-OVARC1001615//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 3100I3, WORKING DRAFT SEQUENCE.//1.3e-19:248:70//AL031658
- R-OVARC1001668//HS\_3228\_A2\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=24 Row=I, genomic survey sequence.//4.6e-13:156:76//AQ188379
- 25 R-OVARC1001702//CITBI-E1-2501P16.TR.1 CITBI-E1 Homo sapiens genomic clone 2501P16, genomic survey sequence.//1.6e-41:217:99//AQ241965
- R-OVARC1001703
- R-OVARC1001711//CITBI-E1-2502N10.TF CITBI-E1 Homo sapiens genomic clone 2502N10, genomic survey sequence.//2.0e-14:220:72//AQ266194
- 30 R-OVARC1001726//CIT-HSP-2320O1.TF CIT-HSP Homo sapiens genomic clone 2320O1, genomic survey sequence.//0.021:170:62//AQ038145
- R-OVARC1001731//Human mRNA for fibroblast tropomyosin TM30 (pl).//2.5e-72:422:90//X05276
- R-OVARC1001745//Human DNA sequence from clone 796I11 on chromosome 20q12. Contains ESTs, an STS and GSSs, complete sequence.//7.6e-44:314:84//AL031257
- 35 R-nnnnnnnnnnn//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//1.6e-08:396:60//M23166
- R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//3.5e-108:567:94//U97670
- R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds.//6.3e-108:529:97//AB014575
- R-OVARC1001768//Caenorhabditis elegans cosmid Y57G11A, complete sequence.//0.24:205:64//Z99279
- 40 R-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//4.6e-58:558:76//AC005066
- R-OVARC1001795
- R-OVARC1001802//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//1.1e-37:346:78//U89337
- 45 R-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//3.0e-112:581:95//AL023694
- R-OVARC1001812//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//6.6e-41:345:81//AL031585
- 50 R-OVARC1001813//CITBI-E1-2508J18.TR CITBI-E1 Homo sapiens genomic clone 2508J18, genomic survey sequence.//1.1e-67:238:95//AQ263046
- R-OVARC1001820//Human PAC clone DJ525N14 from Xq23, complete sequence.//4.8e-41:320:83//AC002086
- 55 R-OVARC1001828//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//3.4e-08:527:58//AC004688
- R-OVARC1001846//CIT-HSP-2014F15.TR CIT-HSP Homo sapiens genomic clone 2014F15, genomic survey sequence.//0.0045:165:67//B58905

- R-OVARC1001861//M.musculus mRNA for pMEM2 protein.//9.5e-28:405:68//X95350
- R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//5.9e-104:571:91//AF070611
- R-OVARC1001879//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//9.1e-20:206:80//AL031864
- R-OVARC1001880//RPC111-42115.TJ RPC111 Homo sapiens genomic clone R-42115, genomic survey sequence.//3.9e-50:287:88//AQ052700
- R-OVARC1001883//Homo sapiens chromosome 17, clone hCIT.123\_J\_14, complete sequence.//6.1e-13:457:63//AC003950
- R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//2.5e-86:346:90//AF061749
- R-OVARC1001901//Homo sapiens testis specific methyl-CpG binding protein MBD2 (MBD2) mRNA, partial cds.//7.2e-89:421:100//AF072246
- R-OVARC1001911//Homo sapiens full-length insert cDNA clone ZD52F10.//8.2e-106:510:98//AF086315
- R-OVARC1001916
- R-OVARC1001928
- R-OVARC1001942//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//0.0013:231:63//M23166
- R-OVARC1001943//Human immunodeficiency virus type 1, strain FRMP329, envelope glycoprotein V3 region (env) gene, partial cds.//0.14:173:64//U58826
- R-OVARC1001949//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//1.3e-09:306:63//M99593
- R-OVARC1001950//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, complete sequence.//8.2e-38:385:75//AC005666
- R-OVARC1001987
- R-OVARC1001989//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11, WORKING DRAFT SEQUENCE.//6.3e-08:355:60//Z92841
- R-OVARC1002044//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//5.0e-42:298:86//AL031286
- R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.4e-107:542:96//AB007934
- R-OVARC1002066//Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence.//0.23:210:61//AC004411
- R-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.4e-99:546:92//AC006015
- R-OVARC1002107//Human DNA sequence from PAC 417G15 on chromosome Xq25-Xq26. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), pseudogene, ESTs.//4.4e-34:375:74//AL009174
- R-OVARC1002127
- R-OVARC1002138//CIT-HSP-2290O18.TF CIT-HSP Homo sapiens genomic clone 2290O18, genomic survey sequence.//2.4e-07:316:62//AQ003988
- R-OVARC1002143//RPC111-54M8.TJ RPC111 Homo sapiens genomic clone R-54M8, genomic survey sequence.//2.3e-35:220:90//AQ083241
- R-OVARC1002156
- R-OVARC1002158//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence.//1.6e-12:140:79//AQ265720
- R-OVARC1002165//CIT-HSP-2307C9.TF CIT-HSP Homo sapiens genomic clone 2307C9, genomic survey sequence.//5.0e-59:291:99//AQ020420
- R-OVARC1002182//P.falciparum SD17 gene for knob-associated histidine-rich protein.//0.74:161:65//Y00060
- R-PLACE1000004//D.discoideum gene for protein kinase.//0.00081:263:59//Z37981
- R-PLACE1000005//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0082:477:58//AC005507
- R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence.//1.2e-14:100:97//AF070557
- R-PLACE1000014//Homo sapiens genomic DNA, chromosome 21q22.2, p1 clone: T1212 and T1601, WORKING DRAFT SEQUENCE.//2.8e-44:405:77//D83253
- R-PLACE1000031//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//1.8e-24:291:73//AC006162
- R-PLACE1000040//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105C5, WORKING DRAFT SEQUENCE.//0.00039:289:61//Z88855
- R-PLACE1000048//Human BAC clone RG210I04, complete sequence.//4.7e-83:518:89//AC002462
- R-PLACE1000050//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING

DRAFT SEQUENCE, 8 unordered pieces.//0.98:73:76//AC005505

R-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//5.9e-21:125:98//L22154

R-PLACE1000066

R-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.2e-87:456:95//AC005848

R-PLACE1000081

R-PLACE1000094//RPCI11-91K6.TV RPCI11 Homo sapiens genomic clone R-91K6, genomic survey sequence.//2.3e-83:409:98//AQ282619

R-PLACE1000133//Homo sapiens chromosome 17, clone hRPK.746\_E\_8, complete sequence.//1.8e-06:420:57//AC005358

R-PLACE1000142

R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.3e-112:594:94//AF058291

R-PLACE1000185

R-PLACE1000213//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//B.2e-80:410:97//AQ022149

R-PLACE1000214//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-09, complete sequence.//1.6e-05:548:59//AL008989

R-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695O20, WORKING DRAFT SEQUENCE.//2.2e-16:118:91//AL032818

R-PLACE1000246//X.laevis mRNA for XLCL2 protein.//6.5e-13:66:95//Z14122

R-PLACE1000292//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111B22, WORKING DRAFT SEQUENCE.//6.6e-41:322:84//Z98200

R-PLACE1000332//Homo sapiens chromosome 17, clone hCIT.281\_F\_24, complete sequence.//1.8e-16:598:62//AC004706

R-PLACE1000347//Homo sapiens PAC clone DJ1090P18 from 7q21-q22, complete sequence.//2.3e-11:237:69//AC005326

R-PLACE1000374//Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.//B.7e-09:492:58//AC005278

R-PLACE1000380//Plasmodium falciparum chromosome 2, section 1 of 73 of the complete sequence.//0.59:354:59//AE001364

R-PLACE1000383//Mus musculus myotubularin related protein 1 (Mtmr1) mRNA, complete cds.//0.55:65:84//AF073997

R-PLACE1000401//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-17:152:83//AC005015

R-PLACE1000406//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence.//0.51:346:58//AB020742

R-PLACE1000420//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.5e-25:243:79//AP000009

R-PLACE1000421//HS\_2251\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=24 Row=N, genomic survey sequence.//1.4e-82:430:95//AQ192807

R-PLACE1000424//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//1.8e-36:483:71//AC002073

R-PLACE1000435//Homo sapiens chromosome 21q22.2 cosmid clone Q71A3, complete sequence.//2.6e-37:371:76//AF015724

R-PLACE1000444//Homo sapiens chromosome 17, clone hRPK.227\_G\_15, complete sequence.//1.0e-54:429:81//AC005899

R-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//0.66:103:72//AF059580

R-PLACE1000481//Human DNA sequence from clone 960O17 on chromosome Xp11.21-11.22 Contains EST, CA repeat(DXS991), STS, GSS, complete sequence.//0.019:171:66//AL022166

R-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//3.2e-17:221:72//U35245

R-PLACE1000540//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00045:480:60//AC005308

R-PLACE1000547//Homo sapiens chromosome 19, cosmid F17987, complete sequence.//9.6e-32:231:85//AC004790

R-PLACE1000562//, complete sequence.//1.8e-45:280:92//AC005409

R-PLACE1000564//Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds.//0.0079:180:65//U41302

R-PLACE1000583//Homo sapiens chromosome 17, clone hRPK.799\_N\_11, complete sequence.//1.5e-37:414:74//AC005323

5 R-nnnnnnnnnnn//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//1.9e-77:542:82//M55542

R-PLACE1000596//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00019:482:59//AC005506

10 R-PLACE1000599//Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S2A1T, TCRBV6S5A1N1, TCRBV3S1P, TCRBV3S1S1, TCRBV13S5, TCRBV6S1A1N1, TCRBV32S1P, TCRBV5S5P, TCRBV1S1A1N1, TCRBV12S2A1T, TCRBV21S1, TCRBV8S4P, TCRBV12S3, TCRBV21S3A2N2T, TCRBV8S5P, TCRBV13S1 genes from bases 1 to 267156 (section 1 of 3).//5.6e-51:369:85//U66059

15 R-PLACE1000610//HS\_3071\_A1\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=9 Row=E, genomic survey sequence.//0.051:147:65//AQ103341

R-PLACE1000636//HS\_3220\_B2\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=18 Row=J, genomic survey sequence.//0.010:253:64//AQ181157

20 R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.6e-99:506:96//AF102265

R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//4.5e-101:559:92//AJ005896

R-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//9.1e-10:331:63//S78219

R-PLACE1000712//Homo sapiens full-length insert cDNA clone ZD76G10.//1.0e-69:345:98//AF086408

25 R-PLACE1000716//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//1.0:174:62//AC002300

R-PLACE1000748//Plasmodium falciparum MAL3P3, complete sequence.//1.0e-06:337:60//Z98547

R-PLACE1000749//cSRL-15g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-15g9, genomic survey sequence.//8.8e-26:236:80//B02791

30 R-PLACE1000755//HS\_2183\_B1\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=21 Row=P, genomic survey sequence.//0.47:151:65//AQ064202

R-PLACE1000769//Homo sapiens clone DJ0647J21, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.0e-38:492:74//AC004847

R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.6e-101:513:96//AB014548

35 R-PLACE1000786//Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds.//0.078:180:68//U58970

R-nnnnnnnnnnn

R-PLACE1000798//Homo sapiens cosmid D66B10, chromosome 21 5' of IFNAR1.//5.1e-26:348:72//AF039904

40 R-PLACE1000841//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//1.4e-26:110:95//U02081

R-nnnnnnnnnnn//Homo sapiens full-length insert cDNA clone ZD55D10.//1.4e-13:93:96//AF086334

R-PLACE1000856//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//2.7e-09:484:59//L04272

45 R-PLACE1000863

R-PLACE1000909//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.0e-05:274:60//AC005505

R-PLACE1000931//RPC11-66P7.TK RPC11 Homo sapiens genomic clone R-66P7, genomic survey sequence.//3.4e-73:369:97//AQ237489

50 R-PLACE1000948//RPC11-64K15.TK RPC11 Homo sapiens genomic clone R-64K15, genomic survey sequence.//6.6e-06:258:62//AQ239337

R-PLACE1000972//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//8.3e-20:223:76//AC005553

55 R-PLACE1000977//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00030:448:59//AC005506

R-PLACE1000979

R-PLACE1001000//CIT-HSP-229718.TF CIT-HSP Homo sapiens genomic clone 229718, genomic survey se-

quence.//7.0e-07:64.95//AQ004997

R-PLACE1001007//Human endothelial nitric oxide synthase gene, complete cds.//0.0078:215.64//D26607

R-PLACE1001010

R-PLACE1001015//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING

DRAFT SEQUENCE.//1.5e-16:452:63//AL022318

R-PLACE1001024//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING

DRAFT SEQUENCE.//0.99:186:63//AL024498

R-PLACE1001036//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.5e-15:313:68//AC005377

R-PLACE1001062//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.3e-16:119:84//AC003664

R-PLACE1001076

R-PLACE1001088//Human DNA sequence from cosmid 203C2, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.97:332:59//Z74696

R-PLACE1001092//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.2e-07:302:62//AC005139

R-PLACE1001104//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//0.057:280:60//AE001372

R-PLACE1001118//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.9e-06:334:60//Z84480

R-PLACE1001136//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-31:331:75//AC005412

R-PLACE1001168//HS\_2036\_A1\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=7 Row=O, genomic survey sequence.//0.40:144:63//AQ230662

R-PLACE1001171

R-PLACE1001185

R-PLACE1001238//Human coxVib gene, last exon and flanking sequence.//3.4e-36:349:76//X58139

R-PLACE1001241//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete sequence.//0.11:258:61//AL008972

R-PLACE1001257//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B4P3; HTGS phase 1, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-46:484:73//AC000016

R-PLACE1001272//Homo sapiens chromosome 21q22.3 PAC 191P10, complete sequence.//0.89:119:65//AF045448

R-PLACE1001279//Caenorhabditis elegans cosmid Y39A1C, complete sequence.//0.99:95:69//AL023839

R-PLACE1001280//CIT-HSP-2328B24.TF CIT-HSP Homo sapiens genomic clone 2328B24, genomic survey sequence.//5.4e-24:147:76//AQ042129

R-PLACE1001294//M.musculus GEG-154 mRNA.//1.3e-22:472:65//X71642

R-PLACE1001304//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-22:139:77//AC003682

R-PLACE1001311//Loligo pealei repeat region.//0.84:232:64//Z18286

R-PLACE1001323//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//7.2e-39:308:83//Z84480

R-PLACE1001351//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y39B6, WORKING DRAFT SEQUENCE.//0.0018:408:59//Z95399

R-PLACE1001366//Human Na<sup>+</sup>/phosphate co-transporter gene, exon 1, partial sequence.//2.2e-46:369:82//D89927

R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//7.1e-80:431:93//AF009615

R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence.//3.6e-35:192:97//AF055030

R-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//2.6e-86:456:94//AJ001319

R-PLACE1001387

R-PLACE1001395//Nyctalus leisleri mitochondrial D-loop, partial sequence.//0.054:148:68//U95355

R-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//6.7e-70:352:98//AC005412

R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//8.0e-44:242:95//AF091087

R-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//0.12:53:84//AC006241



- R-PLACE1001440//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na<sup>+</sup>-isocitrate dehydrogenase gamma subunit (IDH), and translocan-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq281u1 gene and cytochrome C (CCp) pseudogene.//1.0:250:61//U52111
- 5 R-PLACE1001456//Borrelia burgdorferi (section 16 of 70) of the complete genome.//0.0077:173:62//AE001130
- R-PLACE1001468//HS\_3050\_A2\_D07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=14 Row=G, genomic survey sequence.//0.00023:202:65//AQ133920
- R-PLACE1001484//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//7.2e-17:180:80//AC002368
- 10 R-PLACE1001502//RPC11-24F2.TP RPC1-11 Homo sapiens genomic clone RPC1-11-24F2, genomic survey sequence.//0.15:203:66//B84401
- R-PLACE1001503//HS\_2183\_A1\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=19 Row=C, genomic survey sequence.//1.3e-38:181:82//AQ022613
- R-PLACE1001517//Homo sapiens hGAA1 mRNA, complete cds.//6.4e-56:339:90//AB006969
- 15 R-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//8.6e-59:304:97//AL031667
- R-PLACE1001545//Homo sapiens chromosome 3, clone hRPC.165\_1\_16, complete sequence.//2.6e-18:171:82//AC 005669
- R-PLACE1001551
- 20 R-PLACE1001570//M.capricolum DNA for CONTIG MC188.//0.0043:305:57//Z33135
- R-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//2.5e-82:408:98//AB020860
- R-PLACE1001603//Homo sapiens KE05 protein mRNA, complete cds.//1.5e-40:295:84//AF064605
- R-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.5e-39:307:82//AC005037
- 25 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//4.9e-41:217:97//AF054174
- R-PLACE1001632//Homo sapiens DNA binding protein (HPF2) mRNA, complete cds.//1.4e-08:178:65//M27878
- R-PLACE1001634//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone H06C16, WORKING DRAFT SEQUENCE.//0.00026:221:62//Z92791
- 30 R-PLACE1001640//Homo sapiens chromosome 17, clone hRPC.651\_L\_9, complete sequence.//2.6e-83:441:95//AC005971
- R-PLACE1001672//H.sapiens flow-sorted chromosome 6 Tagl fragment, SC6pA26H8.//0.91:115:69//Z79253
- R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.5e-111:545:97//AF069250
- 35 R-PLACE1001692//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.0e-46:478:75//AC005077
- R-PLACE1001705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SEQUENCE.//0.79:91:73//Z99716
- R-PLACE1001716//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//0.96:172:66//AC002349
- 40 R-PLACE1001720
- R-PLACE1001729//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.79:280:60//U31120
- R-PLACE1001739//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.0:109:65//AC005261
- 45 R-PLACE1001740//Homo sapiens BAC clone GS114109 from 7p14-p15, complete sequence.//5.3e-11:249:67//AC006027
- R-PLACE1001745
- R-PLACE1001746//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//6.0e-05:337:61//AC005009
- 50 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-91:540:89//AF061243
- R-PLACE1001756//Human BAC clone RG302F04 from 7q31, complete sequence.//0.074:344:62//AC002463
- R-PLACE1001761
- R-PLACE1001771//Homo sapiens full-length insert cDNA clone ZD79C11.//4.4e-57:298:96//AF086426
- R-PLACE1001781//T.thermophila micronuclear DNA containing to chromosomal breakage sequence Cbs1, clone Tt819.//4.6e-05:282:61//M15711
- 55 R-PLACE1001799//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.015:331:58//AC004710
- R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//

4. 1e-92:463:95//AF058953

R-PLACE1001821//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//3.6e-36:281:82//U14567  
R-PLACE1001845//Mus musculus Paneth cell enhanced expression PCEE mRNA, complete cds.//9.1e-26:313:73//U37351

R-PLACE1001869

R-PLACE1001897//Mus musculus homeobox protein (D1x5) mRNA, complete cds.//0.0043:207:64//AF033011  
R-PLACE1001912//RPC11-25F23.TKBR RPC1-11 Homo sapiens genomic clone RPC1-11-25F23, genomic survey sequence.//6.3e-33:248:67//AQ013567

R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//5.0e-73:363:98//AF070671  
R-PLACE1001923//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//0.98:248:60//AC005245

R-PLACE1001983//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y40H7, WORKING DRAFT SEQUENCE.//0.12:157:61//AL021389

R-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.4e-44:376:80//AL023755

R-PLACE1002046//CITBI-E1-2520J24.TF CITBI-E1 Homo sapiens genomic clone 2520J24, genomic survey sequence.//4.5e-20:144:89//AQ280117

R-PLACE1002052//Human DNA sequence from cosmid U160A4, between markers DXS366 and DXS87 on chromosome X contains STS.//0.025:362:57//Z80900

R-PLACE1002066//Leishmania tarentolae maxicircle DNA fragment.//0.0034:197:62//X02438

R-PLACE1002072//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//9.7e-06:414:60//AC004763

R-PLACE1002073

R-PLACE1002090//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence, complete sequence.//1.8e-06:278:63//AC002302

R-PLACE1002115//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//6.0e-12:327:64//AL022344

R-PLACE1002119//Mus musculus IERS (Ier5) mRNA, complete cds.//5.1e-67:442:86//AF079527

R-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1.

Contains ESTs, STSs and GSSs, complete sequence.//2.2e-80:403:97//AL022162 R-PLACE1002150//Human DNA sequence from PAC 145B12 on chromosome Xq27-Xq28. Contains EST, CA repeat and STS.//0.043:455:59//U008706

R-PLACE1002157//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//9.8e-58:384:79//Z83849

R-PLACE1002163//Canis familiaris MHC class IIA DLA-DQA (DQA 1 allele) gene, exon 2, partial cds.//0.82:96:70//U44785

R-PLACE1002171//Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence.//0.83:196:65//AC004456

R-PLACE1002205//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR1). Contains ESTs, an STS and GSSs, complete sequence.//0.0017:193:61//Z94056

R-PLACE1002213//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//8.0e-42:330:81//AC004152

R-PLACE1002227//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//2.1e-10:126:80//AC003071

R-PLACE1002256//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.7e-06:478:57//AC004907

R-PLACE1002259//Human DNA sequence from cosmid U75A4 on chromosome X.//6.5e-81:501:88//Z82255

R-PLACE1002319//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00023:549:58//AC005505

R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//4.9e-94:501:93//AB018271

R-PLACE1002395//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//1.4e-69:385:93//AC005329

R-PLACE1002399//Human HepG2 3' region cDNA, clone hmd5d06.//2.4e-71:411:92//D16939

R-PLACE1002433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//0.85:176:63//AL031984

- R-PLACE1002437//Human BAC clone RG114A06 from 7q31, complete sequence.//0.0040:213:63//AC002542  
 R-PLACE1002438//CITBI-E1-2501M20.TF.1 CITBI-E1 Homo sapiens genomic clone 2501M20, genomic survey sequence.//0.70:247:61//AQ242104
- 5 R-PLACE1002450//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3.//0.0060:471:59//AJ229041  
 R-PLACE1002465//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//2.5e-10:98.81//AC004854  
 R-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.7e-25:199:71//U69262
- 10 R-PLACE1002477//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.2e-11:382:63//Z92545  
 R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.1e-53:307:91//AF042273  
 R-PLACE1002499//Plasmodium falciparum MAL3P6, complete sequence.//0.56:270:60//Z98551
- 15 R-PLACE1002500//CIT-HSP-2337C20.TR CIT-HSP Homo sapiens genomic clone 2337C20, genomic survey sequence.//3.2e-42:297:85//AQ037614  
 R-PLACE1002514//Human DNA Sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING DRAFT SEQUENCE.//7.8e-16:221:73//Z95114  
 R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.1e-86:582:85//AB018256
- 20 R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//9.0e-91:453:97//AC004774  
 R-PLACE1002537//Hansenuia wingel mitochondrial gene for NADH dehydrogenase subunit 5, complete cds.//0.0042:489:60//D16253  
 R-PLACE1002571//Apis mellifera ligustica complete mitochondrial genome.//0.034:493:55//L06178
- 25 R-PLACE1002578//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//2.5e-44:292:84//AC006084  
 R-PLACE1002583//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//3.1e-17:517:61//AF045555  
 R-PLACE1002591
- 30 R-PLACE1002598//Caenorhabditis elegans cosmid Y37D8A, complete sequence.//0.080:308:60//AL032626  
 R-PLACE1002604//Human cosmid LL12NC01-88A9, ETV6 gene, exons 6, 7 and 8 and partial cds.//0.0013:176:65//U63313  
 R-PLACE1002625//HS\_2233\_B2\_H04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=8 Row=P, genomic survey sequence.//5.2e-13:137:79//AQ146663
- 35 R-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//5.8e-46:272:94//AF079765  
 R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//1.2e-77:390:97//AF068180  
 R-PLACE1002714//Mus musculus clone OST2473, genomic survey sequence.//1.3e-35:328:78//AF046656
- 40 R-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-42:276:89//I73723  
 R-PLACE1002768//Homo sapiens Xp22 bins 169-171 BAC GSHB-383H3 (Genome Systems Human BAC Library) complete sequence.//0.0098:197:64//AC005185  
 R-PLACE1002772//Homo sapiens PAC clone DJ0560O14 from 7q21.1-q21.2, complete sequence.//6.7e-49:378:82//AC008145
- 45 R-PLACE1002782  
 R-PLACE1002794  
 R-PLACE1002811//CIT-HSP-2316H11.TF CIT-HSP Homo sapiens genomic clone 2316H11, genomic survey sequence.//6.0e-50:250:100//AQ034981  
 R-PLACE1002815//Sequence 2 from patent US 5747660.//2.7e-59:312:84//AR005279
- 50 R-PLACE1002816//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.3e-59:339:93//AC004466  
 R-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and-9.//1.4e-78:413:95//M27877  
 R-PLACE1002839//Homo sapiens PAC clone DJ0015123 from 22, complete sequence.//6.5e-25:301:74//AC004819
- 55 R-PLACE1002851//CIT-HSP-2317M9.TR CIT-HSP Homo sapiens genomic clone 2317M9, genomic survey sequence.//0.0011:210:61//AQ040519  
 R-PLACE1002853//Human Interleukin 6 (IL6) gene, 3' flank.//5.8e-06:327:61//J03049

- R-PLACE1002881  
R-PLACE1002908//HS\_3064\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=7 Row=G, genomic survey sequence.//1.9e-09:156:72//AQ142985  
R-PLACE1002941  
5 R-PLACE1002962  
R-PLACE1002968//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPAR $\delta$  for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//1.9e-32:314:77//AL022721  
10 R-PLACE1002991//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.6e-42:343:81//AL023755  
R-PLACE1002993//Homo sapiens PAC clone DJ0899E09 from 7q11.23-q21.1, complete sequence.//0.56:88:72//AC004921  
15 R-PLACE1002996//HS\_2064\_A1\_A05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=9 Row=A, genomic survey sequence.//4.9e-18:117:95//AQ243211  
R-PLACE1003025//Homo sapiens PAC clone DJ0560O14 from 7q21.1-q21.2, complete sequence.//0.26:428:58//AC006145  
20 R-PLACE1003027//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.3e-95:465:98//AC005920  
R-PLACE1003044  
R-PLACE1003092//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//3.6e-05:358:60//AL010266  
R-PLACE1003100//HS\_2244\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2244 Col=24 Row=O, genomic survey sequence.//2.3e-42:288:86//AQ084224  
25 R-PLACE1003108//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00066:233:61//AC004885  
R-PLACE1003136//Plasmodium falciparum MAL3P2, complete sequence.//0.019:429:57//AL034558  
R-PLACE1003145  
30 R-PLACE1003153//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//3.2e-05:390:58//AC004616  
R-PLACE1003174//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence.//2.4e-06:390:60//AB015479  
R-PLACE1003176  
35 R-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-78:406:81//AC005095  
R-PLACE1003200//Plasmodium falciparum MAL3P6, complete sequence.//0.016:411:57//Z98551  
R-PLACE1003205//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00084:288:61//AC005139  
40 R-PLACE1003238//Homo sapiens full-length insert cDNA clone ZD79H11.//7.6e-114:567:96//AF086432  
R-PLACE1003249//Human Chromosome X, complete sequence.//1.3e-45:317:85//AC002416  
R-PLACE1003256//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//1.0e-45:328:85//AC004099  
R-PLACE1003258  
45 R-PLACE1003296//Diphropia sp. 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence.//0.050:228:59//U39952  
R-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, 2, and-9.//1.7e-91:458:96//M27877  
R-PLACE1003334//Homo sapiens DNA sequence from BAC 217C2 on chromosome 22q13-q3.33. Contains a gene for the presumptive isolog of Rat RTP60 (nuclear pore complex protein Np60). Contains ESTs, complete sequence.//4.3e-34:370:71//Z82243  
50 R-PLACE1003342//CIT-HSP-2311D21.TF CIT-HSP Homo sapiens genomic clone 2311D21, genomic survey sequence.//1.0:159:68//AQ020460  
R-PLACE1003343//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-05:330:61//AC004153  
55 R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//3.4e-98:469:98//U92715  
R-PLACE1003361

R-PLACE1003366//Homo sapiens CAG repeated sequence.//0.018:319:61//AJ006805  
 R-PLACE1003369//T18H17-T7 TAMU Arabidopsis thaliana genomic clone T18H17, genomic survey sequence.//0.050:155:63//B20174  
 R-PLACE1003373//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, complete sequence.//1.2e-62:434:83//AC004771  
 R-PLACE1003375//Dictyostellum discoideum golvesin (gol) gene, complete cds.//0.042:263:57//U89350  
 R-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//1.7e-83:429:96//AB020878  
 R-PLACE1003401//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//2.4e-13:175:76//AC005695  
 R-PLACE1003420//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//2.1e-05:340:61//AC005587  
 R-PLACE1003454//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, complete sequence.//0.47:411:58//AL009014  
 R-PLACE1003478//M.capricolum DNA for CONTIG MC175.//0.51:253:59//Z33125  
 R-PLACE1003493//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//4.6e-37:319:81//AC006080  
 R-PLACE1003516//CIT-HSP-2295M19.TF CIT-HSP Homo sapiens genomic clone 2295M19, genomic survey sequence.//1.0e-40:251:90//AQ007480  
 R-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//2.7e-29:163:89//AF064859  
 R-PLACE1003521//HS\_3252\_A2\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=10 Row=M, genomic survey sequence.//0.00017:274:60//AQ221562  
 R-PLACE1003528//HS\_2041\_B1\_B07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=13 Row=D, genomic survey sequence.//6.6e-40:219:83//AQ230483  
 R-PLACE1003537//Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes, and unidentified reading frames A61, 2 and 3.//8.3e-05:300:61//J01404  
 R-PLACE1003553//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.7e-87:450:96//AL031297  
 R-PLACE1003566  
 R-PLACE1003575//Homo sapiens chromosome 16, cosmid clone 325D7, complete sequence.//4.7e-20:148:78//AC003965  
 R-PLACE1003583//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//3.5e-18:287:68//Z99571  
 R-PLACE1003584  
 R-PLACE1003592//Homo sapiens cosmid 223D9 from Xq28, complete sequence.//2.5e-10:153:73//AF061032  
 R-PLACE1003593//Human BAC clone RG030H15 from 7q31, complete sequence.//6.9e-07:240:65//AC002066  
 R-PLACE1003596//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y87G2, WORKING DRAFT SEQUENCE.//0.13:393:60//AL022597  
 R-PLACE1003602//Homo sapiens mRNA expressed in placenta.//2.4e-95:576:88//D83200  
 R-PLACE1003605//Homo sapiens BAC clone RG331C24 from 7q21, complete sequence.//2.9e-19:302:71//AC002081  
 R-nnnnnnnnnnn  
 R-PLACE1003618//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191E19, WORKING DRAFT SEQUENCE.//8.3e-57:469:80//AL034451  
 R-PLACE1003625//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.1e-05:339:62//AC004688  
 R-PLACE1003638//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE.//2.5e-38:279:84//AL022312  
 R-PLACE1003669//HS\_3054\_A2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=14 Row=I, genomic survey sequence.//0.014:265:61//AQ132713  
 R-PLACE1003704//HS\_3213\_A1\_D12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=23 Row=G, genomic survey sequence.//0.80:195:61//AQ176784  
 R-PLACE1003709//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//0.018:152:61//AC002067  
 R-PLACE1003711//Human endothelial nitric oxide synthase gene, complete cds.//1.7e-61:366:89//D26607  
 R-PLACE1003723//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//2.7e-

- 44:505:73//AL022336  
 R-PLACE1003738//H.sapiens DNA sequence.//0.93:185:60//Z22357  
 R-PLACE1003760//Human globin gene.//5.9e-97:538:91//M69023  
 R-PLACE1003762//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//4.6e-13:134:79//  
 5 AC003070  
 R-PLACE1003768//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//5.4e-12:189:  
 71//AC005919  
 R-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//1.7e-119:619:95//  
 10 AC004160  
 R-PLACE1003783  
 R-PLACE1003784//Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.//5.6e-15:  
 204:74//AC004659  
 R-PLACE1003795//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey se-  
 quence.//7.0e-37:234:89//AQ114933  
 15 R-PLACE1003833//Homo sapiens full-length insert cDNA clone ZE15C06.//4.4e-59:313:95//AF086558  
 R-PLACE1003850  
 R-PLACE1003858  
 R-nnnnnnnnnnn  
 R-PLACE1003870//Homo sapiens Chromosome 22q11.2 Cosmid Clone 15a10 In DGCR Region, complete se-  
 20 quence.//8.7e-33:285:81//AC000072  
 R-nnnnnnnnnnn  
 R-PLACE1003886  
 R-PLACE1003888//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//0.73:127:65//  
 AC004069  
 25 R-PLACE1003900//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//1.9e-05:239:59//L78810  
 R-PLACE1003903//Homo sapiens full-length insert cDNA clone ZD78D11.//8.1e-74:369:97//AF086422  
 R-PLACE1003915//Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete  
 cds.//0.56:247:61//U73520  
 R-PLACE1003923//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.67:213:63//Z99281  
 30 R-PLACE1003932//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//8.7e-49:  
 342:85//Z74022  
 R-PLACE1003936//H.sapiens gene for ventricular myosin light chain 2.//2.6e-09:394:61//Z15030  
 R-PLACE1003968//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-62, complete  
 35 sequence.//1.3e-07:245:65//AL010247  
 R-PLACE1004104  
 R-PLACE1004114//Human PAC clone RG212D03, complete sequence.//5.0e-07:336:61//AC002485  
 R-PLACE1004118//HS\_3092\_B1\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2253 Col=1 Row=D, genomic survey sequence.//0.80:207:60//AQ128151  
 40 R-PLACE1004128//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//1.8e-  
 06:193:66//AF022085  
 R-PLACE1004149//HS\_2253\_A2\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=2253 Col=22 Row=K, genomic survey sequence.//2.4e-59:315:95//AQ129711  
 R-PLACE1004156//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC  
 Library) containing Arylsulfatase D and E genes, complete sequence.//8.3e-53:299:76//AC005295  
 45 R-PLACE1004161  
 R-PLACE1004183//Homo sapiens for TOM1-like protein.//1.3e-80:434:93//AJ010071  
 R-PLACE1004197//RPCI11-69N15.TK RPCI11 Homo sapiens genomic clone R-69N15, genomic survey se-  
 quence.//0.0078:170:65//AQ265515  
 50 R-PLACE1004203//Homo sapiens semaphorin L (SEMAL) mRNA, complete cds.//3.4e-105:501:98//AF030698  
 R-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic  
 marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//6.1e-65:373:86//  
 AL021326  
 R-PLACE1004256//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.011:383:  
 61//AC006031  
 55 R-PLACE1004257//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete  
 sequence.//3.4e-09:576:59//AC004470  
 R-PLACE1004258//HS\_3034\_A1\_B12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3034 Col=23 Row=C, genomic survey sequence.//1.4e-35:359:77//AQ128936

- R-PLACE1004270//CITBI-E1-2504K14.TR CITBI-E1 Homo sapiens genomic clone 2504K14, genomic survey sequence.//2.7e-06:150:74//AQ261108
- R-PLACE1004274//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//0.025:116:72//AC005234
- 5 R-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//4.4e-106:581:91//AF084830
- R-PLACE1004284//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.59:231:60//AC005308
- R-PLACE1004289//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//5.8e-31:340:75//AC005920
- 10 R-PLACE1004302//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.4e-90:572:86//AC005095
- R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//1.9e-113:590:94//Y11588
- R-PLACE1004336//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING DRAFT SEQUENCE.//2.3e-65:292:82//AL033383
- 15 R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//2.4e-70:379:93//AF100153
- R-PLACE1004376//CIT-HSP-2287M8.TF CIT-HSP Homo sapiens genomic clone 2287M8, genomic survey sequence.//0.47:173:61//AQ000837
- R-PLACE1004384//CIT-HSP-2316J11.TF CIT-HSP Homo sapiens genomic clone 2316J11, genomic survey sequence.//0.035:109:69//AQ037817
- 20 R-PLACE1004388//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-82, complete sequence.//4.2e-06:381:60//AL010149
- R-PLACE1004405//Homo sapiens clone GS512121, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.20:270:60//AC005027
- 25 R-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//1.3e-96:516:94//AC005532
- R-PLACE1004428//Human DNA sequence from clone 888M10 on chromosome 1p36.11-36.31 Contains part of gene KIAA0453, EST, STS, GSS, complete sequence.//5.8e-10:279:65//AL031296
- R-PLACE1004437//Homo NAD<sup>+</sup>-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.9e-88:516:88//U49283
- 30 R-PLACE1004451//HS\_2258\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=L, genomic survey sequence.//0.82:172:61//AQ221189
- R-PLACE1004460
- R-PLACE1004467//Syrian hamster carbamoylphosphate synthetase-aspartate transcarbamylasedihydroorotase (CAD) gene, exons 1 and 2.//1.2e-24:311:62//M31621
- 35 R-PLACE1004471//Homo Sapiens Chromosome X clone bWXD75, complete sequence.//2.1e-34:333:70//AC004389
- R-PLACE1004473
- R-PLACE1004491//Drosophila melanogaster Oregon-R mitochondrial A+T region.//1.0e-08:485:60//U11584
- 40 R-PLACE1004506
- R-PLACE1004510//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//0.0094:543:56//AE001427
- R-PLACE1004516//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.00011:343:59//AC003071
- 45 R-PLACE1004518
- R-PLACE1004548//Homo sapiens Xp22 BAC GS-551O19 (Genome Systems Human BAC library) and cosmids U199A7 and U209F2 (Lawrence Livermore X chromosome cosmid library) containing part of human chloride channel 4 gene, complete sequence.//4.9e-40:245:80//AC003666
- R-PLACE1004550
- 50 R-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.7e-82:532:86//X75931
- R-PLACE1004629//Homo sapiens chromosome 7 clone UWGC:g3586a230 from 7p14-15, complete sequence.//0.015:437:59//AC004800
- R-PLACE1004645//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.033:76:75//AQ110136
- 55 R-PLACE1004646//Homo sapiens cosmid 120C12 from Xq28, complete sequence.//2.0e-23:237:79//AF036876
- R-PLACE1004658//Homo sapiens Chromosome 12p13.3 BAC RPC111-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.1e-09:94:87//AC005343
- R-nnnnnnnnnnn//RPC111-79G23.TV RPC111 Homo sapiens genomic clone R-79G23, genomic survey se-

quence.//2.2e-81:433:94//AQ283692

R-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//2.7e-24:263:74//U07561

R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.1e-89:513:91//AF035606

R-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.3e-96:498:95//AB020860

R-PLACE1004686

R-PLACE1004691//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 2/11.//2.1e-33:290:80//AB020859

R-PLACE1004693//Caenorhabditis elegans cosmid Y2H9A, complete sequence.//1.0:195:60//AL021448

R-PLACE1004716//CITBI-E1-2519C14. TR CITBI-E1 Homo sapiens genomic clone 2519C14, genomic survey sequence.//5.0e-43:245:93//AQ276965

R-PLACE1004722//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0022:360:60//AC005507

R-PLACE1004736

R-PLACE1004740

R-nnnnnnnnnnn//Homo sapiens ubiquitin-protein ligase E3-alpha (UBR1) mRNA, partial cds.//5.4e-105:575:92//AF061556

R-PLACE1004751//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//9.0e-26:317:76//AC002523

R-PLACE1004773//Homo sapiens Inversin protein mRNA, complete cds.//8.5e-88:437:96//AF084367

R-PLACE1004777//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.050:138:65//AP000010

R-PLACE1004793//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR.//5.1e-58:313:80//U60269

R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds.//5.8e-98:580:88//AB011178

R-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.3e-09:256:64//AC005140

R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//3.5e-107:358:99//AF069250

R-PLACE1004815//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//3.8e-61:353:89//AC004126

R-PLACE1004824//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.7e-42:364:79//AC004666

R-PLACE1004827//Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC library) contains Bmx gene, complete sequence.//2.7e-14:156:79//AC003669

R-PLACE1004836//HS\_2270\_A2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=20 Row=O, genomic survey sequence.//8.6e-51:267:96//AQ164110

R-PLACE1004838//CIT-HSP-2343E10. TR CIT-HSP Homo sapiens genomic clone 2343E10, genomic survey sequence.//0.071:168:63//AQ058544

R-PLACE1004840//Sequence 4 from patent US 5728819.//1.6e-26:150:98//I92820

R-PLACE1004868//Human Chromosome X clone bWDX342, complete sequence.//0.57:344:59//AC004072

R-PLACE1004885//HS\_3235\_B2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=14 Row=J, genomic survey sequence.//1.1e-38:175:78//AQ210193

R-PLACE1004900//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.0e-44:334:84//AL022577

R-PLACE1004902

R-nnnnnnnnnnn//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//7.7e-58:377:87//Z82209

R-PLACE1004918//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.00084:373:60//AC004605

R-PLACE1004930//Homo sapiens MDC-3.13 isoform 1 mRNA, complete cds.//2.0e-100:532:93//AF099936

R-PLACE1004934//Homo sapiens clone RG062N11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00030:198:66//AC005683

R-PLACE1004937//Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds.//1.3e-13:367:61//AF020788



- R-PLACE1004969//Human DNA sequence from clone LUCA7 on chromosome 3, complete sequence.//0.97:116:71//Z84494
- R-PLACE1004972
- R-PLACE1004979//Plasmodium falciparum MAL3P4, complete sequence.//0.74:304:60//AL008970
- 5 R-PLACE1004982//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:495:57//AC005308
- R-PLACE1004985//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE.//2.5e-10:410:60//AL033522
- 10 R-PLACE1005026//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.7e-56:158:99//AC004925
- R-PLACE1005027
- R-PLACE1005046//Homo sapiens chromosome 19, cosmid F20237, complete sequence.//3.1e-63:438:86//AC005775
- R-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//6.1e-87:301:98//AC005867
- 15 R-PLACE1005066//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//1.1e-09:453:61//AL023584
- R-PLACE1005077//H.sapiens genes for semenogelin I and semenogelin II.//2.6e-05:199:66//Z47556
- 20 R-PLACE1005085//Homo sapiens chromosome 17, clone hRPK.293\_K\_20, complete sequence.//2.1e-42:384:69//AC005495
- R-PLACE1005086//RPCI11-30H10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30H10, genomic survey sequence.//0.13:112:67//B87788
- R-PLACE1005101//Homo sapiens (clone zap126) mRNA, 3' end of cds.//2.5e-97:531:92//L40401
- 25 R-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//1.3e-91:504:92//AC004476
- R-PLACE1005108//Homo sapiens BAC129, complete sequence.//4.0e-28:232:84//U85195
- R-PLACE1005111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 566H6, WORKING DRAFT SEQUENCE.//3.0e-18:174:74//AL031845
- 30 R-PLACE1005128
- R-PLACE1005146
- R-PLACE1005162//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.4e-07:273:61//AC005140
- R-nnnnnnnnnnn//Rat alternatively spliced mRNA.//8.1e-20:185:82//M93018
- 35 R-PLACE1005181//HS\_2182\_B2\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=10 Row=D, genomic survey sequence.//4.9e-05:193:65//AQ030787
- R-PLACE1005187//Arabidopsis thaliana chromosome II BAC T14A4 genomic sequence, complete sequence.//0.00073:264:60//AC006161
- R-PLACE1005206//Homo sapiens full-length insert cDNA YN66A06.//6.3e-64:343:93//AF075043
- 40 R-PLACE1005232//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 25J6, WORKING DRAFT SEQUENCE.//1.3e-34:286:81//Z84476
- R-PLACE1005243
- R-PLACE1005261//Caenorhabditis elegans cosmid ZK666, complete sequence.//0.66:180:60//Z49132
- R-PLACE1005266//Homo sapiens clone RG122E10, complete sequence.//1.3e-15:166:78//AC005067
- 45 R-PLACE1005277//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence.//2.5e-34:358:74//AQ265720
- R-PLACE1005287//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//4.1e-07:495:60//AL031744
- R-PLACE1005305//HS\_3180\_B2\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=H, genomic survey sequence.//1.1e-42:308:85//AQ169443
- 50 R-PLACE1005308
- R-PLACE1005313//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.00048:320:60//AC000383
- R-PLACE1005327//chromosome 1 specific transcript KIAA0491.//5.4e-103:537:94//AB007960
- 55 R-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//2.2e-94:536:91//AC004794
- R-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.3e-32:313:79//AC000380

- R-PLACE1005373//Homo sapiens BAC129, complete sequence.//8.8e-10:229:68//U85195  
 R-PLACE1005374//Homo sapiens chromosome 17, clone hRPK.401\_O\_9, complete sequence.//3.0e-44:434:77//AC005291
- 5 R-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//8.8e-105:529:96//AC003991  
 R-PLACE1005453//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.7e-39:302:82//AC002477
- 10 R-PLACE1005467//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING DRAFT SEQUENCE.//1.1e-40:328:81//Z93014  
 R-PLACE1005471//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//6.4e-68:409:90//AL022310
- 15 R-PLACE1005477//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//0.020:216:66//AL023693  
 R-PLACE1005480//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//2.8e-44:327:70//AC005392
- R-PLACE1005481//Homo sapiens-chromosome 17, clone hRPC.1164\_O\_3, complete sequence.//4.2e-23:284:74//AC004703
- 20 R-PLACE1005494//Danio rerio homeobox protein LIM-3 (lim3) gene, exon 4.//0.19:468:60//AF031631  
 R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.6e-55:277:98//AF071185
- R-PLACE1005526//Human mRNA for alpha-1 type II collagen.//0.10:227:63//X16468  
 R-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.3e-76:395:96//AP000038
- 25 R-PLACE1005530//C.familialis CA repeat sequence (isolate ).//0.023:90:75//X86184  
 R-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH1, genomic survey sequence.//2.0e-09:235:64//AL025928
- R-PLACE1005554//Homo sapiens chromosome 17, clone hRPK.215\_P\_18, complete sequence.//0.069:305:60//AC005969
- 30 R-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//4.3e-105:587:91//AC004707  
 R-PLACE1005574//Human BAC 367D17 from chromosome 18, complete sequence.//1.5e-17:274:67//AC003971
- R-PLACE1005584//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//2.7e-15:191:77//AC004991
- 35 R-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//6.4e-90:453:96//AC004126  
 R-PLACE1005603//Homo sapiens cosmid clone U169D2 from Xp22.1-22.2, complete sequence.//0.69:322:61//U72788
- R-PLACE1005611//Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds.//0.059:473:56//U42599
- 40 R-PLACE1005623//Homo sapiens full-length insert cDNA clone ZD76B03.//1.6e-113:575:95//AF086405  
 R-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-79:270:94//AC005840
- R-PLACE1005639//Human BAC clone RG022J17 from 7q21, complete sequence.//8.2e-56:441:83//AC002382
- 45 R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//3.2e-110:585:93//AF083255  
 R-PLACE1005656//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//8.6e-08:505:58//AC005701
- R-PLACE1005666//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//3.2e-27:307:72//Z82203
- 50 R-PLACE1005698//344B22.TV CIT978SKA1 Homo sapiens genomic clone A-344B22, genomic survey sequence.//0.030:91:70//B15144  
 R-PLACE1005727//Human variable number tandem repeat (VNTR) region, allele 17R1 3' to collagen type II (COL2A1) gene.//5.2e-10:587:59//L10171
- R-PLACE1005730//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//0.0039:239:58//L78810
- 55 R-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.2e-21:270:72//U15635  
 R-PLACE1005755//Caenorhabditis elegans cosmid M03F4.//6.9e-08:219:64//U64601
- R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds.//1.0e-45:268:87//ID42087
- R-PLACE1005799//Human X chromosome mRNA for CCG1 protein inv. in cell proliferation.//0.030:91:78//X07024
- R-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.4e-69:391:92//

AC004827

R-PLACE1005803

R-PLACE1005804//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//1.8e-21:175.75//AC002530

5 R-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.9e-56:333.91//AC004150

R-PLACE1005834//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.020:513.55//AL031745

10 R-PLACE1005845//Rabbit mRNA for protein phosphatase 2A-beta.//1.8e-10:182.69//Y00763 R-PLACE1005850 R-PLACE1005851//Homo sapiens clone DJ0789I05, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-06:318.63//AC004887

R-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//6.7e-28:366.72//X75931 R-PLACE1005884//Human DNA sequence from cosmid V526F1, between markers DXS366 and DXS87 on chromosome X contains STS.//1.0e-06:306.64//Z70281

15 R-PLACE1005898//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0094:449.59//AC005139

R-PLACE1005921//CITBI-E1-2509N21.TF CITBI-E1 Homo sapiens genomic clone 2509N21.-genomic survey sequence.//4.8e-84:494.89//AQ261347

20 R-PLACE1005923//RPCI11-65N9.TJ RPCI11 Homo sapiens genomic clone R-65N9, genomic survey sequence.//8.3e-97:520.93//AQ237243

R-PLACE1005925//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//5.2e-67:578.78//AL022719

25 R-PLACE1005932//Caenorhabditis elegans cosmid Y52B11A, complete sequence.//0.0035:176.62//AL032654 R-PLACE1005934

R-PLACE1005936//Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence.//0.00021:272.62//AF069716

26 R-PLACE1005951 R-PLACE1005953//Caenorhabditis elegans cosmid F09E5.//1.3e-07:349.60//U37429

R-PLACE1005955//Human HepG2 3' region MboI cDNA, clone hmd1d01m3.//8.3e-08:128.70//D17131

30 R-PLACE1005966//Pontia protodice large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//7.0e-09:549.59//AF044863

R-PLACE1005968//Rattus norvegicus mRNA for p47, complete cds.//1.1e-51:394.81//AB002086

35 R-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//4.4e-63:369.91//AC005866

R-PLACE1006002//Human cosmid CRI-JC2015 at D10S289 in 10p13.//5.9e-27:299.74//U15177

40 R-PLACE1006003//Mus musculus clone OST18050, genomic survey sequence.//3.5e-07:164.67//AF046375 R-PLACE1006011//Mus musculus poly-(ADPribose)-transferase homolog PARP mRNA, complete cds.//1.1e-32:266.83//AF072521

R-PLACE1006017//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31e In DGCR Region, complete sequence.//1.8e-17:164.82//AC000077

45 R-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//2.0e-49:557.72//U01139 R-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.3e-13:128.81//X99806

R-PLACE1006076//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.3e-18:220.74//AC004885

R-PLACE1006119//Plasmodium berghei (STRAIN ANKA) gamma-GCS gene, complete CDS.//0.0050:271.63//AJ005122

R-PLACE1006129//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//0.43:178.65//AC005454

50 R-PLACE1006139//Homo sapiens PAC clone DJ0658J06 from 7q33-q35, complete sequence.//7.5e-13:222.68//AC004849

R-PLACE1006143//Plasmodium falciparum MAL3P6, complete sequence.//0.00019:455.59//Z98551

R-PLACE1006157//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.00018:351.60//AL034557

55 R-PLACE1006159//Homo sapiens chromosome 10 clone LA10NC01\_124\_D\_3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.0e-113:586.96//AC006103

R-PLACE1006164//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.0e-

- 28.342:75//U91328  
 R-PLACE1006167//Homo sapiens full-length insert cDNA clone ZE14E04.//4.6e-77:426:93//AF086555  
 R-nnnnnnnnnnn//Mouse mRNA for alpha-adaptin (C).//3.0e-46:188:82//X14972  
 R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//1.6e-116:597:95//AF091433  
 5 R-PLACE1006195//Homo sapiens chromosome 19, fosmid 39554, complete sequence.//8.8e-11:148:74//AC004410  
 R-PLACE1006196  
 R-PLACE1006205//Genomic sequence from Mouse 11, complete sequence.//8.4e-44:332:85//AC000398  
 10 R-PLACE1006223//Human DNA sequence from cosmid U74C11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.041:215:61//Z173362  
 R-PLACE1006225//Caenorhabditis elegans cosmid Y69H2, complete sequence.//9.7e-13:358:63//Z98877  
 R-PLACE1006236//Plasmodium falciparum MAL3P4, complete sequence.//0.00019:538:58//AL008970  
 R-nnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//3.1e-96:497:95//AC004142  
 15 R-PLACE1006246//Homo sapiens clone NH0144M13, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.029:499:56//AC006034  
 R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//9.2e-96:499:95//AB014548  
 R-PLACE1006262//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//0.00043:160:66//AC004087  
 20 R-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20N2, WORKING DRAFT SEQUENCE.//3.5e-120:611:96//AL031320  
 R-PLACE1006318  
 R-PLACE1006325//Plasmodium falciparum MAL3P8, complete sequence.//1.0:426:57//AL034560  
 R-PLACE1006335//Human DNA sequence from PAC 849L7 on chromosome Xq21.//0.96:173:66//AL008987  
 25 R-PLACE1006357//P.falciparum complete gene map of plastid-like DNA ((R-B)).//1.9e-07:491:58//X95276  
 R-PLACE1006360//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.25:484:56//AE001398  
 R-PLACE1006368//Caenorhabditis elegans cosmid Y38H6C, complete sequence.//1.0:240:59//AL031630  
 R-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//3.7e-101:574:91//AC004232  
 30 R-PLACE1006382  
 R-PLACE1006385//Mus musculus intersectin-EH binding protein Itp2 mRNA, partial cds.//1.4e-50:350:86//AF057286  
 R-PLACE1006412//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//5.1e-51:339:82//AC004854  
 35 R-PLACE1006414//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-38:297:84//AC004804  
 R-PLACE1006438//Homo sapiens full-length insert cDNA YH73H06.//7.6e-73:422:90//AF074985  
 40 R-PLACE1006445//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018K9, WORKING DRAFT SEQUENCE.//3.0e-07:376:61//AL031726  
 R-PLACE1006469  
 R-PLACE1006470//Mouse B1 repetitive sequence DNA.//1.0:96:66//M24152  
 R-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//3.0e-101:535:94//AL021977  
 45 R-PLACE1006492//Homo sapiens chromosome 17, clone hRPC.180\_P\_8, complete sequence.//0.78:44:95//AC005972  
 R-PLACE1006506//R.norvegicus BSP gene.//1.0:206:60//X86100  
 R-PLACE1006521//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//9.0e-17:414:61//B75158  
 50 R-PLACE1006531//Plasmodium falciparum coronin gene, isolate 3D7.//0.98:186:63//AJ002197  
 R-PLACE1006534//Anopheles gambiae complete mitochondrial genome.//0.051:412:61//L20934  
 R-PLACE1006540//Homo sapiens clone UWGC:y5c025 from 6p21, complete sequence.//7.5e-41:470:70//AC004209  
 R-PLACE1006552//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.57:355:57//Z98865  
 55 R-PLACE1006598//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.016:291:58//AC004710  
 R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//

- 2.9e-116:590:95//U97670  
 R-PLACE1006617//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.2e-45:209:88//AC004050  
 R-PLACE1006626//C. elegans cosmid K12H4.//1.2e-16:344:64//L14331  
 5 R-PLACE1006629//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//2.8e-25:343:70//AC006128  
 R-PLACE1006640//CIT-HSP-2169L1.TF CIT-HSP Homo sapiens genomic clone 2169L1, genomic survey sequence.//0.00020:201:62//B90038  
 10 R-PLACE1006673//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.4e-42:309:84//AC004882  
 R-PLACE1006678//Homo sapiens PAC clone DJ1166G19 from 7p12-p11.2, complete sequence.//6.4e-09:454:59//AC006024  
 R-PLACE1006704//Human DNA sequence from clone 249C1 on chromosome Xq21.1-22.2 Contains GSS, complete sequence.//0.56:226:63//AL022154  
 15 R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence.//6.0e-101:486:98//AF038172  
 R-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.4e-68:381:93//AC005626  
 R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence.//6.2e-72:397:92//AF070622  
 20 R-PLACE1006779//Rattus norvegicus intestinal trefoil factor gene, promoter and partial cds.//1.6e-11:420:61//U20984  
 R-PLACE1006782//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.60:321:58//Z98865  
 R-PLACE1006792//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//2.9e-40:379:77//AC005599  
 25 R-PLACE1006795//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//6.2e-07:291:63//AC005083  
 R-PLACE1006800//HS\_2270\_B1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=3 Row=H, genomic survey sequence.//4.1e-76:367:99//AQ085793  
 R-PLACE1006805//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00058:354:59//AC005507  
 30 R-PLACE1006815//HS\_3028\_B1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=7 Row=D, genomic survey sequence.//1.5e-33:251:77//AQ120174  
 R-PLACE1006819//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.4e-76:544:84//Z86062  
 35 R-PLACE1006829  
 R-PLACE1006860  
 R-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING DRAFT SEQUENCE.//3.2e-107:549:95//AL033378  
 40 R-PLACE1006878//Homo sapiens full-length insert cDNA clone ZB55G05.//1.4e-46:241:97//AF086155  
 R-PLACE1006883//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//1.3e-38:283:85//AC004232  
 R-nnnnnnnnnnn  
 R-PLACE1006904//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//4.1e-15:477:62//Z82203  
 45 R-PLACE1006917//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//1.3e-42:305:87//AC005184  
 R-PLACE1006932  
 R-PLACE1006935//Human DNA sequence from PAC 117P19 on chromosome X.//0.0014:114:74//Z86061  
 50 R-nnnnnnnnnnn//Mouse mRNA for germ cell specific protein APG-1, complete cds.//9.5e-85:590:83//D49482  
 R-PLACE1006961//Homo sapiens chromosome 17, clone hRPC.349\_A\_8, complete sequence.//6.7e-42:295:86//AC005544  
 R-PLACE1006962//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//1.1e-19:302:71//AC002349  
 55 R-PLACE1006966//HS\_2219\_B2\_C02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=4 Row=F, genomic survey sequence.//0.019:180:63//AQ145873  
 R-PLACE1006989  
 R-PLACE1007014

- R-PLACE1007021//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//1.6e-23:362:70//AC005845
- R-PLACE1007045//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//2.3e-90:584:86//AL023693
- 5 R-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.4e-108:550:96//AC004895
- R-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//1.8e-103:552:93//AL021368
- 10 R-PLACE1007105//Mus musculus muskulin mRNA, complete cds.//2.7e-32:379:73//U02194
- R-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.14:422:57//AC004688
- 15 R-PLACE1007112//Cynops cornifex cytb gene.//0.020:427:58//AJ228479
- R-PLACE1007132//Homo sapiens full-length insert cDNA YH77E09.//5.7e-107:535:96//AF074987
- R-PLACE1007140//Homo sapiens clone RG030L05, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.36:408:58//AC005050
- 20 R-PLACE1007178//Homo sapiens clone HEA4 Cri-du-chat region mRNA.//0.99:63:73//AF009283
- R-PLACE1007226
- R-PLACE1007238
- R-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//2.0e-91:534:89//D50495
- 25 R-PLACE1007242//CITBI-E1-2512M9.TF CITBI-E1 Homo sapiens genomic clone 2512M9, genomic survey sequence.//1.3e-05:117:76//AQ279454
- R-PLACE1007243//Prototheca wickerhamii 263-11 complete mitochondrial DNA.//0.21:284:58//U02970
- R-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//6.9e-113:607:93//Y15908
- R-PLACE1007274//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//4.4e-10:135:74//AC006080
- 30 R-PLACE1007276//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//1.7e-36:435:72//AF069291
- R-PLACE1007282//B.garinii (strain T1s1) p83/100 gene (partial).//0.95:183:60//X81533
- R-PLACE1007286//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI11-13L8, genomic survey sequence.//6.1e-55:519:76//B75158
- 35 R-PLACE1007301//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINISITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.75:180:62//Z97195
- R-PLACE1007317//Drosophila dasyncemia 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.59:236:59//U94253
- 40 R-PLACE1007342
- R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//3.7e-65:367:91//AF096870
- R-PLACE1007367//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0e-06:385:62//AC005507
- 45 R-PLACE1007375//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.10:309:59//AC004709
- R-PLACE1007386//Reclinomonas americana mitochondrial DNA, complete genome.//0.0012:403:58//AF007261
- R-PLACE1007402//HS\_2055\_A2\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=8 Row=G, genomic survey sequence.//0.0046:88:79//AQ234824
- 50 R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence.//7.6e-112:590:94//AF093771
- R-PLACE1007416//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.96:98:70//AC005594
- R-PLACE1007450//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-39:308:82//Z98304
- 55 R-PLACE1007452//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.6e-59:389:82//AC004081
- R-PLACE1007460
- R-PLACE1007478//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC II-

brary) complete sequence.//7.0e-08:335:60//AC004241  
 R-PLACE1007484  
 R-PLACE1007488//Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//2.5e-05:421:61//AF072373  
 5 R-PLACE1007507//Plasmodium falciparum MAL3P7, complete sequence.//2.3e-09:577:57//AL034559  
 R-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//1.2e-79:387:96//AC004231  
 R-PLACE1007524//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//3.4e-09:148:73//AC003682  
 10 R-PLACE1007525//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//4.7e-38:297:82//AC004381  
 R-PLACE1007544  
 R-PLACE1007547//Human laminin alpha 4 chain (LAMA4\*-1) mRNA, complete cds.//4.0e-17:108:97//U77706  
 R-PLACE1007557//Human BAC clone RG343P13 from 7q31, complete sequence.//2.2e-45:390:77//AC002465  
 15 R-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 545L17, WORKING DRAFT SEQUENCE.//1.0e-56:302:95//AL031665  
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence.//1.5e-102:554:93//AF038179  
 R-PLACE1007618  
 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence.//1.4e-103:537:94//AF038176  
 20 R-PLACE1007632//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.3e-76:289:94//AC005840  
 R-PLACE1007645//Homo sapiens full-length insert cDNA clone ZD76G10.//0.0080:96:77//AF086408  
 R-PLACE1007649//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//1.1e-82:412:97//AQ022149  
 25 R-PLACE1007677//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0041:470:57//AE001367  
 R-PLACE1007688  
 R-PLACE1007690//Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence.//1.3e-22:162:91//AC002044  
 30 R-PLACE1007697  
 R-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//4.4e-121:624:95//AL031662  
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.8e-73:374:96//AF061243  
 R-PLACE1007725//Caenorhabditis elegans cosmid F38A5.//0.070:186:60//U70854  
 35 R-PLACE1007729//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR.//3.8e-53:415:81//U60269  
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.1e-92:556:89//AB014585  
 R-PLACE1007737//Homo sapiens clone Sb19.12 Alu-Yb8 sequence.//4.0e-43:302:77//AF015169  
 R-PLACE1007743//Plasmodium falciparum MAL3P8, complete sequence.//1.0e-06:533:59//AL034560  
 40 R-PLACE1007746//T.brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds.//0.28:386:58//M14820  
 R-PLACE1007791//D discoideum gene for protein kinase.//0.17:263:60//Z37981  
 R-PLACE1007807//Human DNA sequence from clone 87808 on chromosome Xq21.1-21.33. Contains an EST, STSs, a GSS and genomic marker DXS472, complete sequence.//1.1e-72:324:88//AL031116  
 45 R-PLACE1007810//Homo sapiens chromosome 7 common fragile site, complete sequence.//2.2e-14:325:67//AF017104  
 R-PLACE1007829//Human BAC clone GS165I04 from 7q21, complete sequence.//0.00052:455:61//AC002379  
 R-PLACE1007843//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.0050:447:57//X95275  
 R-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//2.2e-111:570:95//AP000010  
 50 R-PLACE1007852//HS\_3028\_B2\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=8 Row=L, genomic survey sequence.//1.3e-12:209:71//AQ131021  
 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//6.6e-110:574:94//AB018309  
 R-PLACE1007866//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//1.6e-43:551:70//AL022162  
 55 R-PLACE1007877//Homo sapiens chromosome 5, BAC clone 34J15 (LBNL H169), complete sequence.//1.6e-22:222:78//AC005754

- R-PLACE1007897//HS\_3113\_B2\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3113 Col=8 Row=J, genomic survey sequencer.//2.9e-72:381:95//AQ186905
- R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//8.8e-88:460:95//AB007956
- 5 R-PLACE1007946//Human chromosome Y cosmid 54E8 genomic sequence, WORKING DRAFT SEQUENCE.//4.9e-23:172:78//AC003095
- R-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//1.7e-27:303:75//AC006157
- 10 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//3.9e-102:513:95//AF084530
- R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.2e-87:465:93//AF079529
- R-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//4.8e-72:556:81//U13262
- 15 R-PLACE1007990//E. tenella antigen LPMC61 mRNA, partial cds.//0.043:273:63//M30933
- R-PLACE1008000//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING DRAFT SEQUENCE.//8.8e-10:453:62//AL034346
- R-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//9.0e-114:563:96//AC005628
- 20 R-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//2.6e-44:509:72//L31840
- R-PLACE1008045//Homo sapiens chromosome 5, BAC clone 79a6 (LBNL H172), complete sequence.//0.32:137:66//AC005592
- 25 R-PLACE1008080//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//0.082:292:59//AC006232
- R-PLACE1008095//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//5.4e-27:260:76//AC005036
- 30 R-PLACE1008111//Human variable number tandem repeat (VNTR) region, allele 12R1 3' to collagen type II (COL2A1) gene.//2.2e-07:444:59//L10157
- R-PLACE1008122//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//1.9e-11:384:63//AC005919
- R-PLACE1008129//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.0e-10:189:66//AC004955
- 35 R-PLACE1008132//Human HepG2 3' region cDNA, clone hmd5d06.//7.4e-47:320:86//D16939
- R-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.6e-32:410:70//D14849
- R-PLACE1008181//Caenorhabditis elegans cosmid C31H2.//0.055:358:60//U41748
- R-PLACE1008198
- 40 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.8e-103:551:93//AB011102
- R-PLACE1008209//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//4.6e-16:250:71//AL034549
- R-PLACE1008231//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.13:341:60//AC004688
- 45 R-PLACE1008244//P.falciparum P.195 gene.//0.11:212:66//A04562
- R-PLACE1008273//Human MEST mRNA, complete cds.//0.00013:52:100//D78611
- R-nnnnnnnnnnnnn
- R-PLACE1008280//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.5e-05:104:76//AC005272
- 50 R-PLACE1008309//Human 'at-rich region adjacent to alpha satellite DNA.//0.70:138:63//M80308
- R-PLACE1008329//Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence.//0.00061:150:68//AC005886
- R-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//4.8e-74:252:98//AC005176
- R-PLACE1008333//Genomic sequence from Human 13, complete sequence.//1.0:176:65//AC001226
- 55 R-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, 3' UTR.//2.5e-98:556:90//AF036145
- R-PLACE1008368//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.2e-05:375:62//B36336



- R-PLACE1008369//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//2.8e-10:466.61//AP000011
- R-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.471\_L\_13, complete sequence.//1.0e-46:282:82//AC005244
- 5 R-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//4.1e-101:529.94//AL034417
- R-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//0.18:379:58//AC004604
- 10 R-nnnnnnnnnn//Homo sapiens mRNA for p115, complete cds.//1.6e-101:521:95//D86326
- R-PLACE1008405//Human cosmidCRI-JC2015 at D10S289 in 10sp13.//6.8e-22:328:71//U15177
- R-PLACE1008424
- R-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//7.5e-101:505:96//AB020864
- 15 R-PLACE1008429//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.2e-11:118:78//AL022576
- R-PLACE1008437//H.sapiens genomic DNA (PAC 838L14) from chromosome 11, WORKING DRAFT SEQUENCE.//2.2e-06:159:69//Y12335
- R-PLACE1008455
- 20 R-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.2e-109:588:93//AC004526
- R-PLACE1008465//CIT978SK-A-28A11.TVE CIT978SK Homo sapiens genomic clone A-28A11, genomic survey sequence.//1.1e-10:133:77//B78696
- R-PLACE1008488
- 25 R-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34B21, WORKING DRAFT SEQUENCE.//7.3e-120:612:95//AL031778
- R-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//8.5e-98:510:93//AF045555
- R-PLACE1008532
- 30 R-PLACE1008533
- R-PLACE1008568//HS\_3218\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=H, genomic survey sequence.//0.0042:295:62//AQ214623
- R-PLACE1008584//Human PAC clone DJ0596009 from 7p15, complete sequence.//5.0e-26:254:66//AC003074
- 35 R-PLACE1008621//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//4.0e-78:498:86//AC006120
- R-nnnnnnnnnnn
- R-PLACE1008626//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//5.5e-06:228:67//AL031297
- R-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//3.4e-20:335:71//Y12836
- 40 R-PLACE1008629//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.55:326:58//AC004826
- R-PLACE1008630//Homo sapiens genomic DNA, 21q region, clone: B175P11X96, genomic survey sequence.//0.13:440:55//AG011096
- R-PLACE1008643//Human BAC clone RG083J23 from 7q31, complete sequence.//1.3e-58:356:82//AC004001
- 45 R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//2.4e-88:434:97//AF044333
- R-PLACE1008693//CIT-HSP-2025M9.TR CIT-HSP Homo sapiens genomic clone 2025M9, genomic survey sequence.//1.2e-41:300:82//B64742
- R-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//4.8e-31:320:75//AF038406
- 50 R-PLACE1008715//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE.//0.074:478:58//AL022147
- R-PLACE1008748//CIT-HSP-2170P12.TR CIT-HSP Homo sapiens genomic clone 2170P12, genomic survey sequence.//8.5e-42:160:86//B90841
- 55 R-PLACE1008757//Homo sapiens 12q24.2 PAC RPCI4-765H13 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.99:211:61//AC005864
- R-PLACE1008790//Rattus norvegicus clone1 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.052:108:68//U00762

R-PLACE1008798//Homo sapiens full-length insert cDNA clone YZ86C05.//7.7e-58:285:100//AF086088  
 R-PLACE1008807//CIT-HSP-2366014. TR CIT-HSP Homo sapiens genomic clone 2366014, genomic survey sequence.//3.5e-35:223:89//AC0079210  
 R-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//2.3e-97:499:95//AF030933  
 R-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//9.7e-45:394:78//AF032668  
 R-PLACE1008851//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.9e-28:207:87//AC004581  
 R-nnnnnnnnnnn//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//8.9e-30:168:97//B93289  
 R-PLACE1008867//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//3.5e-76:404:95//AC005058  
 R-PLACE1008867//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-37:585:67//AC004932  
 R-PLACE1008902//Homo sapiens chromosome Y, clone hCIT.494\_G\_17, complete sequence.//0.0022:409:60//AC005820  
 R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//8.2e-55:344:89//AB018308  
 R-PLACE1008925//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.0014:398:58//Z92860  
 R-PLACE1008934  
 R-PLACE1009341//Homo sapiens chromosome 17, clone hRPC.293\_K\_20, complete sequence.//9.8e-84:429:92//AC005495  
 R-PLACE1008947  
 R-PLACE1009020  
 R-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.3e-82:434:95//AL031117  
 R-PLACE1009039//Human DNA sequence from clone 276K20 on chromosome 6p22.1-22.3. Contains STSs, GSSs and a putative CpG island, complete sequence.//0.00010:297:58//AL031391  
 R-PLACE1009045//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, complete sequence.//2.9e-06:160:70//AC004707  
 R-PLACE1009048//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//1.3e-16:339:66//AL023694  
 R-PLACE1009050//Aedes aegypti gene sequence, primary transcript.//0.40:393:59//L17023  
 R-PLACE1009060//Mus musculus mRNA for Alix-SF (ALG-2-interacting protein X, short form, complete CDS.//0.00075:79:83//AJ005074  
 R-PLACE1009090//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.7e-13:212:73//AC004783  
 R-PLACE1009094//Caenorhabditis elegans cosmid C49F8, complete sequence.//0.49:221:61//Z70206  
 R-PLACE1009099  
 R-PLACE1009110//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-17:301:66//AC004025  
 R-PLACE1009111//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.2e-06:234:61//AC005140  
 R-PLACE1009130//Plasmodium falciparum MAL3P6, complete sequence.//7.5e-06:426:58//Z98551  
 R-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT SEQUENCE.//2.3e-118:614:95//AJ011929  
 R-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//1.4e-107:584:93//AP000031  
 R-PLACE1009158//Homo sapiens full-length insert cDNA clone YP10D03.//1.9e-105:539:95//AF085876  
 R-PLACE1009160//Homo sapiens chromosome 17, clone hRPC.180\_P\_8, complete sequence.//2.8e-44:360:71//AC005972  
 R-PLACE1009172//Human cosmid QLL2C9 from Xq28.//4.1e-37:401:74//Z47046  
 R-PLACE1009174//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.1e-17:140:81//AC004925  
 R-PLACE1009183//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and



sequence.//0.72:176:62//B81271

R-PLACE1009637//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0068:396:59//X95276

R-PLACE1009639//Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAI project).//0.013:521:58//AL021811

R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.0e-107:589:92//AB011159

R-PLACE1009665//Human PAC clone DJ0658N05 from 7p21, complete sequence.//8.4e-72:487:85//AC003075

R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.0e-61:310:97//AF062534

R-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//2.8e-103:542:94//AC006011

R-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//4.6e-85:518:88//AC000109

R-PLACE1009731//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.0033:215:65//AL022398

R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//6.2e-116:598:95//AF046024

R-PLACE1009794

R-nnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//7.5e-88:191:96//AL030996

R-PLACE1009845//Homo sapiens DNA sequence from PAC 234H5 on chromosome 6q21. Contains an unknown gene, ESTs and STSs, complete sequence.//8.7e-19:226:69//Z98172

R-PLACE1009879//Homo sapiens genomic DNA, 21q region, clone: 149C3A68, genomic survey sequence.//2.1e-29:230:76//AG002672

R-PLACE1009886//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//0.99:203:61//AC004945

R-PLACE1009888//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//5.3e-91:577:88//AC006116

R-nnnnnnnnnnn

R-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//4.7e-81:385:84//M63005

R-PLACE1009924//HS\_3151\_B1\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3151 Col=19 Row=D, genomic survey sequence.//5.5e-47:240:99//AQ167412

R-PLACE1009925//CIT978SK-A-931F6.TV CIT978SK Homo sapiens genomic clone A-931F6, genomic survey sequence.//0.00010:159:68//B51673

R-PLACE1009935//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.081:238:65//AC005308

R-PLACE1009947//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.0:353:58//AC002483

R-PLACE1009971//Homo sapiens full-length insert cDNA clone ZD38E12.//3.7e-11:152:75//AF086247

R-PLACE1009992

R-PLACE1009995//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0019:305:61//AE001367

R-PLACE1009997//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//1.8e-43:462:76//AC005874

R-PLACE1010023//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00013:198:63//AQ093513

R-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.4e-115:581:96//AL031775

R-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//1.9e-05:136:74//X84692

R-PLACE1010069//CIT-HSP-2328B12.TF CIT-HSP Homo sapiens genomic clone 2328B12, genomic survey sequence.//2.6e-60:324:94//AQ042094

R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//4.6e-87:543:88//AF065482

R-PLACE1010076//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0473M13; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.3e-08:489:58//AC005699

R-PLACE1010083

R-PLACE1010089//F19F22-Sp6 IGF Arabidopsis thaliana genomic clone F19F22, genomic survey sequence.//0.14:400:59//B10583

R-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//4.3e-91:562:87//X64411

R-PLACE1010102//Apis mellifera tRNA-Leu cytochrome oxidase II intergenic spacer region, mitochondrial sequence.//1.5e-08:357:60//AF039556

R-PLACE1010105//Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.//4.0e-09:510:59//AE001374

R-PLACE1010106//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.4e-12:194:73//Z98304

R-PLACE1010134

R-PLACE1010148//HS\_3128\_A1\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2328 Col=17 Row=G, genomic survey sequence.//0.17:281:61//AQ140790

R-PLACE1010152//Mouse mRNA for arylhydrocarbon receptor, complete cds.//3.1e-45:351:81//D38417

R-PLACE1010181//Homo sapiens clone DJ0914M06, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.6e-06:207:66//AC004928

R-PLACE101019411HS\_2232\_B1\_H10\_MR CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=2232 Col=17 Row=P, genomic survey sequence.//2.4e-08:134:74//AQ185425

R-PLACE1010202//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//0.00035:383:61//AL031585

R-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SEQUENCE.//1.2e-95:519:94//AL033377

R-PLACE1010261

R-PLACE1010270//H.sapiens CpG island DNA genomic MseI fragment, clone 85a6, reverse read cp985a61rt1a.//0.068:171:63//Z63482

R-PLACE1010274//S.douglasii gene for cytochrome b.//4.5e-07:276:63//X59280

R-PLACE1010293//Homo sapiens chromosome 2 PAC RPC13-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.7e-91:522:90//AC004464

R-PLACE1010321

R-PLACE1010324//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y38E10, WORKING DRAFT SEQUENCE.//5.7e-08:484:57//AL021149

R-PLACE1010329//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//7.9e-35:328:79//AC000024

R-PLACE1010341//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.3e-31:418:66//AC004971

R-PLACE1010362

R-PLACE1010364//Mus cookii mitochondrion DNA fragment.//0.23:162:64//M77098

R-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//1.4e-105:543:95//AC004675

R-PLACE1010401//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.00017:268:62//AC004137

R-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//8.6e-79:556:83//AF003927

R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//7.3e-88:438:96//AF039081

R-PLACE1010492//HS\_3169\_B2\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3169 Col=8 Row=D, genomic survey sequence.//0.98:171:63//AQ169892

R-PLACE1010522//WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.34:407:62//AC006082

R-nnnnnnnnnnn

R-PLACE1010562//CITBI-E1-2503B16.TF CITBI-E1 Homo sapiens genomic clone 2503B16, genomic survey sequence.//6.4e-17:152:84//AC026529

R-PLACE1010579//Torulopsis glabrata mitochondrial gene for ribosomal protein var1.//1.7e-05:271:65//X02893

R-PLACE1010580

R-PLACE1010599

R-PLACE1010616//Human BAC clone RG343P13 from 7q31, complete sequence.//3.0e-13:151:75//AC002465

R-PLACE1010622//Arabidopsis thaliana BAC F1104.//0.00031:366:60//AF096370

R-PLACE1010624//Homo sapiens chromosome 7q22 sequence, complete sequence.//8.2e-34:322:79//AF053356

R-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-97:515:94//AC004846

R-PLACE1010629//HS\_3003\_A2\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=16 Row=E, genomic survey sequence.//5.6e-60:321.95//AQ130493

R-PLACE1010630//Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.//0.051:372.59//AE001382

5 R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds.//2.6e-92:497.93//AB011102

R-PLACE1010661//CIT-HSP-2008K15.TR CIT-HSP Homo sapiens genomic clone 2008K15, genomic survey sequence.//5.7e-27:160.95//B57089

R-PLACE1010662//Caenorhabditis elegans cosmid C12C8, complete sequence.//9.4e-09:151.73//Z81467

10 R-PLACE1010702//CIT-HSP-2314C3.TR CIT-HSP Homo sapiens genomic clone 2314C3, genomic survey sequence.//1.3e-90:459.96//AQ028536

R-PLACE1010714//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//5.3e-08:478.58//U49822

15 R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//3.8e-55:300.95//AF092564

R-PLACE1010739//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//3.4e-89:507.90//Z95400

R-PLACE1010743

20 R-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//3.0e-103:511.97//AC005921

R-PLACE1010771

R-PLACE1010786

R-PLACE1010800//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//1.8e-43:545.71//AC005682

25 R-PLACE1010802//Phoebeis agarithe large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//1.9e-09:492.59//AF044862

R-PLACE1010811//Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence.//0.041:415.59//AC002524

30 R-PLACE1010833

R-PLACE1010856//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:512.55//AC004153

R-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11//4.9e-85:507.90//AB020868

35 R-PLACE1010870//RPC11-59K21:TK RPC11 Homo sapiens genomic clone R-59K21, genomic survey sequence.//8.2e-85:422.97//AQ195697

R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//7.0e-100:501.96//AB011182

R-PLACE1010891//Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.10:162.61//AC002489

40 R-PLACE1010896//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00032:409.59//AC005505

R-PLACE1010900//Homo sapiens DNA, trinucleotide repeats region.//3.2e-07:180.71//AB018488

R-PLACE1010916//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.041:205.60//AL034557

45 R-PLACE1010917

R-PLACE1010925//HS\_2027\_B2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=18 Row=D, genomic survey sequence.//1.6e-46:404.77//AQ247031

R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//4.2e-65:402.89//AB011126

50 R-NNNNNNNNNN//Homo sapiens intersectin short form mRNA, complete cds.//1.9e-80:441.93//AF064243

R-PLACE1010944

R-PLACE1010947//D. discoideum rasG gene.//0.00044:181.65//Z11533

R-PLACE1010954//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-51:518.74//AC005077

55 R-PLACE1010960//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE.//0.022:292.63//AL033522

R-PLACE1010965//Human mariner1 transposase gene, complete consensus sequence.//1.0e-64:444.84//U52077

R-PLACE1011026//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.59:345.61//

AJ235272

R-PLACE1011032//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//0.62:82:75//Z93242

R-PLACE1011041//H.sapiens DNA sequence.//0.051:162:66//Z22248

R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds.//2.9e-100:563:91//AB011153

R-PLACE1011054//Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.//4.7e-29:280:73//Z84483

R-PLACE1011056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//1.7e-39:288:84//Z97985

R-PLACE1011057//CIT-HSP-2014F10.TF CIT-HSP Homo sapiens genomic clone 2014F10, genomic survey sequence.//2.4e-60:370:90//B58896

R-PLACE1011090//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//0.12:489:59//AC005509

R-PLACE1011109//Homo sapiens chromosome Y, clone 486, O, 2, complete sequence.//8.4e-43:427:76//AC002531

R-PLACE1011114//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hi1-14).//1.7e-29:179:94//Y16709

R-PLACE1011133//HS-1058-B1-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=3 Row=P, genomic survey sequence.//1.0:133:63//44006

R-PLACE1011143//H.sapiens CpG island DNA genomic MseI fragment, clone 127a4, forward read cpg127a4.ftta.//1.0:127:67//Z56550

R-PLACE1011160//Homo sapiens HRIHFB2038 mRNA, partial cds.//2.4e-95:534:91//AB015333

R-PLACE1011165//Human Cosmid g5129s232 from Tq31.3, complete sequence.//0.47:355:58//AC003968

R-PLACE1011185//Homo sapiens clone DJ003810, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.3e-26:403:70//AC004820

R-PLACE1011203//paramecium species 4.51er mt dna dimer: replication init. region, clone 1.//1.0e-10:379:60//K00908

R-PLACE1011219//HS\_3036\_B1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=15 Row=L, genomic survey sequence.//2.6e-39:253:88//AQ104587

R-PLACE1011221//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//0.32:279:60//AE000659

R-PLACE1011229//HS\_3002\_B1\_E10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=19 Row=J, genomic survey sequence.//9.3e-31:317:74//AQ303626

R-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.2e-109:571:94//AC005014

R-PLACE1011273//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.00027:337:61//M97514

R-PLACE1011291

R-PLACE1011296//H.sapiens steroid reductase pseudogene.//4.2e-37:326:80//M68887

R-PLACE1011310//H.sapiens 5' flanking sequence of gene for corticotropin.//0.0017:416:60//X67661

R-PLACE1011325//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.3.0e-10:511:59//AE001398

R-PLACE1011332//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.3e-06:250:64//AC002344

R-PLACE1011340//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//0.67:290:58//AC002530

R-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.8e-23:190:86//AJ010310

R-PLACE1011399//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.22:359:60//AC005140

R-PLACE1011419//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//5.1e-32:282:81//Z74022

R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//1.5e-112:600:94//AB011102

R-PLACE1011452//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.9e-77:303:85//AC006013

R-PLACE1011465

R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//7.9e-103:515:96//AB018255

R-PLACE1011492//A-837A4.TP CIT978SK Homo sapiens genomic clone A-837A4, genomic survey sequence.//6.5e-37:234:82//B14085

R-PLACE1011503//Homo sapiens chromosome 17, clone hRPC.1171\_1\_10, complete sequence.//0.99:267:60//

AC004687

R-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//2.0e-116:591:96//AC004968

R-PLACE1011563//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-13:566:59//AC004688

R-PLACE1011567//Plasmodium-falciparum MAL3P6, complete sequence.//0.62:358:61//Z98551

R-PLACE1011576//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.7e-45:400:78//AC003973

R-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.2e-59:338:93//AC004477

R-PLACE1011635//C.pasteurianum pfl gene and act gene.//0.71:288:60//X93463

R-PLACE1011641//Mycoplasma genitalium random genomic clone sg11, partial cds.//0.023:232:60//U02205

R-PLACE1011643//Homo sapiens chromosome 19, cosmid R33590, complete sequence.//1.4e-21:432:67//AC005620

R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence.//7.8e-72:414:91//AF070535

R-PLACE1011650//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//5.1e-27:174:79//AC002477

R-PLACE1011664//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone. 460D19, WORKING DRAFT SEQUENCE.//7.4e-05:238:65//AL031905

R-PLACE1011675//CIT-HSP-2370M16.TR CIT-HSP Homo sapiens genomic clone 2370M16, genomic survey sequence.//1.3e-27:233:81//AQ108283

R-PLACE1011682//H.sapiens HLA-DMB gene.//2.3e-22:390:67//X76776

R-PLACE1011719//Homo sapiens 12q24.2 BAC RPC111-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.1e-24:409:66//AC004806

R-PLACE1011725//Homo sapiens unknown mRNA downregulated by induced differentiation with 13-cis retinoic acid.//0.13:143:65//AF026526

R-PLACE1011729//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//1.1e-15:157:82//AL022345

R-PLACE1011749//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:314:81//AC005089

R-PLACE1011762//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//1.9e-35:538:68//AC002383

R-PLACE1011778//CIT-HSP-2326C17.TV CIT-HSP Homo sapiens genomic clone 2326C17, genomic survey sequence.//2.8e-58:346:91//AQ028782

R-PLACE1011783//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//4.6e-38:288:84//Z86090

R-PLACE1011858//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//4.1e-104:524:97//AL031321

R-PLACE1011874//Homo Sapiens Chromosome X clone bWDX312, complete sequence.//2.1e-100:511:95//AC004478

R-PLACE1011875

R-PLACE1011891//Human lens membrane protein (mp19) gene, exon 11.//0.0011:195:64//L04193

R-PLACE1011896//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.010:110:74//AL022398

R-PLACE1011922//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//3.5e-10:152:74//AF042090

R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//7.0e-98:546:92//AF059617

R-PLACE1011962//CIT-HSP-2294L24.TF CIT-HSP Homo sapiens genomic clone 2294L24, genomic survey sequence.//0.31:131:63//AQ006352

R-PLACE1011964//Homo sapiens chromosome 17, clone HRPC897K16, complete sequence.//2.5e-08:393:63//AC002994

R-PLACE1011982//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence.//9.6e-09:463:62//AB016889

R-PLACE1011995//Human Down Syndrome region of chromosome 21, clone A12H1-2H4.//2.7e-39:294:82//U44738

R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//2.5e-104:540:95//AB018256

R-PLACE2000003//Human PAC clone DJ404F18 from Xq23, complete sequence.//4.9e-10:439:63//AC004000



- R-PLACE2000007//Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 3.//1.0:151.66//L78722
- R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.5e-103:524.95//AF091080
- R-PLACE2000015//Homo sapiens PAC clone DJ269005 from Xq23, complete sequence.//0.94:372.57//AC005191
- 5 R-PLACE2000017//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence.//3.0e-55:299.86//AC006236
- R-PLACE2000021//CIT-HSP-2343C18. TR CIT-HSP Homo sapiens genomic clone 2343C18, genomic survey sequence.//4.5e-54:295.94//AQ058140
- R-PLACE2000033//H. sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//6.5e-38:298.82//X69907
- 10 R-PLACE2000034//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.3e-34:200.79//AC005628
- R-PLACE2000039//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//1.8e-49:274.89//AC003083
- R-PLACE2000047//CIT-HSP-2373C2. TR CIT-HSP Homo sapiens genomic clone 2373C2, genomic survey sequence.//1.8e-48:389.79//AQ112243
- 15 R-PLACE2000050//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117715, WORKING DRAFT SEQUENCE.//0.0027:95.76//AL022315
- R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds.//2.9e-39:429.72//AB011147
- R-PLACE2000062//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.9e-40:310.84//AC004832
- 20 R-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//1.9e-109:550.95//AF072719
- R-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-106:553.95//AC005910
- R-PLACE2000100//Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.//1.8e-38:285.84//AL031730
- 25 R-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//4.3e-113:559.97//AL031848
- R-PLACE2000111//Rat MLC1V gene encoding alkali myosin ventricle light chain, exon 1.//0.00041:347.61//X16325
- 30 R-PLACE2000115//Cervus elaphus MHC class II DRB pseudogene, intron 2 microsatellite.//0.50:165.63//U63067
- R-PLACE2000132
- R-PLACE2000136//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-30, complete sequence.//0.0032:310.61//AL008974
- R-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING
- 35 DRAFT SEQUENCE.//1.1e-111:566.96//AL020995
- R-PLACE2000164
- R-PLACE2000170//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.9e-40:390.76//AC005598
- R-PLACE2000172
- 40 R-PLACE2000176
- R-PLACE2000187//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING DRAFT SEQUENCE.//8.7e-45:298.87//AL008718
- R-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end.//5.6e-88:495.92//L02897
- R-PLACE2000223
- 45 R-PLACE2000235//HS\_3159\_B1\_B06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3159 Col=11 Row=D, genomic survey sequence.//1.8e-88:454.96//AQ179271
- R-PLACE2000246//Homo sapiens chromosome 3p clone RPC14-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//9.1e-41:282.86//AC005902
- R-PLACE2000264//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//8.3e-35:305.80//Z97181
- 50 R-PLACE2000274//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//3.5e-18:325.67//AC002394
- R-PLACE2000302//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.5e-39:287.85//AC003043
- 55 R-PLACE2000305//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING DRAFT SEQUENCE.//1.2e-43:295.85//Z93015
- R-PLACE2000317//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Tsp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNC-

TION 43 KD HEART PROTEIN)), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-05:284.65//Z92542

R-PLACE2000335//Homo sapiens clone DJ0755D09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.5e-26:334:70//AC006147

R-PLACE2000342//Fugu rubripes cosmid 258N02 containing IGF1I, TH, NAP2 genes.//4.0e-05:254:64//AL021880  
R-PLACE2000347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE.//1.6e-82:504:88//AL022147

R-PLACE2000359//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 40E16, WORKING DRAFT SEQUENCE.//2.0e-36:314:80//AL031963

R-PLACE2000366//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//2.0e-48:389:80//AL031291

R-PLACE2000371  
R-PLACE2000373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 324M8, WORKING DRAFT SEQUENCE.//0.61:231:61//AL008734

R-PLACE2000379//Homo sapiens clone DJ0892G19, complete sequence.//3.5e-11:287:67//AC004917  
R-PLACE2000394//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//6.8e-108:553:96//AL031432

R-PLACE2000398//Homo sapiens clone RG07A24, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.9e-26:326:73//AC005059

R-PLACE2000399  
R-PLACE2000404//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//6.5e-84:434:96//AC005216

R-PLACE2000411//P.clarkii mRNA; repeat region (ID R2).//0.47:104:70//Z54273  
R-PLACE2000419

R-PLACE2000425//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.9e-40:447:74//AF003528  
R-PLACE2000427

R-PLACE2000433//Human Chromosome 15 pac pDJ24m8, complete sequence.//3.5e-40:286:85//AC000379  
R-PLACE2000435

R-PLACE2000438//Homo sapiens full-length insert cDNA clone ZE04D01.//2.2e-107:523:98//AF086521  
R-PLACE2000450 4.1e-42:328:79//AG006257  
R-PLACE2000455

R-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete-sequence.//5.1e-116:570:97//AC005740

R-PLACE2000465//Human BAC clone RG191D16, complete sequence.//6.3e-37:408:75//AC002460  
R-PLACE2000477//M.musculus tex264 mRNA (3'region).//7.5e-06:117:76//X80427  
R-PLACE3000004

R-PLACE3000029//Human DNA sequence from PAC 506G2 contains STSs and a CpG island.//5.8e-34:308:78//Z82976  
R-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-36:273:87//Y17267

R-PLACE3000070//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//2.3e-10:181:71//AC004648  
R-PLACE3000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.2e-48:495:74//AL022156

R-PLACE3000119//Homo sapiens Chromosome 22q12 BAC Clone 58B8 In Meningioma Deletion Region, complete sequence.//3.4e-39:283:85//AC000026  
R-PLACE3000124//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//9.2e-23:171:76//AC005200

R-PLACE3000136//U. arcatus microsatellite DNA, clone UarMU23.//0.00052:171:65//Y09645  
R-PLACE3000142//HS\_3037\_82\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=4 Row=D, genomic survey sequence.//0.88:121:66//AQ097023

R-PLACE3000147//Mus musculus DNA for ADAMTS-1, complete cds.//3.3e-23:472:66//AB001735  
R-PLACE3000148//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//3.5e-11:176:73//Z49237

R-PLACE3000155//Homo sapiens chromosome 17, clone hRPK\_57\_M\_12, complete sequence.//6.9e-106:549:94//AC005277  
R-PLACE3000156//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//7.0e-38:545:70//AC002383

R-PLACE3000157  
 R-PLACE3000158// complete sequence.//1.4e-33:283.81//AC005500  
 R-PLACE3000160  
 R-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//5.2e-43:229.85//  
 AC006130  
 R-PLACE3000194  
 R-PLACE3000197//Homo sapiens chromosome 17, clone hRPC.401\_O\_9, complete sequence.//7.2e-61:394.89//  
 AC005291  
 R-PLACE3000199//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for  
 neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD)1 N-  
 acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1  
 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene.//0.23:309.57//U52112  
 R-PLACE3000207//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey se-  
 quence.//1.1e-15:156.81//B54637  
 R-PLACE3000208//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 591N18, WORKING  
 DRAFT SEQUENCE.//1.3e-16:139.87//AL031594  
 R-PLACE3000218//HS\_3185\_B1\_B01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3185 Col=1 Row=D, genomic survey sequence.//3.5e-07:120.75//AQ155720  
 R-PLACE3000220//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//2.4e-44:363.80//  
 AC004167  
 R-PLACE3000226//Caenorhabditis elegans cosmid M01G5.//0.88:95.77//AF078786  
 R-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and  
 lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.3e-69:536.81//U95626  
 R-PLACE3000242//Sequence 1 from patent US 5599918.//3.2e-62:546.78//U35489  
 R-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.7e-45:404.75//X80169  
 R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds.//7.5e-28:174.94//AB002307  
 R-PLACE3000271//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING  
 DRAFT SEQUENCE.//3.9e-54:492.77//AL034379  
 R-PLACE3000276//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//5.4e-12:176.69//  
 AC004081  
 R-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//5.7e-114:555.97//  
 AC005328  
 R-PLACE3000310//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467L1, WORKING  
 DRAFT SEQUENCE.//6.2e-51:314.84//Z98884  
 R-PLACE3000320//Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds.//2.5e-  
 44:289.90//U93037  
 R-PLACE3000322//Human argininosuccinate lyase (ASL) gene, exon 3.//5.9e-20:153.88//M21006  
 R-PLACE3000331//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//  
 1.1e-43:230.84//AC005480  
 R-PLACE3000339  
 R-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roswell Park Cancer Institute Human PAC  
 Library) complete sequence.//2.5e-111:550.97//AC006055  
 R-PLACE3000350//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and  
 GSSs, complete sequence.//1.5e-44:314.78//AL022323  
 R-PLACE3000352//HS\_3095\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3095 Col=17 Row=J, genomic survey sequence.//8.5e-73:356.99//AQ123142  
 R-PLACE3000353//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y22F5,  
 WORKING DRAFT SEQUENCE.//0.21:194.63//Z99712  
 R-PLACE3000362//Plasmodium falciparum coronin gene, isolate 3D7.//0.26:360.60//AJ002197  
 R-PLACE3000363  
 R-PLACE3000365//Human BAC clone RG343P13 from 7q31, complete sequence.//4.6e-52:487.76//AC002465  
 R-PLACE3000373//HS\_3202\_B1\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3202 Col=9 Row=N, genomic survey sequence.//2.4e-75:437.90//AQ252699  
 R-PLACE3000388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING  
 DRAFT SEQUENCE.//6.4e-61:515.81//AL008722  
 R-PLACE3000399//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//  
 0.00098:444.60//AC005231  
 R-PLACE3000400//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING

DRAFT SEQUENCE, 7 unordered pieces.//0.78:155:66//AC005506  
 R-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//8.0e-47:223:81//AC006023  
 R-PLACE3000402//Homo sapiens chromosome 17, clone 104H12, complete sequence.//1.0:179:63//AC000003  
 5 R-PLACE3000405//Homo sapiens chromosome 7qtel0 BAC F6, complete sequence.//2.4e-44:466:74//AF104455  
 R-PLACE3000406//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING DRAFT SEQUENCE.//7.7e-49:471:75//AL008718  
 R-PLACE3000413  
 10 R-PLACE3000416//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SEQUENCE.//5.4e-42:416:77//AJ009612  
 R-PLACE3000425//Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal protein L29 pseudogene, ESTs and STSs.//1.1e-41:366:78//AL008627  
 R-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//3.8e-98:549:92//AL031284  
 15 R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds.//1.9e-82:440:92//U43999  
 R-PLACE3000477  
 R-PLACE4000009//R.norvegicus mRNA encoding 45kDa protein which binds to heymann nephritis antigen gp330.//6.6e-17:344:68//Z11995  
 20 R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//2.7e-83:433:95//AB018352  
 R-PLACE4000034//cSRL-51C5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-51C5, genomic survey sequence.//0.54:116:66//B04984  
 R-PLACE4000049//Human BAC clone GS165I04 from 7q21, complete sequence.//0.29:313:59//AC002379  
 R-PLACE4000052//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MALP1, WORKING DRAFT SEQUENCE.//0.0058:466:57//AL034557  
 25 R-PLACE4000063//Homo sapiens chromosome 7q22 sequence, complete sequence.//0.98:246:61//AF053356  
 R-PLACE4000089//RPCI11-151.TUB RPCI-11 Homo sapiens genomic clone RPCI-11-151, genomic survey sequence.//3.2e-07:284:60//B82414  
 R-PLACE4000093//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.4e-07:429:60//AC005506  
 30 R-PLACE4000100  
 R-PLACE4000106//Homo sapiens clone 24561 unknown mRNA, partial cds.//9.3e-100:419:91//AF055010  
 R-PLACE4000128//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//9.6e-45:284:90//AC003007  
 35 R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//1.6e-19:118:100//AB007969  
 R-PLACE4000147//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//8.9e-17:208:73//AC005034  
 R-PLACE4000156//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-43:281:90//AL021939  
 40 R-PLACE4000192  
 R-PLACE4000222//Homo sapiens clone DJ1129J21, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.4e-44:280:82//AC005631  
 45 R-PLACE4000233//Homo sapiens full-length insert cDNA YH59G06.//1.8e-79:414:97//AF074981  
 R-PLACE4000247//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//5.7e-59:558:76//AC005821  
 R-PLACE4000250//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.7e-44:313:84//AQ037381  
 50 R-PLACE4000252//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, complete sequence.//1.5e-39:311:83//AC005920  
 R-PLACE4000261//H.sapiens BF1P-g1H03np gene for immunoglobulin heavy chain variable region.//0.33:197:61//Z80410  
 R-PLACE4000269//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//1.4e-31:327:68//AC005510  
 55 R-PLACE4000270//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.3e-32:345:74//D87675  
 R-PLACE4000300//Sequence 61 from patent US 5744300.//0.0017:51:98//AR003339  
 R-PLACE4000320//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete

sequence.//8.2e-41:295:85//Z99495

R-PLACE4000323//Human chromosome 11 187a8 cosmid, complete sequence.//1.3e-32:404:75//U73640

R-PLACE4000326

R-PLACE4000344//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//0.32:135:68//AC005587

R-PLACE4000367//H.sapiens gene encoding RING finger protein.//0.61:146:67//Y07829

R-PLACE4000369//HS\_3181\_A1\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3181 Col=3 Row=C, genomic survey sequence.//7.1e-80:424:94//AQ173222

R-PLACE4000379//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE.//1.7e-05:160:65//AL022312

R-PLACE4000387//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.4e-47:351:81//AC004913

R-PLACE4000392//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//8.5e-88:541:88//AL034377

R-PLACE4000401//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//2.7e-17:143:83//AC000406

R-PLACE4000411

R-PLACE4000445//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.028:91:78//AC005628

R-PLACE4000465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-43:532:71//AL022156

R-PLACE4000489//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//4.1e-06:357:61//AE001427

R-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-37:416:74//AC005865

R-PLACE4000522

R-PLACE4000548//Homo sapiens 12p13.3 PAC RPCI5-1096D14 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.0020:383:60//AC005342

R-PLACE4000558//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//2.9e-44:465:75//AC002996

R-THYRO1000026//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 37E16, WORKING DRAFT SEQUENCE.//2.2e-43:354:82//Z83844

R-THYRO1000034//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.022:327:60//AE001422

R-THYRO1000035//HS\_3018\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=20 Row=L, genomic survey sequence.//2.3e-36:228:91//AQ092318

R-THYRO1000040//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0:367:56//AC004157

R-THYRO1000070//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence.1/1e-44:284:89//U14573

R-THYRO1000072//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//6.6e-33:150:83//U14567

R-THYRO1000085

R-THYRO1000092//Homo sapiens chromosome 7qtel0 BAC F6, complete sequence.//3.3e-36:301:78//AF104455

R-THYRO1000107//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 125I3, WORKING DRAFT SEQUENCE.//1.4e-35:282:82//AL033528

R-THYRO1000111//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//4.0e-32:351:65//AC002300

R-THYRO1000121//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//6.6e-77:507:85//U91318

R-THYRO1000124//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.66:334:59//AC005840

R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//2.3e-88:449:96//AF087142

R-THYRO1000132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING DRAFT SEQUENCE.//1.1e-40:298:84//Z95114

R-THYRO1000156//Homo sapiens chromosome 17, clone hRPK.849\_N\_15, complete sequence.//3.4e-37:425:73//AC005703

R-THYRO1000163//RPCI11-1B20.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1B20, genomic survey sequence.//8.4e-38:276:84//B63536

R-THYRO1000173//Human DNA sequence from PAC 323B6 on chromosome X contains ESTs CpG island.//1.1e-

70:553:81//Z83841

R-THYRO1000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410I8, WORKING DRAFT SEQUENCE.//6.7e-41:345:81//AL031732

R-THYRO1000187//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.3e-43:356:80//U18271

R-THYRO1000190//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//2.6e-40:386:77//AC004139

R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//1.1e-108:535:97//AJ005698

R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.4e-113:559:97//AB014552

R-THYRO1000206//Rat PMSG-induced ovarian mRNA, 3' sequence, N4.//4.0e-43:318:86//D84482

R-THYRO1000221//Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//2.7e-44:452:76//AC002115

R-THYRO1000241//Homo sapiens Cosmid Clone p129d11 unknown chromosomal location, complete sequence.//4.8e-58:447:81//AC000039

R-THYRO 1000242

R-THYRO1000253//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//3.4e-56:300:84//Z95152

R-THYRO1000270

R-THYRO1000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//4.8e-113:584:96//AL031664

R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//1.1e-98:566:91//AB016068

R-THYRO1000320//HS\_2033\_B1\_A07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=13 Row=B, genomic survey sequence.//0.97:211:63//AQ233366

R-THYRO1000327//Sequence 1 from patent US 5541298.//2.8e-52:289:93//I24058

R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//1.1e-111:559:96//AB018333

R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//4.6e-47:317:87//U29091

R-THYRO1000368//HS\_3049\_A1\_E12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=23 Row=I, genomic survey sequence.//7.0e-11:111:83//AQ126777

R-nnnnnnnnnnn

R-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//2.4e-101:545:93//AC006019

R-THYRO1000394//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.6e-46:233:88//AC006078

R-THYRO1000395//Mouse MIPP mRNA for a placenta-expressed gene.//2.3e-57:395:85//X58523

R-THYRO 1000401

3.3e-111:546:97//AF051907

R-THYRO1000438//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.7e-44:289:89//AC005231

R-THYRO1000452//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, complete sequence.//6.7e-27:222:82//AC005668

R-THYRO1000471//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//2.4e-36:369:76//AL021391

R-THYRO1000484//Homo sapiens clone DJ1099N07, complete sequence.//1.6e-43:288:81//AC004962

R-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.6e-95:512:94//AC005740

R-THYRO1000501//HS\_2208\_A1\_G11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=21 Row=M, genomic survey sequence.//0.0063:189:63//AQ091586

R-THYRO1000502//Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, complete cds.//0.19:468:60//AF000987

R-THYRO1000505//Homo sapiens chromosome 19, cosmid R31546, complete sequence.//0.20:214:58//AC004798

R-THYRO1000558

R-THYRO 1000569

R-THYRO1000570//Homo sapiens full-length insert cDNA clone ZD76G10.//4.3e-41:209:100//AF086408

R-nnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds.//8.2e-107:533:97//AF075587

R-THYRO 000596//Mus musculus mitochondrial DNA polymerase accessory subunit (MtPolB) mRNA, nuclear gene encoding mitochondrial protein, partial cds.//0.36:170:67//AF006072

- R-THYRO1000602//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.2e-53:289:92//D87675  
R-THYRO 1000605  
R-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//1.3e-31:261:82//AC005546
- 5 R-THYRO1000637//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-06:249:63//AL022323  
R-THYRO1000641//P.falcapurum glutamic acid-rich protein gnen, complete cds.//3.1e-08:244:68//J03998  
R-THYRO1000658//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.9e-49:282:93//U14572  
R-nnnnnnnnnnn
- 10 R-THYRO1000666//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//1.9e-20:215:77//AL031005  
R-THYRO1000676//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//1.2e-06:227:64//AC004069  
R-THYRO1000684  
R-THYRO1000699  
R-THYRO1000712
- 15 R-THYRO1000734//Human BAC clone RG19D16, complete sequence.//3.7e-14:468:64//AC002460  
R-THYRO1000748//Homo sapiens cosmid 123E15, complete sequence.//2.6e-11:182:73//AF024533  
R-THYRO1000756//Sequence 21 from patent US 5552281.//1.4e-15:106:98//U25660  
R-THYRO1000777//Plasmodium falcapurum MAL3P2, complete sequence.//1.0:175:66//AL034558  
R-THYRO1000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 2335P6, genomic survey sequence.//1.2e-81:391:99//A0038226  
R-THYRO1000787//Homo sapiens chromosome Y, clone 264.M,20, complete sequence.//9.4e-07:494:58//AC004617
- 25 R-THYRO1000793  
R-THYRO1000796//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING DRAFT SEQUENCE.//1.7e-42:379:79//Z93014  
R-THYRO1000805//Human Chromosome 11 pac pDJ610/20, WORKING DRAFT SEQUENCE, 18 unordered pieces.//4.7e-40:362:76//AC002555
- 30 R-THYRO1000815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//4.0e-58:295:92//Z82199  
R-THYRO1000829//Sequence 7 from patent US 5716622.//0.97:362:61//87788  
R-THYRO1000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence.//3.3e-57:522:76//AC004738
- 35 R-THYRO1000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//4.2e-17:291:69//AC005849  
R-THYRO1000855//Human DNA sequence from clone 366B10 on chromosome 22q12.2-12.3. Contains GSSs, complete sequence.//1.1e-41:419:75//AL031592  
R-THYRO1000865//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//9.0e-47:294:84//AL034549  
R-THYRO1000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380F5, WORKING DRAFT SEQUENCE.//3.7e-111:569:96//AL031719  
R-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0e-97:554:92//AC006015
- 45 R-THYRO1000926//Homo sapiens CAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.6e-109:566:94//AF079529  
R-THYRO1000934//Homo sapiens full-length insert cDNA clone ZD69A10.//1.6e-104:539:95//AF086378  
R-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ5714, WORKING DRAFT SEQUENCE, 29 unordered pieces.//8.9e-61:478:81//AC004229
- 50 R-THYRO1000952//Human autoimmune thyroid disease-related antigen mRNA.//5.3e-16:116:93//M28639  
R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds.//3.2e-59:321:95//AF047440  
R-THYRO1000975//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//1.9e-44:396:79//AC006126
- 55 R-THYRO1000983//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//0.99:71:78//AC005562  
R-THYRO1000984//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.7e-42:320:84//AC006078

R-THYRO1000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z84466

R-THYRO1001003//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//2.5e-39:310:83//AQ253727

5 R-THYRO1001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//2.5e-50:300:88//Z84466

R-THYRO1001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 2007J14, genomic survey sequence.//5.1e-26:143:100//B56677

10 R-THYRO1001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2386P3, genomic survey sequence.//1.4e-48:316:87//AQ239882

R-THYRO1001093

R-THYRO1001100//Homo sapiens BAC clone RG152G17 from 7q22-q31.1, complete sequence.//0.47:102:73//AC005070

R-THYRO1001120

15 R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D.//8.9e-81:429:94//AJ006417

R-THYRO1001133//CIT-HSP-2381110.TR CIT-HSP Homo sapiens genomic clone 2381110, genomic survey sequence.//4.7e-12:237:67//AQ111077

R-THYRO1001134

20 R-THYRO1001142//H.sapiens CpG island DNA genomic Mse1 fragment, clone 81d1, reverse read cpg81d1.rt1a.//0.95:214:60//Z56037

R-THYRO1001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence.//4.6e-26:262:77//B04145

R-THYRO1001177

25 R-THYRO1001189//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-41:281:87//AC003973

R-THYRO 1001204

R-THYRO1001213//Human Alu repeat sequence A6.//3.8e-38:236:88//U12581

R-THYRO1001262//Homo sapiens, clone hRPK\_16\_A\_1, complete sequence.//8.7e-53:442:79//AC006227

R-THYRO1001271//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0224P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered pieces.//0.53:330:61//AC004630

30 R-THYRO 1001290

R-THYRO1001313//H.sapiens CpG island DNA genomic Mse1 fragment, clone 195h3, forward read cpg195h3.ft1b.//0.046:126:66//Z57783

R-THYRO1001320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//3.0e-58:476:80//Z82207

35 R-THYRO100132//Plasmodium falciparum MAL3P2, complete sequence.//1.0e-08:408:62//AL034558

R-nnnnnnnnnnn

R-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//3.2e-08:266:64//AB018288

40 R-THYRO1001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence.//1.7e-85:471:92//B05884

R-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence.//1.8e-109:584:94//AC005660

R-THYRO1001374

R-THYRO1001401//Human pigment epithelium-derived factor gene, complete cds.//4.2e-51:333:88//U29953

45 R-THYRO1001403//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//8.7e-38:307:82//AC002377

R-THYRO1001405

R-THYRO1001406//RPC11-69F22.TK RPC11 Homo sapiens genomic clone R-69F22, genomic survey sequence.//1.9e-67:400:90//AQ238297

50 R-THYRO1001411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 80N2, WORKING DRAFT SEQUENCE.//2.2e-06:349:63//AL031123

R-THYRO1001428//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118122) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.2e-89:506:86//AJ002553

R-THYRO1001434//Microcentrus caryae 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//1.0:176:61//U77877

55 R-THYRO1001458//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//3.3e-07:196:67//AL021578



- R-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered piece.//1.2e-99:517:95//AC006001
- R-THYRO1001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//8.5e-14:221:70//AC004085
- 5 R-THYRO10001534//HS\_2242\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence.//0.00012:141:68//AQ182326
- R-THYRO1001537//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//0.42:323:60//AL023876
- 10 R-THYRO1001541//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.7e-42:370:78//AC005077
- R-THYRO1001559//Homo sapiens 12q24.2 PAC RPCi5-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0:144:67//AC005868
- R-THYRO1001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.43:268:61//AC005308
- 15 R-THYRO1001573//M.avium rpsL gene.//0.98:131:66//X80120
- R-THYRO1001584//A. longa plastid genes for ribosomal proteins and tRNAs.//0.29:502:58//X75653
- R-THYRO1001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.5e-33:319:78//AL023808
- R-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//4.4e-13:320:67//AC005919
- 20 R-THYRO1001605//Human DNA sequence from PAC 358H7 on chromosome X.//1.9e-32:391:76//Z77249
- R-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//1.9e-81:448:92//AJ002190
- R-THYRO1001637//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 688G8, WORKING DRAFT SEQUENCE.//5.4e-41:381:78//AL031671
- 25 R-THYRO1001656//HS\_2201\_B2\_A08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=B, genomic survey sequence.//0.096:162:63//AQ293168
- R-THYRO1001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds.//1.0:229:62//U22954
- 30 R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//4.8e-110:562:95//AJ225089
- R-THYRO1001673//CIT-HSP-2327D12. TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequence.//1.5e-17:224:68//AQ042426
- R-THYRO1001703//Homo sapiens clone 198 unknown mRNA, partial sequence.//1.6e-44:251:93//AF091072
- 35 R-THYRO1001706//Homo sapiens clone DJ0935K16, complete sequence.//1.8e-26:378:68//AC006011
- R-THYRO1001721//, complete sequence.//1.3e-101:571:92//AC005500
- R-nnnnnnnnnnn
- R-THYRO1001745//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//1.1e-15:193:70//AC004777
- 40 R-THYRO1001746//Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 3.//0.54:260:61//M88244
- R-THYRO1001772//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-12:285:64//AL022156
- R-THYRO1001793
- R-THYRO1001809//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING DRAFT SEQUENCE.//2.5e-43:486:74//AL031728
- 45 R-THYRO1001854//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//5.0e-41:245:87//AC005696
- R-THYRO1001895//Human Chromosome 11p14.3 PAC clone 6-106f23, complete sequence.//4.4e-12:419:61//AC005137
- 50 R-THYRO1001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b In DGCR Region, complete sequence.//8.1e-35:340:78//AC000075
- R-VESEN1000122//Homo sapiens Luman mRNA, complete cds.//1.3e-23:138:98//AF009368
- R-Y79AA1000013
- 55 R-Y79AA1000033//Homo sapiens BAC clone GS114109 from 7p14-p15, complete sequence.//9.9e-112:551:97//AC006027
- R-Y79AA1000037//CIT-HSP-2334F3. TR CIT-HSP Homo sapiens genomic clone 2334F3, genomic survey sequence.//0.16:308:60//AQ036673
- R-Y79AA1000059//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.1e-

56:314:88//AC002300

R-Y79AA1000065//Human carboxylesterase gene, exon 5.//0.64:203.63//D21079

R-Y79AA1000131//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0548N01; HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//7.0e-18:169.79//AC004795

R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.1e-106:474.98//AL031864

R-Y79AA1000202//CIT978SK-A-518G2.TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey sequence.//1.0e-10:78.97//B68074

R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//6.5e-59:386.90//AC004854

R-Y79AA1000230//Cyttauxoon felis 18S ribosomal RNA.//1.0:167.62//L19080

R-Y79AA1000231//HS\_3009\_A1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=5 Row=O, genomic survey sequence.//6.4e-52:348.88//AQ090225

R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds.//0.65:127.65//D10558  
R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//4.7e-40:300.84//Z98047

R-Y79AA10003131//Human DNA sequence from PAC 179I15. BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//5.0e-14:136.83//Z92540

R-Y79AA1000328

R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence).//0.55:189.65//X54107

R-Y79AA1000346//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//8.8e-36:300.81//X84692

R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//5.7e-45:403:80//AL022163

R-Y79AA1000368

R-Y79AA1000405//RPCI11-16B12.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16B12, genomic survey sequence.//0.10:171.65//B88000

R-Y79AA1000410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING

DRAFT SEQUENCE.//4.1e-50:361.83//Z93097

R-Y79AA1000420//Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds.//0.071:474.57//AF033037

R-Y79AA1000469//Homo sapiens clone NH0140K04, complete sequence.//1.8e-86:221.90//AC005033

R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//2.1e-14:179:72//AC004057

R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.5e-43:321.83//AC005282

R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//0.0012:275.59//AC006143

R-Y79AA1000540//Z.diploperennis repetitive DNA (clone ZEAR 260).//0.0017:258.62//X53609

R-Y79AA1000560//Mouse mRNA for alpha-adaptin (c).//6.1e-32:390.70//X14972

R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 23B4, complete sequence.//0.96:224.61//AC002325

R-Y79AA1000627//Homo sapiens full-length insert cDNA ZA77G02.//6.3e-100:533.94//AF075117

R-Y79AA1000705//RPCI11-76G7.TV RPCI11 Homo sapiens genomic clone R-76G7, genomic survey sequence.//4.6e-88:429.98//AQ268433

R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//2.7e-112:586:95//AF093670

R-Y79AA1000748

R-Y79AA1000752

R-Y79AA1000774//CIT-HSP-2288K24.TF CIT-HSP Homo sapiens genomic clone 2288K24, genomic survey sequence.//5.3e-45:316.86//AQ005014

R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds.//5.0e-17:107:100//D87433

R-Y79AA1000784//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00034:520:55//AC005505

R-Y79AA1000794//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 989H11, WORKING DRAFT SEQUENCE.//0.015:322:60//Z83851

R-Y79AA1000800//M.musculus tex264 mRNA (3'region).//1.1e-06:104:78//X80427

R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,

- complete sequence.//1.3e-35:207:95//AL034430  
 R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.7e-44:285:81//D14336
- 5 R-nnnnnnnnnnnn//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//0.70:365:60//AL023574  
 R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L36151  
 R-Y79AA1001555  
 R-Y79AA1001585
- 10 R-Y79AA1001594//Human DNA sequence from PAC 80G11 on chromosome X; contains STS.//6.6e-19:241:76//Z94722  
 R-Y79AA1001603//H.sapiens CpG island DNA genomic MseI fragment, clone 72f8, forward read cpq72f8.ft1a.//3.3e-21:131:96//Z62766  
 R-Y79AA1001613  
 R-Y79AA1001647//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//6.3e-08:338:63//Z82975
- 15 R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//3.2e-11:114:84//AP000008  
 R-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//M22743  
 R-nnnnnnnnnnnn//RPC111-42M5.TJ RPC111 Homo sapiens genomic clone R-42M5, genomic survey sequence.//0.013:64:89//AQ052792
- 20 R-Y79AA1001696//Apis mellifera ligustica complete mitochondrial genome.//9.3e-09:428:58/L06178  
 R-Y79AA1001705  
 R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ro gene, partial cds.//2.2e-45:554:75//AF042139  
 R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//1.0:414:57//AE001402
- 25 R-nnnnnnnnnnnn//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//2.8e-05:329:61//Z98044  
 R-Y79AA1001827//Oryctolagus cuniculus PIUS mRNA, complete cds.//2.3e-90:557:89//U74297  
 R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//2.1e-34:306:78//Z95152
- 30 R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//14369  
 R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0089:527:58//AB016874
- 35 R-Y79AA1001874  
 R-Y79AA1001875//M.musculus mRNA for Rab7 protein.//5.8e-45:170:92//X89650  
 R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.0:138:68//AL022577
- 40 R-Y79AA1002027//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.71:153:67//X04465  
 R-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 172B20, WORKING DRAFT SEQUENCE.//1.0:178:64//AL022319
- 45 R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.3e-49:377:81//AC005011  
 R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA.//4.0e-32:174:99//L77612  
 R-Y79AA1002103//CIT-HSP-2328I21.TR CIT-HSP Homo sapiens genomic clone 2328I21, genomic survey sequence.//1.9e-44:245:96//AQ044502
- 50 R-Y79AA1002115//CITBI-E1-2514F10.TF CITBI-E1 Homo sapiens genomic clone 2514F10, genomic survey sequence.//1.8e-24:249:78//AQ265752  
 R-Y79AA1002125//RPC11-15J6.TV RPC11-15J6 Homo sapiens genomic clone RPC11-15J6, genomic survey sequence.//8.5e-21:147:91//B75354
- 55 R-Y79AA1002139  
 R-Y79AA1002204  
 R-nnnnnnnnnnnn//Human ankyrin G (ANK-3) mRNA, complete cds.//0.040:319:59//U13616  
 R-Y79AA1002209//Psilotum nudum RT gene for reverse transcriptase (PT4).//0.99:106:65//X65415  
 R-Y79AA1002210

R-Y79AA1002211//H.sapiens NGAL gene.//1.0.311:59//X99133  
 R-Y79AA1002220//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING  
 DRAFT SEQUENCE.//5.9e-07:535:57//AL034557  
 R-Y79AA1002229  
 5 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//6.1e-117:564:98//AB014592  
 R-Y79AA1002246  
 R-Y79AA1002258//Homo sapiens mRNA for HIP3, complete cds.//1.3e-92:453:97//AB013384  
 R-Y79AA1002298//HS\_3071\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-  
 nomic clone Plate=3071 Col=16 Row=J, genomic survey sequence.//1.9e-56:384:87//AQ171331  
 10 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//2.5e-108:403:99//AB014534  
 R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173112 map 10q25, complete sequence.//  
 1.1e-07:368:61//AC005887  
 R-Y79AA1002351  
 R-Y79AA1002361//H.sapiens CpG island DNA genomic MseI fragment, clone 65b9, reverse read cp95b9.rt1a.//  
 0.57:59:79//Z62206  
 15 R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPC.700\_H\_6, complete sequence.//2.0e-98:385:99//  
 AC005920  
 R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//5.4e-59:490:  
 76//AC004662  
 20 R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete se-  
 quence.//6.3e-08:103:80//AC004087  
 R-Y79AA1002431  
 R-nnnnnnnnnnn//Mouse transcriptional control element.//0.064:84:71//M17284  
 R-Y79AA1002472//Homo sapiens chromosome 19, BAC CTY-B-39315 (BC301323), complete sequence.//1.6e-  
 103:525:96//AC006116  
 25 R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//9.7e-38:302:  
 83//AC006238  
 R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.23:266:61//X95276

# Homology Search Result Data 4.

**[0307]** The result of the homology search of the Human Unigene using the clone sequence of 5'-end.

**[0308]** Data include

the name of clone,  
 title of the top hit data,  
 the P-value: the length of the compared sequence: identity (%), and  
 the Accession No. of the top hit data, as in the order separated by //.

**[0309]** Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069  
 F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:  
 L40157  
 45 F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U83668  
 F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078  
 F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247  
 F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharo-  
 myces cerevisiae]//0.00019:192:65//Hs.7900:W22411  
 50 F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI336759  
 F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417910  
 F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734  
 F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//0.27:  
 342:61//Hs.14207:U86453  
 55 F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//6.8e-169:791:98//Hs.27197:  
 AB018340  
 F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4e-37:243:88//Hs.2397:Z70200  
 F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]//5.3e-80:383:98//

Hs.135552:Al215187

F-HEMBA1000158//Homo sapiens OPA-containing protein mRNA, complete cds//2.1e-07:265.63//Hs.85313:AF071309

F-HEMBA1000168//ESTs//6.1e-35:257.85//Hs.13533:H23079

5 F-HEMBA1000180//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [H.sapiens]//1.3e-18:111.96//Hs.163863:W28729

F-HEMBA1000185//H.sapiens ERF-2 mRNA//1.0:125.68//Hs.78909:U07802

F-HEMBA1000193//EST//1.5e-48:266.95//Hs.160642:Al240133

F-HEMBA1000201//Human Ini1 mRNA, complete cds//6.5e-75:440.92//Hs.155626:U04847

10 F-HEMBA1000213//ESTs//0.21:239.62//Hs.26838:AA527529

F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequence//1.1e-57:529.68//Hs.8136:U81984

F-HEMBA1000227//Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA, complete cds//1.3e-05:311.64//Hs.81248:U63289

F-HEMBA1000231

15 F-HEMBA1000243//EST//5.9e-52:359.85//Hs.141433:N23377

F-HEMBA1000244//H.sapiens mRNA for cytokine inducible nuclear protein//0.0022:350.60//Hs.74019:X83703

F-HEMBA1000251//ESTs//3.2e-84:443.95//Hs.21068:N47460

F-HEMBA1000264//ESTs//0.76:227.61//Hs.5159:AA588562

F-HEMBA1000280//EST//1.7e-12:149.75//Hs.103418:AA035568

20 F-HEMBA1000282//ESTs//1.7e-16:164.79//Hs.123111:AA813186

F-HEMBA1000288//ESTs//5.4e-06:154.68//Hs.54174:N64406

F-HEMBA1000290//Human novel homeobox mRNA for a DNA binding protein//3.8e-07:412.61//Hs.37035:U07664

F-HEMBA1000302//EST//1.2e-41:238.94//Hs.147245:Al206095

F-HEMBA1000303

25 F-HEMBA1000304//ESTs//3.5e-11:96.87//Hs.163057:AA728946

F-HEMBA1000307//EST//7.7e-05:280.62//Hs.146462:Al24898

F-HEMBA1000327//ESTs//5.3e-92:435.99//Hs.100605:AA305965

F-HEMBA1000333//Human mRNA for KIAA0206 gene, partial cds//0.84:395.56//Hs.79299:D86961

F-HEMBA1000338//ESTs, Moderately similar to novel stromal cell protein [M.musculus]//2.4e-38:317.80//Hs.99189:X84712

30 F-HEMBA1000351//Human Line-1 repeat mRNA with 2 open reading frames//0.020:334.59//Hs.23094:M19503

F-HEMBA1000355//Myosin, heavy polypeptide 11, smooth muscle//0.11:336.61//Hs.78344:AF001548

F-HEMBA1000356//H.sapiens ERF-2 mRNA//0.031:317.59//Hs.78909:U07802

F-HEMBA1000357//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:441.78//Hs.154326:D42087

35 F-HEMBA1000368//ESTs//0.025:56.87//Hs.141629:H74010

F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 from 7q33-q35//0.99:433.58//Hs.159899:AC004853

F-HEMBA1000376//Oxytocin receptor//3.4e-43:569.70//Hs.2820:X64878

F-HEMBA1000387//ESTs//8.2e-104:535.94//Hs.78110:AA741320

F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15//2.3e-141:712.95//Hs.22900:AC004520

40 F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequence//1.7e-47:461.74//Hs.139088:AF070533

F-HEMBA1000396//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.2e-26:351.70//Hs.138992:C14008

F-HEMBA1000411//EST//2.6e-27:401.71//Hs.138719:N52915

F-HEMBA1000418//ESTs//0.0094:375.61//Hs.40140:Al079253

F-HEMBA1000422//EST//6.2e-23:225.78//Hs.132635:A1032875

45 F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//7.6e-31:616.66//Hs.159897:AB007970

F-HEMBA1000434//EST//0.0031:157.64//Hs.162328:AA559034

F-HEMBA1000442//EST//1.0:201.61//Hs.162434:AA577398

F-HEMBA1000456//Fanconi anemia complementation group C//0.58:362.59//Hs.37953:X66893

50 F-HEMBA1000459//EST//9.2e-21:157.86//Hs.132635:Al032875

F-HEMBA1000460//ESTs//2.9e-77:409.95//Hs.27135:W49590

F-HEMBA1000464//ESTs//6.6e-17:365.65//Hs.150675:AA127853

F-HEMBA1000469

55 F-HEMBA1000488//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//0.15:253.58//Hs.104640:AF000561

F-HEMBA1000490//Homo sapiens kinectin mRNA, complete cds//0.71:539.56//Hs.82709:Z22551

F-HEMBA1000491//ESTs//2.0e-21:361.65//Hs.152453:AA864970

F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.5e-39:312.77//Hs.5247:AF029750

- F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)/1.3e-08:57:100//Hs.155095:D13666
- F-HEMBA1000505//Homo sapiens KE04p mRNA, complete cds//1.0:197:62//Hs.131962:AF064093
- F-HEMBA1000508//EST//0.67:156:60//Hs.162898:AA659646
- 5 F-HEMBA1000518
- F-HEMBA1000519//EST//6.8e-52:300:91//Hs.149580:AI281881
- F-HEMBA1000520//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]/2.9e-16:132:84//Hs.155871:AA533783
- 10 F-HEMBA1000523//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]/2.1e-25:192:87//Hs.22383:R51067
- F-HEMBA1000531//ESTs, Weakly similar to heat shock protein [H.sapiens]/2.4e-57:288:97//Hs.116022:AA455706
- F-HEMBA1000534//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.8e-47:153:88//Hs.113283:AF018080
- F-HEMBA1000540//ESTs//8.6e-07:60:100//Hs.109755:AA180809
- 15 F-HEMBA1000542//Human lysyl oxidase-like protein mRNA, complete cds//0.088:581:57//Hs.65436:U24389
- F-HEMBA1000545//Human kpnI repeat mma (cDNA clone pcd-kpnI-4), 3' end//7.8e-106:731:83//Hs.139107:K00629
- F-HEMBA1000555//Human mRNA for KIAA0242 gene, partial cds//0.75:283:58//Hs.77495:D87684
- 20 F-HEMBA1000557//ESTs//3.9e-27:389:71//Hs.125087:AA495729
- F-HEMBA1000561//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.8e-64:665:72//Hs.137168:AB018303
- F-HEMBA1000563//ESTs//3.8e-51:257:98//Hs.47122:AI338977
- F-HEMBA1000568//EST//0.12:270:61//Hs.134833:AI091046
- F-HEMBA1000569//H.sapiens mRNA encoding GPI-anchored protein p137//3.8e-19:409:62//Hs.119283:Z48042
- 25 F-HEMBA1000575//EST//0.060:156:64//Hs.126277:AA826681
- F-HEMBA1000588//ESTs, Weakly similar to weakly similar to myosin heavy chain [C.elegans]/7.7e-41:217:96//Hs.55084:AA479162
- F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-44:228:97//Hs.155218:AJ007509
- 30 F-HEMBA1000592//ESTs, Weakly similar to sorting nexin 1 [H.sapiens]/1.7e-27:463:65//Hs.13794:AA203241
- F-HEMBA1000594//Human clone 230971 defective mariner transposon Hsma2 mRNA sequence//4.0e-68:574:79//Hs.159176:U92019
- F-HEMBA1000604//ESTs//3.3e-21:158:74//Hs.142924:AI092535
- F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.7e-120:561:99//Hs.5003:AB007925
- 35 F-HEMBA1000622//Homo sapiens DEC-205 mRNA, complete cds//5.2e-34:592:68//Hs.153563:AF011333
- F-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]/7.4e-22:166:84//Hs.26252:AA643235
- F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//2.1e-138:639:99//Hs.60103:AB014590
- 40 F-HEMBA1000655//ESTs//1.2e-54:503:77//Hs.140864:AA176174
- F-HEMBA1000657//Mucin 1, transmembrane//0.99:219:61//Hs.89603:J05582
- F-HEMBA1000662//ESTs//2.2e-52:257:99//Hs.63243:AI123912
- F-HEMBA1000673//H.sapiens mRNA for translin associated protein X//1.7e-47:366:79//Hs.96247:X95073
- F-HEMBA1000682//Oxytocin receptor//4.7e-59:873:72//Hs.2820:X64878
- 45 F-HEMBA1000686
- F-HEMBA1000702
- F-HEMBA1000705//EST//0.047:363:60//Hs.136379:AA521309
- F-HEMBA1000719//ESTs//2.7e-68:333:98//Hs.146195:AI039850
- F-HEMBA1000722//ESTs//0.49:283:60//Hs.21108:N92630
- 50 F-HEMBA1000726//EST//1.1e-45:183:87//Hs.149580:AI281881
- F-HEMBA1000727//ESTs//4.8e-95:442:100//Hs.22119:AA885491
- F-HEMBA1000747
- F-HEMBA1000749//ESTs//8.0e-14:108:77//Hs.154892:AI091568
- F-HEMBA1000752//EST//1.3e-25:344:69//Hs.160992:H52716
- 55 F-HEMBA1000769//ESTs//0.0018:206:63//Hs.153268:AA887239
- F-HEMBA1000773//ESTs//0.56:336:58//Hs.105964:N35803
- F-HEMBA1000774//EST//4.0e-38:312:79//Hs.162197:AA535216
- F-HEMBA1000791//ESTs//2.8e-87:413:99//Hs.112050:AA431300

- F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536  
 F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542  
 F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367  
 F-HEMBA1000843
- 5 F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.89764:X69962  
 F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572  
 F-HEMBA1000867  
 F-HEMBA1000869//ESTs//5.1 e-33:166:77//Hs.141186:R99609  
 F-HEMBA1000870//EST//0.032:130:66//Hs.157351:AI367237
- 10 F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047  
 F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660  
 F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:AI203154  
 F-HEMBA1000910//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-Kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.8e-11:309:65//Hs.4943:Z98046  
 F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537  
 F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:221:64//Hs.109804:D64142  
 F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete cds//3.8e-09:360:62//Hs.36850:AB011119
- 20 F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repair protein [H.sapiens]//9.4e-10:77:93//Hs.111445:H00596  
 F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [Homo sapiens]//0.0039:54:92//Hs.58338:AA609476
- 25 F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide-synthetase, phosphoribosylaminimidazole synthetase//0.93:132:66//Hs.82285:X54199  
 F-HEMBA1000960//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//0.080:128:71//Hs.118972:AA761369  
 F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87//Hs.84775:M23161
- 30 F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:AI127903  
 F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775  
 F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314  
 F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.3e-05:424:59//Hs.159564:AF061936
- 35 F-HEMBA1000985//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.0036:389:60//Hs.127338:AB007961  
 F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132  
 F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:193:84//Hs.24756:U43895  
 F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835
- 40 F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.9e-43:472:74//Hs.46468:U45984  
 F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//Hs.75758:X58529  
 F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//1.4e-140:661:98//Hs.158287:AB007937
- 45 F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:AI239572  
 F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.78160:AF010238  
 F-HEMBA1001022  
 F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.8e-28:376:72//Hs.159897:AB007970
- 50 F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:745:57//Hs.94592:AB005142  
 F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515  
 F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:AI281881  
 F-HEMBA1001052//EST//0.94:149:67//Hs.31216:AI017971  
 F-HEMBA1001059//N-ACETYLGLACTOSAMINE-6-SULFATASE PRECURSOR//4.6e-165:777:98//Hs.159479:U06088
- 55 F-HEMBA1001060//ESTs//6.8e-14:150:78//Hs.24821:AA044813  
 F-HEMBA1001071//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.119571:X14420  
 F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary factor 1 [H.sapiens]//1.1e-98:487:97//



- Hs.147802:R71297  
 F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//0.013:385:58//Hs.69949:M94172
- 5 F-HEMBA1001085//Human hSIAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U76248  
 F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//Hs.83987:U09284  
 F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017  
 F-HEMBA1001099  
 F-HEMBA1001109//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.4-61:341:85//Hs.5247:AF029750  
 F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497
- 10 F-HEMBA1001122//Human sapiens mRNA for KIAA0471 protein, complete cds//0.066:649:56//Hs.5347:AB007940  
 F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.5e-10:231:68//Hs.27349:AB007917  
 F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015474  
 F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.2e-73:527:77//Hs.159277:AB018341
- 15 F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.020:141:65//Hs.7482:AB014582  
 F-HEMBA1001172//EST//0.77-158:60//Hs.158894:AI378457  
 F-HEMBA1041174//ESTs//1.4e-63:363:92//Hs.132798:AA922226  
 F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//5.0e-54:555:71//Hs.55165:AA573499
- 20 F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463  
 P-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57//Hs.48824:D87717  
 F-HEMBA1001226//ESTs//1.9e-11:407:65//Hs.157977:AI369694  
 F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748
- 25 F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058  
 F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7647:M94046  
 F-HEMBA1001265  
 F-HEMBA1001281  
 F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL021155
- 30 F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-30:530:64//Hs.154050:AC004131  
 F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119534:AJ224741  
 F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:77//Hs.155464:AF088219  
 F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53:272:97//Hs.154563:AI129590
- 35 F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.norvegicus]//2.6e-66:241:99//Hs.120847:AA731201  
 F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873  
 F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.23:562:58//Hs.22039:AB018301  
 F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2.5e-31:165:99//Hs.152213:L20861
- 40 F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-08:185:68//Hs.108734:AI073427  
 F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013  
 F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569
- 45 F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//3.6e-105:516:97//Hs.9006:AF057358  
 F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794  
 F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425:AI198074  
 F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156
- 50 F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353  
 F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.0e-132:643:97//Hs.124217:AA020848  
 F-HEMBA1001388  
 F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660
- 55 F-HEMBA1001398  
 F-HEMBA1001405//EST//1.0:135:63//Hs.146833:AI151117  
 F-HEMBA1001407//ESTs//10.53:390:57//Hs.150447:AI017798  
 F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108

F-HEMBA1001413  
 F-HEMBA1001415//EST//1.3e-12:176.75//Hs.133172:AI051605  
 F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040  
 F-HEMBA1001433//ESTs//1.3e-21:333.69//Hs.131648:AI025726  
 5 F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-74:469:80//Hs.1361:M55053  
 F-HEMBA1001442//EST//0.29:181.64//Hs.116883:AA663031  
 F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//6.8e-47:550.71//Hs.55165:AA573499  
 10 F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIP1) mRNA, complete cds//0.82:312:58//Hs.7019:AB005666  
 F-HEMBA1001454//ESTs//1.2e-46:297.80//Hs.152395:AA533107  
 F-HEMBA1001455//ESTs//7.3e-103:502.97//Hs.112860:AA442412  
 F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323.88//Hs.40100:AB002390  
 15 F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2e-104:489.99//Hs.14409:AB011144  
 F-HEMBA1001478//EST//0.013:205.61//Hs.157309:AI365451  
 F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307.84//Hs.155464:AF088219  
 F-HEMBA1001510//H. sapiens mRNA for G13 protein//2.1e-71:405.92//Hs.42853:X98054  
 20 F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-105:773.82//Hs.23094:M19503  
 F-HEMBA1001517//EST//3.6e-09:271.65//Hs.162347:AA564902  
 F-HEMBA1001522//ESTs//4.3e-13:85.95//Hs.126707:AI376869  
 F-HEMBA1001526  
 25 F-HEMBA1001533//EST//1.0:75.73//Hs.145360:AI252476  
 F-HEMBA1001557//EST//3.5e-13:261.64//Hs.161496:N66580  
 F-HEMBA1001566//EST//3.7e-07:354.64//Hs.43830:N26652  
 F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338.97//Hs.91589:M36205  
 30 F-HEMBA1001570//ESTs//1.5e-47:369.82//Hs.107657:AA126814  
 F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//7.0e-175:678.99//Hs.159597:AJ012449  
 F-HEMBA1001581//ESTs//4.4e-07:237.67//Hs.152304:AA605184  
 F-HEMBA1001585//ESTs//1.1e-11:81.100//Hs.16364:AI357228  
 35 F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210.64//Hs.115778:D79988  
 F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855.78//Hs.90998:D50918  
 F-HEMBA1001608//EST//1.0:201.60//Hs.136747:AA749210  
 F-HEMBA1001620//ESTs//1.5e-39:211.98//Hs.131063:AI016400  
 F-HEMBA1001635//ESTs//4.0e-33:168.100//Hs.122655:AI361870  
 40 F-HEMBA1001636//ESTs, Moderately similar to !!! ALU SUBFAMILY SP WARNING ENTRY !!! [H.sapiens]//0.038:198.64//Hs.34579:AI338536  
 F-HEMBA1001640//ESTs//1.1e-24:315.71//Hs.34114:AA776899  
 F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629.61//Hs.79706:U53204  
 F-HEMBA1001651//EST//3.6e-07:285.63//Hs.132558:AA948560  
 45 F-HEMBA1001655//ESTs//1.4e-95:497.96//Hs.59563:AA203283  
 F-HEMBA1001658//EST//0.18:251.59//Hs.117724:H47121  
 F-HEMBA1001661  
 F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//7.9e-146:669.99//Hs.107254:AC005943  
 50 F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//2.0e-57:447.79//Hs.158095:AB007953  
 F-HEMBA1001678//ESTs//4.0e-50:360.83//Hs.146811:AA410788  
 F-HEMBA1001681//EST//1.0:165.58//Hs.136790:AA776060  
 F-HEMBA1001702//EST//0.015:312.61//Hs.162839:AA648760  
 55 F-HEMBA1001709//EST//0.85:131.65//Hs.131451:AI023995  
 F-HEMBA1001711//ESTs//0.084:425.56//Hs.125346:AI302836  
 F-HEMBA1001712//EST//0.26:214.59//Hs.159088:AI383114  
 F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus nor-

- vegicus//J.3.0e-30:195:92//Hs.132948:AA194452  
 F-HEMBA1001718//EST//J.0.0044:275:60//Hs.125969:AA889554  
 F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//J.0.24:50:1:57//Hs.101524:U58197  
 F-HEMBA1001731//EST//J.1.2e-06:261:63//Hs.132331:AI028363  
 5 F-HEMBA1001734//ESTs//J.0.018:177:63//Hs.129631:AI000415  
 F-HEMBA1001744//EST//J.7e-77:420:92//Hs.133226:AI052250  
 F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//J.0.37:300:62//Hs.10887:AB013924  
 F-HEMBA1001746//ESTs//J.0.31:168:66//Hs.27237:N68328  
 F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//J.0.76:218:60//Hs.135553:  
 10 N41598  
 F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//J.0.98:219:60//Hs.98776:AC005622  
 F-HEMBA1001784//Homo sapiens mRNA for KJAA0474 protein, complete cds//J.6.4e-09:265:67//Hs.158232:  
 AB007943  
 F-HEMBA1001791  
 15 F-HEMBA1001800//EST//J.3.1e-41:331:81//Hs.127142:AA937570  
 F-HEMBA1001803//EST//J.0.0062:269:59//Hs.49075:N64817  
 F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//J.1.8e-07:439:59//Hs.266:U06233  
 F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//J.2.-5e-175:809:98//Hs.  
 118164:AB007969  
 20 F-HEMBA1001809//ESTs//J.6.0e-101:497:97//Hs.155127:AA625305  
 F-HEMBA1001815  
 F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds//J.4.9e-80:842:70//Hs.  
 158174:U66561  
 F-HEMBA1001820//EST//J.0.057:214:62//Hs.148715:A1223845  
 25 F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//J.6.7e-42:510:65//Hs.66392:  
 AF064244  
 F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//J.5.2e-13:253:68//Hs.85313:  
 AF071309  
 F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//J.0.96:288:60//Hs.6151:D87078  
 30 F-HEMBA1001844//ESTs//J.1.1e-29:197:80//Hs.155243:N70293  
 F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//J.2.0e-23:379:68//Hs.6833:AB002324  
 F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//J.2.8e-185:865:98//Hs.78946:  
 AB014517  
 F-HEMBA1001864//EST//J.0.27:145:63//Hs.162585:AA593121  
 35 F-HEMBA1001866//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE  
 PRECURSOR [D.melanogaster]//J.3.2e-39:293:84//Hs.152332:AI141922  
 F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//J.8.1e-70:367:95//Hs.15423:T84036  
 F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//J.5.4e-86:835:76//Hs.  
 158095:AB007953  
 40 F-HEMBA1001896  
 F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds//J.0.43:114:71//Hs.6133:U93436  
 F-HEMBA1001912//ESTs//J.4.1e-79:398:97//Hs.26660:AI312633  
 F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds//J.0.00031:  
 200:62//Hs.9573:AF027302  
 45 F-HEMBA1001915//EST//J.0.082:128:64//Hs.126542:AA916511  
 F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//J.0.46:374:59//Hs.31575:AF100141  
 F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//J.6.7e-186:  
 855:99//Hs.154934:AF000145  
 F-HEMBA1001939//ESTs//J.4.9e-34:342:77//Hs.132711:AI377295  
 50 F-HEMBA1001940//ESTs//J.8.6e-15:149:81//Hs.141129:R86221  
 F-HEMBA1001942//ESTs//J.0.0014:271:62//Hs.124514:AI219882  
 F-HEMBA1001945//EST//J.0.98:142:64//Hs.161540:N85943  
 F-HEMBA1001950//ESTs//J.0.99:188:64//Hs.28639:R78360  
 F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MB2 (MB2D) mRNA, complete cds//J.0.30:85:69//  
 55 Hs.25674:AF072242  
 F-HEMBA1001962//ESTs//J.0.0012:289:59//Hs.125492:AA938930  
 F-HEMBA1001964//EST//J.0.73:153:64//Hs.112161:AA477708  
 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/

Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178  
 F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732  
 F-HEMBA1001987//ESTs, Moderately similar to hTAF1I68 [H.sapiens]//2.8e-29:151:100//Hs.124106:AA948100  
 5 F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581  
 F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//9.8e-09:294:63//Hs.99936:X14487  
 F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803:W63582  
 10 F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64//Hs.78867:MG3426  
 F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545:U32907  
 F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:AI049827  
 F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057  
 15 F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-26:223:81//Hs.105292:AA504776  
 F-HEMBA1002084  
 F-HEMBA1002092  
 F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds//5.6e-21:124:96//Hs.101842:L32832  
 20 F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09:434:62//Hs.135102:AI190276  
 F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:AI129973  
 F-HEMBA1002119  
 F-HEMBA1002125//H.sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802  
 F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393  
 25 F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:60//Hs.79170:D86980  
 F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6e-06:353:62//Hs.23741:AB018263  
 F-HEMBA1002151  
 F-HEMBA1002153//EST//10.014:328:60//Hs.149115:AI244695  
 F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//5.6e-49:303:79//Hs.158241:AB007976  
 30 F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-40:616:67//Hs.929:M57965  
 F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.44766:AJ007590  
 F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs.155464:AF088219  
 F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//Hs.114808:AF026245  
 35 F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141  
 F-HEMBA1002189//EST//5.1e-24:193:81//Hs.163161:AA778363  
 F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.27:382:59//Hs.21992:AB014589  
 F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.2e-14:199:72//Hs.159897:AB007970  
 40 F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696  
 F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767  
 F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//1.6e-47:251:96//Hs.59906:AA001281  
 F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.4e-57:375:71//Hs.67619:AB007957  
 45 F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80//Hs.43681:AL022394  
 F-HEMBA1002237//EST//0.044:137:66//Hs.144448:AA812455  
 F-HEMBA1002241  
 F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887  
 50 F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKI) mRNA, complete cds//1.1e-152:731:97//Hs.159564:AF061936  
 F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420  
 F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//1.0:395:60//Hs.150926:AF017445  
 55 F-HEMBA1002270//ESTs//2.5e-87:504:89//Hs.124440:H95404  
 F-HEMBA1002321//Homo sapiens oxidized low-density lipoprotein receptor mRNA, complete cds//0.17:338:60//Hs.77729:AB010710  
 F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982

- F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//Hs.154326:D42087  
 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-187:872:98//Hs.6162:AB018314  
 F-HEMBA10023481//EST//1.0e-19:285:70//Ms.121860:AA776692  
 F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996  
 5 F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//2.4e-189:872:99//Hs.119023:AF092563  
 F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216  
 F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144  
 F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:97//Hs.25527:AC005954  
 10 F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141  
 F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.90798:U9289  
 F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//0.11:111.67//Hs.162154:AA528561  
 15 F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B, 6.8K [H.sapiens]//1.3e-71:346:98//Hs.136121:W26490  
 F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160  
 F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783  
 20 F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:92//Hs.154583:D50912  
 F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89631:U48508  
 F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8e-45:331:83//Hs.6189:AB011133  
 F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235  
 F-HEMBA1002495  
 25 F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161  
 F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74//Hs.19949:X98173  
 F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:460:83//Hs.113283:AF018080  
 F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//9.0e-159:738:98//Hs.6764:AJ011972  
 30 F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795  
 F-HEMBA1002538//EST//0.97:68:73//Hs.134672:AI087951  
 F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete cds//6.1e-46:238:87//Hs.10458:AF088219  
 F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138:655:98//Hs.68900:AF016903  
 35 F-HEMBA1002552//Human Hep27 protein mRNA, complete cds//2.8e-08:173:68//Hs.102137:U31875  
 F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.00020:603:57//Hs.20912:AB012162  
 F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205  
 F-HEMBA1002561//Humancore 23574 mRNA sequence//4.7e-17:268:72//Hs.79385:U90905  
 40 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//4.3e-142:457:99//Hs.151411:AF075587  
 F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//2.8e-30:156:100//Hs.32170:AB015132  
 F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159  
 F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363  
 45 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4e-176:820:99//Hs.20141:AB011169  
 F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013  
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.2e-189:632:97//Hs.91338:AB018351  
 50 F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65//Hs.125129:AB002334  
 F-HEMBA1002629//Human density enhanced phosphatase 1 mRNA, complete cds//1.3e-07:473:61//Hs.1177:U10886  
 F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390  
 F-HEMBA1002651  
 55 F-HEMBA1002659//Human vascular endothelial growth factor related protein VRP mRNA, complete cds//0.74:223:60//Hs.79141:U43142  
 F-HEMBA1002661//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-122:781:85//Hs.23094:M19503

- F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497  
 F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368  
 F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 1 (alpha)/0.00096:418:61//Hs.1323:S42457
- 5 F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.8e-11:541:601//Hs.124161:AF065164  
 F-HEMBA10026961//Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e-06:345:61//Hs.155647:AC004221
- 10 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.0e-12:327:62//Hs.13245:AB007924  
 F-HEMBA1002712  
 F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800  
 F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942:AB014521
- 15 F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGST3) mRNA, complete cds//0.21:157:66//Hs.111811:AB007867  
 F-HEMBA1002742//EST//0.97:138:60//Hs.160545:71596  
 F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061:X59372  
 F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806:AA018786
- 20 F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817  
 F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834:98//Hs.74750:AB011126  
 F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:492:96//Hs.11833:AI299947  
 F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 mRNA, complete cds//3.9e-05:528:59//Hs.128208:U63809
- 25 F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W60392  
 F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326  
 F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756  
 F-HEMBA1002801//ESTs//2.1e-24:162:67//Hs.124633:AA856938
- 30 F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169:820:97//Hs.28307:AF071185  
 F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744  
 F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733:89//Hs.6059:AF093119  
 F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:M279904
- 35 F-HEMBA1002833  
 F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550  
 F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823  
 F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730
- 40 F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AE79429  
 F-HEMBA1002896//ESTs//2.1e-1172:100//Hs.149215:AI051679  
 F-HEMBA1002921  
 F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001  
 F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915
- 45 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6e-174:803:99//Hs.14687:AB011148  
 F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:GenBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA130053  
 F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1.1e-05:479:59//Hs.74019:X83703
- 50 F-HEMBA1002944//Human putative endothelin receptor type B-like protein mRNA, complete cds//0.83:326:58//Hs.27747:U87460  
 F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.26762:AA913925  
 F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099  
 F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092  
 F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828
- 55 F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA454219  
 F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) //1.5e-37:247:89//Hs.188:L20971

- F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.7e-05:797:58//Hs.50758:AF092564
- F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525
- F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs.155464:AF088219
- 5 F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486
- F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:330:78//Hs.113283:AF018080
- F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.159425:AJ001454
- F-HEMBA1003037//EST//0.53:59:74//Hs.148011:M268003
- 10 F-HEMBA1003041//ESTs, Weakly similar to F58G11.6 [C.elegans]//1.7e-64:337:95//Hs.I05907:AA186514
- F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182
- F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438
- F-HEMBA1003067
- 15 F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164
- F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62//Hs.48998:AB007865
- F-HEMBA1003078//CYTOCHROME P450 IVF3//2.0e-29:452:67//Hs.106242:AB002454
- F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461
- F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881
- 20 F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721
- F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M.musculus]//0.98:216:61//Hs.97865:AA405872
- F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721
- F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802
- 25 F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//Hs.12432:AF070575
- F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.038:288:63//Hs.6162:AB018314
- F-HEMBA1003136
- F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279
- F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99//Hs.63931:AJ005670
- 30 F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.1e-24:171:83//Hs.I41874:AB014588
- F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740
- F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' region [E.coli]//4.7e-20:118:97//Hs.II8831:AA211895
- 35 F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523
- F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135
- F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412
- F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:154:85//Hs.113283:AF018080
- 40 F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765
- F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784
- F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310
- F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012
- F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.00054:432:58//Hs.I32206:AF039694
- 45 F-HEMBA1003250
- F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds//4.3e-08:426:64//Hs.49585:AF075292
- F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991
- F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020
- 50 F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864
- F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867
- F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds//2.9e-146:539:97//Hs.13225:AF038662
- F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//1.6e-167:799:98//Hs.12836:AB011109
- 55 F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R44912
- F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160
- F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.I05486:AA521012

- F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//1.5e-189;865.99//Hs.142224:AB001872
- F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49;399.80//Hs.154782:X99459
- F-HEMBA1003327//EST//7.7e-10;165.72//Hs.114826:AA056254
- 5 F-HEMBA1003328//EST//0.00023;128.67//Hs.126467:AA913328
- F-HEMBA1003330
- F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-26;256.78//Hs.146395:AB002329
- F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmid R31240, R30272 and R28549 containing the EKLf, GCDH, CRTc, and RAD23A genes, genomic sequence//0.37;187.65//Hs.80265:AD000092
- 10 F-HEMBA1003370//ESTs//8.2e-36;196.79//Hs.139158:AA226159
- F-HEMBA1003373//ESTs//1.0;195.61//Hs.127307:AI263819
- F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29;606.64//Hs.73919:X81637
- F-HEMBA1003380//ESTs//2.5e-21;303.70//Hs.37528:H58017
- F-HEMBA1003384//ESTs//0.14;281.61//Hs.159650:N95552
- 15 F-HEMBA1003395//ESTs//0.53;121.70//Hs.144873:AI202488
- F-HEMBA1003402//EST//0.029;148.66//Hs.116798:AA633813
- F-HEMBA1003403//Adducin 2 (beta) (alternative products)//5.0e-05;445.61//Hs.90951:U43959
- F-HEMBA1003408//ESTs//9.0e-12;87.98//Hs.70266:Z78309
- F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//9.5e-05;541.58//Hs.89709:L35546
- 20 F-HEMBA1003418//ESTs//3.5e-85;399.100//Hs.154489:AA564962
- F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0e-149;686.99//Hs.25812:AF058696
- F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43;271.60//Hs.47822:AB0002378
- F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8e-08;775.58//Hs.3847:U59632
- 25 F-HEMBA1003463//ESTs//3.3e-22;121.99//Hs.130847:AA058578
- F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cds//0.16;321.60//Hs.13999:AB014600
- F-HEMBA1003528//ESTs//3.8e-53;315.91//Hs.129688:AA057443
- F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-51;451.78//Hs.22271:D26067
- F-HEMBA1003538//ESTs//1.2e-82;415.96//Hs.162075:AI392811
- 30 F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (islet-1)//5.0e-75;736.73//Hs.505:U07559
- F-HEMBA1003548//ESTs//8.7e-77;411.95//Hs.163443:R23311
- F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cds//3.6e-33;562.64//Hs.81469:U01833
- F-HEMBA1003556
- F-HEMBA1003560//EST//3.7e-29;202.86//Hs.136858:AA767122
- 35 F-HEMBA1003568//ESTs//2.4e-06;214.65//Hs.143371:AI342327
- F-HEMBA1003569//Human metastasis-associated mtal mRNA, complete cds//2.0e-58;455.66//Hs.101448:U35113
- F-HEMBA1003571//ESTs//0.0025;198.63//Hs.116448:AA648972
- F-HEMBA1003579//ESTs//6.0e-110;513.99//Hs.97372:AA398546
- 40 F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19;108.99//Hs.18420:AA599232
- F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85;467.92//Hs.57937:W68285
- F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)//2.8e-06;439.62//Hs.83532:X59405
- F-HEMBA1003597//ESTs//0.0025;200.64//Hs.8473:T40827
- 45 F-HEMBA1003598//ESTs//0.18;187.63//Hs.98641:AA429916
- F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]//2.4e-133;644;97//Hs.3566:AA314782
- F-HEMBA1003617//Homo sapiens mRNA for HRIHFB2157, partial cds//7.9e-171;501.97//Hs.124956:AB015344
- 50 F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein PIASX-alpha mRNA, complete cds//4.4e-16;161.78//Hs.111323:AF077954
- F-HEMBA1003622//EST//0.0085;251.62//Hs.97343:AA401750
- F-HEMBA1003630//ESTs//7.5e-05;304.61//Hs.87131:AA233159
- F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds//7.9e-26;546.63//Hs.109901:AF013591
- 55 F-HEMBA1003640//ESTs//1.1e-11;267.66//Hs.34359:AI122719
- F-HEMBA1003645
- F-HEMBA1003646
- F-HEMBA1003656



- F-HEMBA1003662  
 F-HEMBA1003679//ESTs//1.5e-27.235.81//Hs.55855:AA621381  
 F-HEMBA1003680//ESTs//4.3e-49.251.97//Hs.152811:AA630906  
 F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06.464.61//Hs.79706:U53204  
 5 F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]/1.6e-100.478.98//Hs.118866:AI017072  
 F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5e-74.606.77//Hs.9028:AF039691  
 F-HEMBA1003692//ESTs//4.2e-43.252.92//Hs.39748:AA487187  
 F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.81:254.62//Hs.32316:AB011116  
 10 F-HEMBA1003714//ESTs//6.4e-98.495.95//Hs.43846:N49995  
 F-HEMBA1003715//ESTs//1.3e-11.228.69//Hs.101237:AA078760  
 F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45.692.68//Hs.91916:AF035317  
 F-HEMBA1003725//EST//2.5e-46.228.100//Hs.160069:AA926921  
 F-HEMBA1003729//ESTs//4.1e-48.253.96//Hs.26270:AA258839  
 15 F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6e-102.753.81//Hs.23094:M19503  
 F-HEMBA1003742//Homo sapiens chromosome 19, cosmid R31180//0.16:242.62//Hs.153325:AC005390  
 F-HEMBA1003758//ESTs//9.3e-12.408.61//Hs.148459:AI198946  
 20 F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35.430.69//Hs.8136:U81984  
 F-HEMBA1003773//EST//0.76:191.61//Hs.127020:AA934920  
 F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]/1.7e-24.224.81//Hs.18171:AA524327  
 F-HEMBA1003784//ESTs//0.13:120.67//Hs.161993:AA503172  
 F-HEMBA1003799//Interleukin 9 receptor//2.0e-17.263.70//Hs.1702:L39064  
 25 F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.13:222.61//Hs.89230:AF031815  
 F-HEMBA1003804//ESTs//1.4e-112.275.98//Hs.72132:AF039239  
 F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11.523.60//Hs.119537:M88108  
 F-HEMBA1003807//ESTs//4.1e-08.279.68//Hs.115679:AI379721  
 30 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3e-85.586.87//Hs.6051:AB014516  
 F-HEMBA1003836//EST//6.8e-06.98.74//Hs.I45447:AI204220  
 F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]/3.8e-40:151.88//Hs.139007:H74314  
 F-HEMBA1003856//ESTs//8.6e-53286.95//Hs.116645:AI005167  
 35 F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144.66//Hs.21355:AB002367  
 F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.3e-30.580.63//Hs.27621:U52840  
 F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10.87.95//Hs.89563:D32002  
 F-HEMBA1003880  
 40 F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cds//4.2e-18.302.67//Hs.23711:AB018295  
 F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]/1.2e-49.295.92//Hs.114673:W72675  
 F-HEMBA1003902//ESTs//1.1e-11.165.74//Hs.54632:AA976236  
 F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cds//0.081:345.58//Hs.78494:AB011097  
 45 F-HEMBA1003926//EST//2.5e-32.253.83//Hs.132635:AI032875  
 F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-38.313.69//Hs.154668:AB002389  
 F-HEMBA1003939//ESTs//3.4e-07.150.71//Hs.148926:R59562  
 F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis]/0.0029:222.61//Hs.I44236:W52380  
 F-HEMBA1003950//ESTs//0.98:200.62//Hs.163912:W20055  
 50 F-HEMBA1003953//Zinc finger protein 7 (KOX 4, clone HF.16)//0.00014:271.66//Hs.2076:M29580  
 F-HEMBA1003958//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/2.1e-44:243.76//Hs.91146:N73230  
 F-HEMBA1003959//ESTs//0.067:251.59//Hs.39915:H78567  
 F-HEMBA1003976//EST//6.7e-09.109.81//Hs.154635:AI138965  
 55 F-HEMBA1003978  
 F-HEMBA1003985//EST//0.32:115.69//Hs.102617:N47009  
 F-HEMBA1003987//ESTs//7.8e-07.60.100//Hs.66058:AA424456  
 F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//

0.022:349:58//Hs.104640:AF000561  
 F-HEMBA1004000//EST//7.2e-07:200.66//Hs.119082:AA358468  
 F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493  
 F-HEMBA1004012//ESTs//3.6e-09:177.68//Hs.106132:AA812573  
 5 F-HEMBA1004015//ESTs//3.0e-86:407.99//Hs.115679:AJ379721  
 F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.2e-51:359.84//Hs.15519:  
 AB018315  
 F-HEMBA1004038//ESTs//1.2e-58:324.94//Hs.61658:AI239930  
 F-HEMBA1004042//EST//0.00088:272.6//Hs.155763:AI312281  
 10 F-HEMBA1004045//EST//2.7e-20:408.66//Hs.162529:AA584160  
 F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.6101:M60315  
 F-HEMBA1004049//ESTs//8.1e-68:430.86//Hs.146307:AA584638  
 F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:457.58//Hs.82837:L13435  
 F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.5e-46:199.80//Hs.  
 15 46328:D87942  
 F-HEMBA1004074//ESTs//3.0e-23:219.74//Hs.70279:AA757426  
 F-HEMBA1004086//EST//0.36:189.62//Hs.156218:AA770107  
 F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.75666:M28713  
 F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.3e-39:335.79//Hs.  
 20 46468:U45984  
 F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-24:610.61//Hs.80712:D86957  
 F-HEMBA1004132//EST//3.5e-06:143.70//Hs.136799:AA780064  
 F-HEMBA1004133//ESTs//1.0:157.68//Hs.161226:AI419759  
 F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1//0.00055:343.62//Hs.5923:X82260  
 25 F-HEMBA1004143  
 F-HEMBA1004146  
 F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:AI186056  
 F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete cds//1.8e-15:591.60//Hs.159277:  
 AB016341  
 30 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:649.97//Hs.59988:AF067855  
 F-HEMBA1004199  
 F-HEMBA1004200//ESTs//0.0083:150.66//Hs.116424:AI375427  
 F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.2e-35:205.94//Hs.  
 10092:AI189282  
 35 F-HEMBA1004203//ESTs//3.9e-14:237.70//Hs.118273:AA626040  
 F-HEMBA1004207//Leptin receptor//1.1e-167:791.98//Hs.54515:U50748  
 F-HEMBA1004225//ESTs//0.00087:231.64//Hs.13109:AA192514  
 F-HEMBA1004227//ESTs, Weakly similar to F55A11.4 [C.elegans]//0.012:156.67//Hs.163588:AI073878  
 F-HEMBA1004238  
 40 F-HEMBA1004241//ESTs//8.7e-05:51.96//Hs.162826:AA679571  
 F-HEMBA1004246//EST//1.2e-36:198.96//Hs.121343:AA758522  
 F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds//1.1e-28:295.72//Hs.  
 56205:U96876  
 F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:553.60//Hs.83634:U52112  
 45 F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 protein, complete cds//4.9e-73:490.77//Hs.141874:  
 AB014588  
 F-HEMBA1004272  
 F-HEMBA1004274//EST//0.43:154.61//Hs.125347:AA876444  
 F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:118.65//Hs.155313:AB002331  
 50 F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.0:364.56//Hs.118738:AB018343  
 F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.9e-187:868:  
 99//Hs.101766:AF022795  
 F-HEMBA1004289  
 F-HEMBA1004295//EST//0.20:149.62//Hs.162415:AA573484  
 55 F-HEMBA1004306//ESTs//0.041:177.64//Hs.158234:AI270047  
 F-HEMBA1004312//ESTs//0.83:253.59//Hs.121898:AI336314  
 F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:452.65//Hs.69740:U09367  
 F-HEMBA1004323//EST//0.44:134.64//Hs.145464:AI204532

- F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//0.017:209:64//Hs.43627:U35612
- F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062
- F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888
- 5 F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete cds//0.49:80:73//Hs.139648:AB014606
- F-HEMBA1004341
- F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//2.7e-39:270:86//Hs.80686:D89667
- 10 F-HEMBA1004354//Human CHL1 potential helicase (CHLR1), complete cds//1.3e-46:190:92//Hs.27424:U75968
- F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:62//Hs.3022:D85376
- F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]//7.8e-10:396:61//Hs.33688:AA020928
- F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800
- F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//Hs.112180:AF039019
- 15 F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250
- F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818
- F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199
- F-HEMBA1004408//ESTs, Weakly similar to The ha1539 protein is related to cyclophilin. [H.sapiens]//1.4e-20:144:88//Hs.121076:A1246426
- 20 F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//4.8e-18:248:72//Hs.69747:M35531
- F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:AF088219
- F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080
- F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606
- 25 F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984
- F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450
- F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600
- F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431
- F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-69:758:76//Hs.23094:M19503
- 30 F-HEMBA1004507//ESTs, Weakly similar to T19B10.6 [C.elegans]//1.4e-61:296:99//Hs.114622:AA693492
- F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014:265:61//Hs.43543:AF042800
- F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//Hs.76279:X53416
- F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381
- 35 F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.74:74:75//Hs.87497:U90552
- F-HEMBA1004554
- F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331
- F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802
- F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2e-17:334:67//Hs.24536:AA479825
- 40 F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1e-35:337:78//Hs.78160:AF010238
- F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661
- F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds//0.42:186:66//Hs.84136:1170370
- 45 F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606
- F-HEMBA1004617//EST//0.027:188:61//Hs.159094:AI383198
- F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178
- F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416
- 50 F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891
- F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI346780
- F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522
- F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083
- F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796
- 55 F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582
- F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141
- F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:AI093252
- F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue//0.64:313:61//Hs.118578:X80821

- F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73//Hs.155174:AB007892  
 F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515  
 F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:244:57//Hs.99975:X55019  
 F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328:60//Hs.68900:AF016903  
 5 F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.9e-32:476:70//Hs.116874:AA524909  
 F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515  
 F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004  
 10 F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0e-61:663:71//Hs.23094:M19503  
 F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813  
 F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504  
 F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400:AB006626  
 15 F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.I53563:AF011333  
 F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082  
 F-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:L39060  
 F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.I55657:M61120  
 20 F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-115:909:78//Hs.23094:M19503  
 F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139  
 F-HEMBA1004771  
 F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235  
 25 F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:A1222106  
 F-HEMBA1004795  
 F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952  
 F-HEMBA1004806//EST//0.080:142:65//Hs.160268:A1146971  
 30 F-HEMBA1004807//Human HIV1 tate element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042  
 F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646  
 F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:AI300481  
 F-HEMBA1004847//ESTs//2.1e-09:66:98//Hs.158161:AA312511  
 35 F-HEMBA1004850//EST//0.033:253:64//Hs.158782:A376601  
 F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150  
 F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:AA446987  
 F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077  
 40 F-HEMBA1004880//H. sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633  
 F-HEMBA1004889//Growth arrest-specific //0.20:146:68//Hs.65029:L13698  
 F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304  
 F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106  
 F-HEMBA1004918//EST//0.78:122:61//Hs.I45491:AI254348  
 45 F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172  
 F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X52947  
 F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959  
 F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331  
 50 F-HEMBA1004934  
 F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981  
 F-HEMBA1004954//ESTs//0.04:404:60//Hs.11177:AA417813  
 F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:A174478  
 F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274  
 55 F-HEMBA1004972  
 F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.073:574:58//Hs.154139:AB007914  
 F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946

- F-HEMBA1004978//ESTs//0.097:337.60//Hs.114157:AA703013  
 F-HEMBA1004980//EST//3.2e-10:169.65//Hs.149123:AI244750  
 F-HEMBA1004983//EST//0.93:85.71//Hs.162267:AA553589  
 F-HEMBA1004995//ESTs//0.46:296.61//Hs.135168:AI394026  
 5 F-HEMBA1005008//ESTs//1.5e-20:156.85//Hs.114140:U35429  
 F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379.72//Hs.151887:AF053356  
 F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693.98//Hs.31921:AB014548  
 10 F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215.65//Hs.6727:AB014560  
 F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503.98//Hs.21362:AF039237  
 F-HEMBA1005039//Human kpni repeat mna (cdna clone pcd-kpni-8), 3' end//5.8e-60:272.89//Hs.103948:K00627  
 F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds//0.078:442.59//Hs.100602:AF010193  
 15 F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251.63//Hs.78909:U07802  
 F-HEMBA1005062//ESTs//0.020:268.59//Hs.146181:AI264462  
 F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//1.5e-59:411.85//Hs.129727:AF035587  
 F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395.57//Hs.27590:AB002381  
 20 F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344.72//Hs.89479:X66785  
 F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631.59//Hs.27910:AF049105  
 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762.98//Hs.11170:AF080561  
 25 F-HEMBA1005113//ESTs//0.52:109.68//Hs.106330:AI031916  
 F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468.78//Hs.93121:AB018304  
 F-HEMBA1005133//ESTs//1.6e-27:366.73//Hs.151467:N51106  
 F-HEMBA1005149//EST//3.3e-37:304.80//Hs.132635:AI032875  
 30 F-HEMBA1005152//ESTs//3.9e-09:285.62//Hs.155876:AA593021  
 F-HEMBA1005159//EST//8.4e-05:289.64//Hs.125563:AA884216  
 F-HEMBA1005185//ESTs//1.4e-22:129.96//Hs.14920:AA910914  
 F-HEMBA1005201//EST//4.0e-16:96.98//Hs.89002:AA282197  
 F-HEMBA1005202  
 35 F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431.58//Hs.144029:Y13436  
 F-HEMBA1005219//ESTs//4.3e-47:299.88//Hs.5019:VW26547  
 F-HEMBA1005223//ESTs//0.00030:168.66//Hs.76487:N37081  
 F-HEMBA1005232//EST//0.0078:209.61//Hs.46852:N48302  
 F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//6.0e-54:399.79//Hs.129735:AF010144  
 40 F-HEMBA1005244//ESTs//2.5e-14:85.10011Hs.128744:AI191922  
 F-HEMBA1005251//ESTs//0.012:49.95//Hs.161554:AA393896  
 F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7e-151:705.98//Hs.72660:AB011157  
 45 F-HEMBA1005274//ESTs//7.1e-09:298.64//Hs.145522:AI261380  
 F-HEMBA1005275//ESTs//7.9e-13:375.63//Hs.148974:AA001777  
 F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338.65//Hs.12451:U97018  
 F-HEMBA1005296//ESTs//0.055:299.60//Hs.86320:AI149232  
 F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322.85//Hs.155464:AF088219  
 50 F-HEMBA1005311  
 F-HEMBA1005314//ESTs//8.1e-39:199.98//Hs.119974:AI279516  
 F-HEMBA1005315//ESTs//1.9e-07:266.64//Hs.141440:N21615  
 F-HEMBA1005318//ESTs//5.3e-06:161.72//Hs.119411:AA937117  
 F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.00075:310.63//Hs.111597:U68723  
 55 F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//4.4e-153:740.97//Hs.29361:AJ007581  
 F-HEMBA1005353//EST//5.4e-09:22.68//Hs.119508:AA485732  
 F-HEMBA1005359//Zinc finger protein 137 (clone pHZ-30)//5.7e-100:500.88//Hs.151689:U09414  
 F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds//2.5e-70:572.73//Hs.43265:

AF071787

F-HEMBA1005372//ESTs//0.00045:163.66//Hs.164058:A1417905

F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.1e-43:341.81//Hs.154069:U06452

F-HEMBA1005382//EST//2.4e-32:167.99//Hs.147186:A193053

F-HEMBA1005389//ESTs//0.0021:245.59//Hs.104463:AA804448

F-HEMBA1005394//ESTs, Weakly similar to No definition line found [C.elegans]//1.0e-130:620.98//Hs.108990:N25951

F-HEMBA1005403//ESTs, Weakly similar to No definition line found [C.elegans]//7.7e-151:727.97//Hs.17118:AI033807

F-HEMBA1005408//ESTs//3.2e-70:426.89//Hs.158078:H24513

F-HEMBA1005410//EST//2.5e-25:406.67//Hs.138765:N70347

F-HEMBA1005411

F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:537.99//Hs.4854:AF041248

F-HEMBA1005426//EST//1.0:148.64//Hs.44469:N33323

F-HEMBA1005443//Zinc finger protein 157 (HZF22)//9.0e-34:259.72//Hs.89897:U28687

F-HEMBA1005447//EST//3.9e-10:211.70//Hs.145960:AI276783

F-HEMBA1005468//ESTs//8.4e-53:390.81//Hs.152395:AA533107

F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cds//3.1e-29:155.99//Hs.75104:L37368

F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-88:481.92//Hs.23094:M19503

F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257.78//Hs.155464:AF088219

F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414.60//Hs.132206:AF039694

F-HEMBA1005497//Glucocorticoid receptor alpha { alternative products}//8.7e-41:588.69//Hs.102761:U25029

F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21//1.1e-28:318.73//Hs.159530:AC004957

F-HEMBA1005508//Human mRNA for KIAA0010 gene, complete cds//0.67:351.58//Hs.155287:D13635

F-HEMBA1005508//ESTs//0.45:326.59//Hs.102756:AA526911

F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400.79//Hs.153014:AB002353

F-HEMBA1005513//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378.97//Hs.22767:N99220

F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0.54:623.56//Hs.143551:AF048693

F-HEMBA1005518//ESTs//0.10:207.60//Hs.72447:AA160575

F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.1e-55:288.85//Hs.144563:AF057280

F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176.76//Hs.155464:AF088219

F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//1.2e-30:166.96//Hs.17035:AI080471

F-HEMBA1005530

F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18:391.64//Hs.30250:AF055376

F-HEMBA1005552//ESTs//1.8e-46:238.88//Hs.138856:H47461

F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501.60//Hs.157091:M13903

F-HEMBA1005568//ESTs//0.013:259.63//Hs.13669:H47257

F-HEMBA1005570//ESTs//0.0084:442.59//Hs.125384:AI346507

F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610.98//Hs.77738:AB007932

F-HEMBA1005577//ESTs//0.98:199.61//Hs.146226:A1312873

F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830.64//Hs.57929:AB011538

F-HEMBA1005582

F-HEMBA1005583

F-HEMBA1005588//ESTs//1.3e-35:386.70//Hs.55855:AA621381

F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA

FORMS//0.54:439.59//Hs.2137:D49357

F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378.57//Hs.7720:AB002323

- F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609  
 F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982  
 F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)/8.2e-22:721:61//Hs.144563:AF057280  
 5 F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]/1.8e-89:454:96//Hs.19400:AA662845  
 F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535  
 F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734  
 F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199  
 10 F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AA16956  
 F-HEMBA1005666  
 F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.7e-45:255:79//Hs.114293:AB011142  
 F-HEMBA1005679//Human kpni repeat mma (cdna clone pcd-kpni-4), 3' end//1.2e-37:356:77//Hs.139107:K00629  
 15 F-HEMBA1005680  
 F-HEMBA1005685  
 F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406  
 F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678  
 20 F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143  
 F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, geranyltransferase)/2.6e-20:151:88//Hs.77393:D14697  
 F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754  
 F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024  
 25 F-HEMBA1005755//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//1.8e-48:425:78//Hs.103948:K00627  
 F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs.155464:AF088219  
 F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141  
 F-HEMBA10058131//ESTs//0.012:209:63//Hs.113365:R77747  
 F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds//2.0e-07:439:62//Hs.6133:U94346  
 30 F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577  
 F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788  
 F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9e-42:690:66//Hs.23094:M19503  
 F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//Hs.79706:U53204  
 F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150  
 35 F-HEMBA1005884//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.4e-53:332:83//Hs.158095:AB007953  
 F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097  
 F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete cds//7.2e-45:411:77//Hs.46468:U45984  
 40 F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.00054:477:59//Hs.37125:U42766  
 F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081  
 F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006  
 F-HEMBA1005933//ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]/1.2e-46:228:100//Hs.152178:AI224880  
 45 F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588  
 F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883  
 F-HEMBA1005963  
 F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.26285:AF082516  
 50 F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:AI127530  
 F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526  
 F-HEMBA1006002  
 F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]/0.98:197:61//Hs.5184:AA709151  
 55 F-HEMBA1006031  
 F-HEMBA1006035  
 F-HEMBA1006036//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080  
 F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.41186:R99609

- F-HEMBA1006067//ESTs//2.0e-74:354.99//Hs.43321:Al139422  
F-HEMBA1006081  
F-HEMBA1006090//EST//1.2e-12:340.62//Hs.61195:Al418788  
F-HEMBA1006091//ESTs//4.7e-98:473.98//Hs.9658:AA506313  
5 F-HEMBA1006100//ESTs//1.7e-22:273.73//Hs.144407:AA737799  
F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273.66//Hs.8763:W30741  
F-HEMBA1006121//EST//0.00012:232.59//Hs.117096:AA677968  
F-HEMBA1006124//EST//0.047:251.62//Hs.132257:Al027222  
10 F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150.62//Hs.74061:X59372  
F-HEMBA1006138//ESTs//1.8e-27:132.84//Hs.141575:AA211734  
F-HEMBA1006142//EST//2.5e-47:310.87//Hs.149580:Al281881  
F-HEMBA1006155  
F-HEMBA1006158//ESTs//5.1e-105:506.98//Hs.93468:N40575  
F-HEMBA1006173//ESTs//2.5e-24:195.84//Hs.79092:H29627  
15 F-HEMBA1006182//ESTs//2.5e-19:237.72//Hs.141840:AA028117  
F-HEMBA1006198//ESTs//0.017:133.67//Hs.142168:AA292540  
F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836.98//Hs.109268:AF070557  
F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221.67//Hs.7647:M94046  
F-HEMBA1006252  
20 F-HEMBA1006253//EST//1.3e-100:467.100//Hs.146619:Al140706  
F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.00037:158.69//Hs.159277:AB018341  
F-HEMBA1006268//ESTs//1.1e-20:376.67//Hs.72814:AA706631  
F-HEMBA1006272//EST//4.8e-20:252.69//Hs.162992:AA688140  
25 F-HEMBA1006278//H. sapiens PAP mRNA//6.5e-57:610.71//Hs.49007:X76770  
F-HEMBA1006283  
F-HEMBA1006284//ESTs//0.00017:248.63//Hs.143840:Al189964  
F-HEMBA1006291  
F-HEMBA1006293  
30 F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.76:416.58//Hs.46465:U45285  
F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3e-49:637.68//Hs.37656:AB011174  
F-HEMBA1006328//ESTs//1.8e-71:429.88//Hs.139922:AA281350  
F-HEMBA1006334//EST//0.082:267.57//Hs.136449:AA572789  
35 F-HEMBA1006344//ESTs//6.2e-09:67.94//Hs.42302:Al032142  
F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378.97//Hs.22767:N99220  
F-HEMBA1006349//ESTs//0.87:276.60//Hs.23628:H03287  
F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823.81//Hs.74107:X59244  
40 F-HEMBA1006364//EST//0.0012:168.66//Hs.156756:Al351026  
F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POB1) mRNA, complete cds//0.0028:422.59//Hs.80667:AF010233  
F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:265.61//Hs.8813:AF032922  
45 F-HEMBA1006381//ESTs//3.8e-78:382.98//Hs.132171:Al042531  
F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1e-49:395.80//Hs.23094:M19503  
F-HEMBA1006416//EST//7.3e-12:154.77//Hs.134086:Al077477  
F-HEMBA1006419//EST//4.6e-51:179.86//Hs.149580:Al281881  
50 F-HEMBA1006421//HsLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517.72//Hs.51048:X68830  
F-HEMBA1006424//ESTs//2.7e-08:380.60//Hs.44369:Al206835  
F-HEMBA1006426//ESTs//3.0e-98:465.99//Hs.129251:AA993264  
F-HEMBA1006438//EST//1.3e-29:183.93//Hs.147412:Al209194  
F-HEMBA1006445  
F-HEMBA1006446//EST//0.14:200.59//Hs.160695:Al282889  
55 F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210.72//Hs.51124:AF019369  
F-HEMBA1006467  
F-HEMBA1006471//ESTs//1.4e-05:391.60//Hs.121282:Al091453  
F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346.63//Hs.31257:



AA875998

F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386.82//Hs.89887:D38081

F-HEMBA1006485//EST//5.4e-111:516.99//Hs.61925:AA039532

F-HEMBA1006486//EST//4.7e-23:266.72//Hs.137800:AA866897

5 F-HEMBA1006489//ESTs//2.5e-06:137.71//Hs.28621:AA910431

F-HEMBA1006492

F-HEMBA1006494//ESTs//8.5e-24:299.72//Hs.153413:AI248625

F-HEMBA1006497//EST//0.00034:431.61//Hs.130057:AA903389

F-HEMBA1006502//ESTs//2.6e-11:131.80//Hs.141267:H22072

10 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470.98//Hs.153858:AB014566

F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]//3.9e-98:483.97//Hs.94811:AA011185

F-HEMBA1006530//EST//1.7e-42:530.71//Hs.163207:AA808002

15 F-HEMBA1006535//ESTs//2.9e-84:404.98//Hs.128679:AI160081

F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173:654.98//Hs21301:AF093419

F-HEMBA1006546//ESTs//2.8e-45:391.78//Hs.146307:AA584638

F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363.79//Hs.21490:AB007898

20 F-HEMBA1006562//ESTs//4.5e-09:116.75//Hs.142368:AI198425

F-HEMBA1006566//EST//0.85:100.68//Hs.13052:T67136

F-HEMBA1006569//ESTs//2.7e-06:213.64//Hs.44372:AI346522

F-HEMBA1006579//EST//0.064:160.62//Hs.126244:AA873479

F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533.60//Hs.106387:AF029778

25 F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328.81//Hs.155464:AF088219

F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6e-38:441.69//Hs.23711:AB018295

F-HEMBA1006612//ESTs//8.8e-135:668.97//Hs.7942:AA205862

F-HEMBA1006617//EST//4.6e-31:254.81//Hs.132635:AI032875

30 F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION [S. cerevisiae]//2.5e-75:379.97//Hs.40911:AI391502

F-HEMBA1006631//ESTs//1.4e-126:612.98//Hs.131737:AI343331

F-HEMBA1006635//EST//0.65:145.63//Hs.104560:AA340589

F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185

35 F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259.65//Hs.105747:AA505003

F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//3.9e-28:108.93//Hs.6196:U40282

40 F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:452.96//Hs.159574:AA190615

F-HEMBA1006653

F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:438.98//Hs.8173:AC005189

F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180.80//Hs.91916:AF035317

F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:122.90//Hs.5092:Y12065

45 F-HEMBA1006676

F-HEMBA1006682//EST//0.12:193.61//Hs.128367:AA974575

F-HEMBA1006695//ESTs//5.6e-27:110.80//Hs.159510:AA297145

F-HEMBA1006696//EST//3.2e-12:160.75//Hs.146472:AI128198

F-HEMBA1006708

50 F-HEMBA1006709//ESTs//0.69:60.80//Hs.152752:AA643545

F-HEMBA1006717//ESTs//12.6e-31:286.78//Hs.55573:W37226

F-HEMBA1006737//ESTs//1.6e-37:189.99//Hs.97490:AA394105

F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360.84//Hs.154326:D42087

55 F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.0e-92:817.78//Hs.129727:AF035587

F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0e-10:576.56//Hs.149323:AB002325

F-HEMBA1006767//ESTs//1.7e-18:252.72//Hs.141073:W72720

F-HEMBA1006779//EST//9.1e-26:395.69//Hs.145366:AI252657

- F-HEMBA1006780//EST//1.0:93.69//Hs.116946:AA680250  
 F-HEMBA1006789//ESTs//0.0060:276.59//Hs.144121:AI369798  
 F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-37:781.64//Hs.23094:M19503  
 F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202.68//Hs.34054:U79298  
 5 F-HEMBA1006807//ESTs. Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMO-SOME III [C.elegans]//4.8e-110:523.98//Hs.125790:AA287723  
 F-HEMBA1006821//EST//5.1e-11:246.66//Hs.150542:AI051551  
 F-HEMBA1006824//ESTs//1.4e-29:158.98//Hs.127712:AA961624  
 F-HEMBA1006832//EST//3.1e-24:277.74//Hs.139357:AA420970  
 10 F-HEMBA1006849//ESTs//0.99:332.57//Hs.128993:AA985327  
 F-HEMBA1006865  
 F-HEMBA1006877//ESTs. Highly similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//2.4e-61:311.97//Hs.127793:W25938  
 F-HEMBA1006885//ESTs. Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC REGION [Saccharomyces cerevisiae]//9.1e-128:805.87//Hs.32376:AA758214  
 15 F-HEMBA1006900//EST//6.8e-05:255.63//Hs.163173:AA781592  
 F-HEMBA1006914//EST//0.065:366.621//Hs.162914:AA666199  
 F-HEMBA1006921//ESTs//2.9e-42:347.82//Hs.159266:AI376989  
 F-HEMBA1006926//Human I kappa BR mRNA, complete cds//0.90:545.59//Hs.154764:U16258  
 20 F-HEMBA1006929//EST//0.00013:403.61//Hs.162642:AA602539  
 F-HEMBA1006936//ESTs//0.00014:60.93//Hs.8737:W22712  
 F-HEMBA1006938//ESTs//4.7e-51:256.98//Hs.143651:AI150382  
 F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//4.4e-92:437.98//Hs.42644:AJ010841  
 25 F-HEMBA1006949//H. sapiens mRNA for retrotransposon//6.9e-43:385.76//Hs.6940:Z48633  
 F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.8e-144:740.94//Hs.14934:AF004828  
 F-HEMBA1006976//H. sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase//1.9e-79:447.89//Hs.75268:X74570  
 30 F-HEMBA1006993//ESTs//5.4e-19:380.66//Hs.152635:AA600968  
 F-HEMBA1006996//ESTs//0.17:242.59//Hs.106879:AA054723  
 F-HEMBA1007002  
 F-HEMBA1007017//EST//1.0:59.72//Hs.113400:R39282  
 F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete cds//2.5e-78:827.70//Hs.43003:AF035812  
 35 F-HEMBA1007045  
 F-HEMBA1007051//EST//0.85:65.73//Hs.158641:AI370659  
 F-HEMBA1007052  
 F-HEMBA1007062  
 40 F-HEMBA1007066//ESTs//0.94:160.63//Hs.56071:W52212  
 F-HEMBA1007073//ESTs//3.6e-50:246.80//Hs.142678:H37845  
 F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//6.7e-75:417.91//Hs.80510:M74002  
 F-HEMBA1007080  
 45 F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-06:568.61//Hs.1974:M92432  
 F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA, complete cds//0.95:541.57//Hs.3828:U49260  
 F-HEMBA1007112//ESTs//3.4e-104:494.98//Hs.19207:AA039595  
 F-HEMBA1007113//ESTs//0.71:246.62//Hs.96235:AA196354  
 50 F-HEMBA1007121//ESTs//3.7e-69:335.98//Hs.140519:AA643182  
 F-HEMBA1007129  
 F-HEMBA1007147//ESTs//3.2e-07:235.641//Hs.124813:W46172  
 F-HEMBA1007149//ESTs//7.2e-08:161.68//Hs.121179:AA757136  
 F-HEMBA1007151  
 55 F-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//6.6e-64:318.97//Hs.22396:AF062085  
 F-HEMBA1007178//ESTs. Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-39:248.90//Hs.157148:AA311921  
 F-HEMBA1007194//ESTs//2.3e-107:503.99//Hs.100605:AA305965

- F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.6e-158:478:98//Hs.3363: D86987
- F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252
- 5 F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6e-177:839:98//Hs.27197: AB018340
- F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//2.7e-56:647:69//Hs. 82314:M31642
- F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//Hs.79706:U53204
- 10 F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:6411Hs.12432:AF070575
- F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//0.99:239:60//Hs.111749: U13695
- F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836
- F-HEMBA1007279//ESTs//6.1e-36:185:78//Hs.141022:H06475
- 15 F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529
- F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637
- F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI300062
- F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-09:406:61//Hs.111913:Z74615
- F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506
- F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634
- 20 F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241
- F-HEMBA1007327//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens]//3.5e-09:144:76//Hs.20597: W56370
- F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130
- F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006
- 25 F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561
- F-HEMBA1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568
- F-HEMBA1000008//H.sapiens mRNA for translin associated protein X//1.1e-43:370:78//Hs.96247:X95073
- F-HEMBA1000018//Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)//1.0:108:70//Hs. 83428:M58603
- 30 F-HEMBA1000024//EST//5.4e-07:137:70//Hs.125389:AA878307
- F-HEMBA1000025//EST//0.99:362:58//Hs.121221:AA757392
- F-HEMBA1000030//H.sapiens mRNA for cyclin III//1.3e-10:525:62//Hs.3232:Z46788
- F-HEMBA1000036
- 35 F-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//6.2e-102:450: 98//Hs.20815:AF084928
- F-HEMBA1000039//EST//0.0034:97:73//Hs.141684:W35358
- F-HEMBA1000044//ESTs//0.0048:218:63//Hs.123161:AA807319
- F-HEMBA1000048//EST//0.00025:222:62//Hs.122474:AA765131
- 40 F-HEMBA1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717
- F-HEMBA1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3e-54:259:88//Hs.23094:M19503
- F-HEMBA1000055//ESTs//0.0017:289:62//Hs.125755:AA286923
- F-HEMBA1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9e-59:286:84//Hs.93121:AB018304
- 45 F-HEMBA1000083
- F-HEMBA1000089//EST//0.0016:192:661//Hs.137093:AA917621
- F-HEMBA1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645
- F-HEMBA1000103//Human kpni repeat mna (cdna clone pcd-kpni-8), 3' end//4.9e-43:418:74//Hs.103948:K00627
- F-HEMBA1000113//EST//4.6e-23:221:76//Hs.142065:AA173763
- F-HEMBA1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521
- 50 F-HEMBA1000136//ESTs//12.3e-101:507:96//Hs.12659:AA195207
- F-HEMBA1000141//ESTs//2.1e-15:283:69//Hs.126257:AI279044
- F-HEMBA1000144//EST//4.5e-52:298:91//Hs.149580:AI281881
- F-HEMBA1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs.3057:X92715
- F-HEMBA1000175//EST//1.0:101:65//Hs.162898:AA659646
- 55 F-HEMBA1000198//EST//0.99:179:56//Hs.116880:AA662457
- F-HEMBA1000215//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.4e-15:139:82//Hs.101414: AB011129
- F-HEMBA1000217//ESTs//3.4e-06:81:88//Hs.121151:T66277
- F-HEMBA1000218//EST//0.11:136:63//Hs.134683:AI092013

- F-HEMBB1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X69962  
 F-HEMBB1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y08612  
 F-HEMBB1000244//ESTs//3.2e-15:139:81//Hs.134549:AI078483  
 F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds//2.1e-156:735:981//Hs.151411:AF075587  
 F-HEMBB1000258//EST//0.0091:325:60//Hs.97533:AA435884  
 F-HEMBB1000264//Human CHL1 potential helicase (CHLR1), complete cds//1.4e-33:100:100//Hs.27424:U75968  
 F-HEMBB1000266//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.0019:373:60//Hs.16533:D87930  
 F-HEMBB1000272//ESTs//1.3e-93:440:99//Hs.I09224:A46684  
 F-HEMBB1000274//ESTs//0.41:221:65//Hs.71990:AA151796  
 F-HEMBB1000284//EST//0.00024:108:73//Hs.100725:F13689  
 F-HEMBB1000307//EST//3.6e-10:149:73//Hs.140415:AA778574  
 F-HEMBB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.00092:252:65//Hs.41153:AB018326  
 F-HEMBB1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787  
 F-HEMBB1000318//EST//0.014:184:61//Hs.155758:AI311870  
 F-HEMBB1000335//EST//0.99:187:63//Hs.137424:AA243729  
 F-HEMBB1000336//EST//1.0:209:63//Hs.150410:AI003611  
 F-HEMBB1000337//EST//0.086:133:66//Hs.128207:AA972330  
 F-HEMBB1000338//EST//7.1e-07:129:72//Hs.140488:AA767127  
 F-HEMBB1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:7611//Hs.155464:AF088219  
 F-HEMBB1000341  
 F-HEMBB1000343//EST//0.66:163:63//Hs.150822:AI302729  
 F-HEMBB1000354//ESTs//7.6e-61:292:100//Hs.152266:AA926874  
 F-HEMBB1000369//ESTs, Highly similar to t-BOP [M.musculus]/10.013:157:64//Hs.129982:AI420970  
 F-HEMBB1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934  
 F-HEMBB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348  
 F-HEMBB1000391//ESTs//0.033:237:64//Hs.135289:AI092963  
 F-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//9.4e-165:762:98//Hs.16184:AJ001642  
 F-HEMBB1000402//EST//0.013:291:59//Hs.149191:AI246155  
 F-HEMBB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194  
 F-HEMBB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925  
 F-HEMBB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//9.4e-73:364:83//Hs.129735:AF010144  
 F-HEMBB1000438//ESTs//0.073:446:58//Hs.134632:AI223429  
 F-HEMBB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627  
 F-HEMBB1000449//EST//5.5e-21:356:671//Hs.157848:AI362501  
 F-HEMBB1000455//ESTs//0.092:147:65//Hs.106446:N93227  
 F-HEMBB1000472  
 F-HEMBB1000480//EST//0.98:83:71//Hs.146462:AI124898  
 F-HEMBB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206  
 F-HEMBB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI057560  
 F-HEMBB1000491  
 F-HEMBB1000493//ESTs//0.019:103:69//Hs.138358:T66178  
 F-HEMBB1000510//Glucocorticoid receptor alpha (alternative products)//1.6e-46:409:77//Hs.102761:U25029  
 F-HEMBB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413  
 F-HEMBB1000523//ESTs//0.69:332:59//Hg.106845:W19543  
 F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus//2.1e-38:138:96//Hs.36131:Y11710  
 F-HEMBB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//7.7e-31:554:67//Hs.157142:U85996  
 F-HEMBB1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-27:282:75//Hs.158095:AB007953  
 F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds//2.0e-33:537:65//Hs.5444:AB018293  
 F-HEMBB1000564  
 F-HEMBB1000573//H.sapiens HCG II mRNA//7.5e-27:197:76//Hs.146333:X81001

- F-HEMBA1000575//Von Hippel-Lindau syndrome//2.7e-72:255.79//Hs.78160:AF010238  
 F-HEMBA1000586//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:M18533  
 F-HEMBA1000589//PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228.79//Hs.73734:Z23031  
 5 F-HEMBA1000591//ESTs//1.0e-17:370.64//Hs.58156:W71990  
 F-HEMBA1000592//EST//0.0038:51.88//Hs.148022:AI269323  
 F-HEMBA1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:503.99//Hs.3386:AF053356  
 F-HEMBA1000598//Ribosomal protein L5//3.5e-29:537.66//Hs.118781:U66589  
 F-HEMBA1000623//H. sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X91809  
 10 F-HEMBA1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//Hs.105850:AB007864  
 F-HEMBA1000631//ESTs//1.7e-06:247.61//Hs.156864:AI346481  
 F-HEMBA1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811.65//Hs.29963:AB002349  
 F-HEMBA1000637//Sialophorin (gp115, leukosialin, CD43)//2.4e-79:304:85//Hs.80738:X52075  
 F-HEMBA1000638//EST//0.0076:92.75//Hs.125496:AA883735  
 15 F-HEMBA1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477.74//Hs.51048:X68830  
 F-HEMBA1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:533.75//Hs.51011:L19778  
 F-HEMBA1000652//ESTs//1.6e-49:345.84//Hs.132722:AA618531  
 F-HEMBA1000665//EST//0.44:152.63//Hs.149534:AI280924  
 F-HEMBA1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2e-79:280.85//Hs.23094:M19503  
 20 F-HEMBA1000673//ESTs//0.99:177.59//Hs.149864:N80474  
 F-HEMBA1000684//Protein kinase, interferon-inducible double stranded RNA dependent//2.6e-31:220.87//Hs.73821:M35663  
 F-HEMBA1000693//Homo sapiens neuroan mRNA, complete cds//5.3e-120:575.97//Hs.158300:AF040723  
 F-HEMBA1000705//ESTs//4.7e-65:350.94//Hs.24610:R33125  
 25 F-HEMBA1000706//EST//8.6e-14:373.61//Hs.138281:RS5703  
 F-HEMBA1000709//EST//0.99:110.651//Hs.162437:AA577510  
 F-HEMBA1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635.77//Hs.123109:X56741  
 F-HEMBA1000726//EST//1.3e-43:257.84//Hs.162197:AA535216  
 F-HEMBA1000738//EST//5.9e-13:259.64//Hs.159699:AI417328  
 30 F-HEMBA1000749//EST//3.1e-42:271.871//Hs.162197:AA535216  
 F-HEMBA1000763  
 F-HEMBA1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]//0.021:111:72//Hs.38178:AA921830  
 F-HEMBA1000774//ESTs, Weakly similar to mTERF [H.sapiens]//2.5e-116:580.97//Hs.5009:AA081390  
 35 F-HEMBA1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426.74//Hs.86201:U78876  
 F-HEMBA1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds//3.0e-65:672.71//Hs.155983:AB014577  
 F-HEMBA1000790//ESTs//1.2e-52:344.86//Hs.35254:AI133727  
 F-HEMBA1000794//ESTs//0.00098:289.59//Hs.138782:N73572  
 40 F-HEMBA1000807//ESTs//2.1e-91:434.99//Hs.61334:AI298375  
 F-HEMBA1000810//ESTs//0.038:92.71//Hs.148763:AA66887  
 F-HEMBA1000821//EST//0.94:129.62//Hs.162299:AA555154  
 F-HEMBA1000822//ESTs//7.5e-05:199.63//Hs.117018:AA832421  
 F-HEMBA1000826//ESTs//4.8e-13:343.65//Hs.153429:AI283069  
 45 F-HEMBA1000827  
 F-HEMBA1000831  
 F-HEMBA1000835//EST//4.3e-27:201.851//Hs.141451:N29915  
 F-HEMBA1000840//EST//6.3e-75:380.96//Hs.142557:AA464948  
 F-HEMBA1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-135:875.85//Hs.23094:M19503  
 50 F-HEMBA1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292.61//Hs.311:U00238  
 F-HEMBA1000870//EST//0.00091:246.62//Hs.126502:AA913831  
 F-HEMBA1000876//Homo sapiens ELIS-1 mRNA, partial cds//4.9e-34:200.94//Hs.128434:AF085351  
 F-HEMBA1000883//ESTs//0.42:107.67//Hs.154173:AI379823  
 55 F-HEMBA1000887  
 F-HEMBA1000888//ESTs//1.0:137.67//Hs.8121:AA521290  
 F-HEMBA1000890//ESTs//1.0:116.65//Hs.7105:T23433  
 F-HEMBA1000893//EST//0.0079:408.58//Hs.146504:AI129834

- F-HEMBB1000908//EST//9.2e-21:205.79//Hs.132635:AI032875  
 F-HEMBB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327.60//Hs.7938:D86984  
 F-HEMBB1000913//ESTs//1.0e-12:233.68//Hs.137545:AA487049  
 F-HEMBB1000915//ESTs//2.5e-90:423.99//Hs.135254:AI095468  
 5 F-HEMBB1000917//EST//2.8e-49:241:100//Hs.162216:AA548069  
 F-HEMBB1000927//Hippocalcin//1.2e-31:528.65//Hs.89692:D16593  
 F-HEMBB1000947  
 F-HEMBB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9.3e-48:572.72//Hs.2379:U23942  
 10 F-HEMBB1000973//ESTs//4.5e-26:286.76//Hs.137393:AA142938  
 F-HEMBB1000975//ESTs//0.78:180.66//Hs.104789:AA417124  
 F-HEMBB1000981  
 F-HEMBB1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.7e-07:308.62//Hs.122967:AF059569  
 F-HEMBB1000991//EST//0.12:125.66//Hs.22945:R43713  
 15 F-HEMBB1000996//ESTs//6.9e-05:273.63//Hs.133116:AI054055  
 F-HEMBB1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.62:193.62//Hs.119004:AB014565  
 F-HEMBB1001008//EST//4.7e-09:203.65//Hs.105221:AA489025  
 20 F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17:384.67//Hs.108604:AC002310  
 F-HEMBB1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284.60//Hs.161547:W04991  
 F-HEMBB1001020//ESTs//9.7e-37:186.76//Hs.138852:AA284247  
 F-HEMBB1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242.61//Hs.129982:AI420970  
 F-HEMBB1001037//EST//0.0057:192.66//Hs.149987:AI291177  
 25 F-HEMBB1001047//ESTs//1.6e-22:360.70//Hs.120734:W58721  
 F-HEMBB1001051//H.sapiens mRNA for FAN protein//3.8e-29:160.98//Hs.78687:X96586  
 F-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.0e-42:149.96//Hs.15832:AB014518  
 F-HEMBB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349.82//Hs.155464:AF088219  
 30 F-HEMBB1001060//ESTs//1.6e-62:464.81//Hs.138663:N24942  
 F-HEMBB1001063  
 F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:736.95//Hs.12953:AF034803  
 F-HEMBB1001096//EST//0.017:154.66//Hs.130403:AA908272  
 F-HEMBB1001102//ESTs//2.1e-18:120.95//Hs.163767:R06293  
 35 F-HEMBB1001105//Human BRCA2 region, mRNA sequence  
 CG016//0.30:84.75//Hs.112434:U50529  
 F-HEMBB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//9.3e-38:341.77//Hs.14038:R06800  
 F-HEMBB1001114//EST//6.4e-07:296.62//Hs.126420:AA975062  
 40 F-HEMBB1001117//EST//1.6e-99:464.99//Hs.130493:AA928139  
 F-HEMBB1001119  
 F-HEMBB1001126  
 F-HEMBB1001133//H.sapiens mRNA for translin associated protein X//1.2e-28:739.61//Hs.96247:X95073  
 F-HEMBB1001137  
 45 F-HEMBB1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23:340.69//Hs.146395:AB002329  
 F-HEMBB1001151//ESTs//2.6e-30:252.79//Hs.6880:W26854  
 F-HEMBB1001153//ESTs//7.6e-16:97.96//Hs.113307:H16716  
 F-HEMBB1001169//ESTs//1.4e-32:374.71//Hs.161682:AA206863  
 F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509.66//Hs.73073:D78334  
 50 F-HEMBB1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:100//Hs.86878:AA599183  
 F-HEMBB1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:199.64//Hs.74047:X71129  
 F-HEMBB1001199  
 F-HEMBB1001208//ESTs//0.12:120.69//Hs.130093:AA928802  
 55 F-HEMBB1001209//EST//0.00028:215.65//Hs.118276:W15258  
 F-HEMBB1001210//EST//2.9e-05:297.60//Hs.88840:AA281452  
 F-HEMBB1001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5e-37:260.76//Hs.72660:AB011157  
 F-HEMBB1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//0.00046:650.58//Hs.

- 158241:AB007976  
 F-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Mus musculus]/6.7e-103.477:100//Hs.127835:AI378790
- 5 F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31.458:67//Hs.129918:AB005754  
 F-HEMBB1001249//EST//0.26:203:63//Hs.140791:AA935909  
 F-HEMBB1001253//ESTs//4.0e-91.433:98//Hs.120636:AA325219  
 F-HEMBB1001254//ESTs//2.0e-24.180.85//Hs.136391:H04977  
 F-HEMBB1001267//Ataxia telangiectasia mutated (includes complementation groups A, C and D)/6.1e-24.146:78//Hs.51187:U82828
- 10 F-HEMBB1001271//ESTs//2.5e-05.686:58//Hs.115423:AI359248  
 F-HEMBB1001282//GA-binding protein transcription factor, beta subunit 2 (47kd)/0.39:531:57//Hs.78915:U13045  
 F-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]/4.9e-10.91:89//Hs.16606:W81021
- 15 F-HEMBB1001289//ESTs//6.4e-100.467:99//Hs.151720:AI287890  
 F-HEMBB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]/1.3e-135.654:98//Hs.124217:AA020848  
 F-HEMBB1001302  
 F-HEMBB1001304//ESTs//0.98:109:68//Hs.138972:AA047725
- 20 F-HEMBB1001314//ESTs//7.4e-39.285:77//Hs.144749:AI217339  
 F-HEMBB1001315//Small inducible cytokine A5 (RANTES)/1.9e-40.355:78//Hs.155464:AF088219  
 F-HEMBB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98.625:85//Hs.23094:M19503  
 F-HEMBB1001326//ESTs//0.00030:257:63//Hs.62208:H12380  
 F-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]/1.0e-48.332:87//Hs.43071:AA206222
- 25 F-HEMBB1001335  
 F-HEMBB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56.282:87//Hs.15731:AB011135  
 F-HEMBB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694  
 F-HEMBB1001346//Oxytocin receptor//4.2e-42.456:73//Hs.2820:X64878
- 30 F-HEMBB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293:AB011142  
 F-HEMBB1001356//EST//0.32:292:59//Hs.135771:AI005648  
 F-HEMBB1001364  
 F-HEMBB1001366//EST//7.8e-24.367:69//Hs.138765:N70347
- 35 F-HEMBB1001367//Small inducible cytokine A5 (RANTES)/8.7e-50:326:86//Hs.155464:AF088219  
 F-HEMBB1001369//EST//0.17:211.63//Hs.120066:AA707973  
 F-HEMBB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36.225:79//Hs.129748:AB011099  
 F-HEMBB1001384
- 40 F-HEMBB1001387//ESTs//0.61:215:60//Hs.145915:AI342230  
 F-HEMBB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94.568:83//Hs.23094:M19503  
 F-HEMBB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750:AF065988  
 F-HEMBB1001424//EST//0.20:307:58//Hs.135336:AI049827
- 45 F-HEMBB1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17.205:72//Hs.83466:AF038174  
 F-HEMBB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]/5.5e-153.729:96//Hs.21679:AF034175  
 F-HEMBB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345  
 F-HEMBB1001443
- 50 F-HEMBB1001449//Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216  
 F-HEMBB1001454//ESTs//1.4e-46.279:93//Hs.104866:AA426038  
 F-HEMBB1001458//EST//1.7e-09:106:83//Hs.141422:N20920  
 F-HEMBB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220
- 55 F-HEMBB1001464//Homo sapiens Coch-5B2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740  
 F-HEMBB1001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27.292:74//Hs.137168:AB018303  
 F-HEMBB1001500//ESTs//8.1e-28.312:74//Hs.18498:N52088

- F-HEM BB1001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942
- F-HEM BB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815
- F-HEM BB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735
- 5 F-HEM BB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093
- F-HEM BB1001536//ESTs//0.0047:120:68//Hs.144858:R67748
- F-HEM BB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D. melanogaster]//3.7e-20:297:73//Hs.42457:AA523306
- 10 F-HEM BB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//Hs.102877:U41315
- F-HEM BB1001562//ESTs//0.95:161:61//Hs.145075:A1208240
- F-HEM BB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953
- 15 F-HEM BB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080
- F-HEM BB1001585
- F-HEM BB1001586//EST//0.84:132:64//Hs.145264:A1218708
- F-HEM BB1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.90798:U92899
- F-HEM BB1001603//ESTs//1.3e-12:84:96//Hs.13380:R60414
- F-HEM BB1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680
- 20 F-HEM BB1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314
- F-HEM BB1001630//EST//1.4e-07:334:62//Hs.145698:A1266713
- F-HEM BB1001635//ESTs//0.92:282:60//Hs.126980:AA934077
- F-HEM BB1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.116549:AL009172
- F-HEM BB1001641//EST//0.11:53:81//Hs.112445:AA594279
- 25 F-HEM BB1001653//EST//0.91:124:64//Hs.144213:T40480
- F-HEM BB1001665//Human mRNA for apolipoprotein E receptor 2, complete cds//7.0e-13:473:63//Hs.54481:D86407
- F-HEM BB1001668//ESTs//0.94:83:69//Hs.146202:A1252519
- F-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.3e-172:803:98//Hs.24439:AB014546
- 30 F-HEM BB1001684//ESTs, Highly similar to Tbc1 [M. musculus]//5.4e-20:110:100//Hs.106104:AA599496
- F-HEM BB1001685//EST//2.2e-05:112:73//Hs.130984:A1015430
- F-HEM BB1001695//Human novel homeobox mRNA for a DNA binding protein//1.6e-08:425:62//Hs.37035:U07664
- F-HEM BB1001704//EST//5.8e-20:295:69//Hs.140231:A1054398
- 35 F-HEM BB1001706
- F-HEM BB1001707//EST//0.091:241:60//Hs.136830:AA769219
- F-HEM BB1001717//ESTs//2.9e-06:325:60//Hs.150063:A1298064
- F-HEM BB1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs.155464:AF088219
- F-HEM BB1001736//ESTs, Weakly similar to E04D5.1 [C. elegans]//5.4e-99:485:97//Hs.120581:W25578
- 40 F-HEM BB1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244
- F-HEM BB1001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.5e-75:315:83//Hs.129735:AF010144
- F-HEM BB1001753//ESTs//0.00013:35:100//Hs.139643:H06263
- F-HEM BB1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077
- 45 F-HEM BB1001760//ESTs//6.5e-06:503:58//Hs.21766:A1357639
- F-HEM BB1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//2.9e-13:498:60//Hs.158241:AB007976
- F-HEM BB1001785//EST//0.16:262:60//Hs.162526:AA584102
- F-HEM BB1001797//ESTs//0.37:201:63//Hs.91559:AA806370
- 50 F-HEM BB1001802//ESTs//1.6e-06:447:58//Hs.134672:A1087951
- F-HEM BB1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.3e-54:311:81//Hs.92381:AB007956
- F-HEM BB1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017
- F-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//7.6e-164:763:98//Hs.159396:AF056209
- 55 F-HEM BB1001834//TRICHOHYALIN//7.1e-05:548:60//Hs.82276:L09190
- F-HEM BB1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:86//Hs.22271:D26067
- F-HEM BB1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370



- F-HEM BB1001850//EST//0.0035:204.61//Hs.7311:T23858  
 F-HEM BB1001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357.82//Hs.155464:AF088219  
 F-HEM BB1001867//ESTs//2.2e-40:265.88//Hs.146323:AI251752  
 F-HEM BB1001868//ESTs//5.2e-06:131.73//Hs.123362:AA811371  
 5 F-HEM BB1001869//ESTs//1.0e-86:429.96//Hs.141208:AA825503  
 F-HEM BB1001872  
 F-HEM BB1001874//H.sapiens mRNA for CHD5 protein//0.0033:388.60//Hs.19923:Y12478  
 F-HEM BB1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//0.32:346:60//Hs.100555:X98743  
 10 F-HEM BB1001880//EST//4.0e-28:171.92//Hs.151194:AI125868  
 F-HEM BB1001899//ESTs//0.17:242:62//Hs.136969:AA830918  
 F-HEM BB1001905  
 F-HEM BB1001906//ESTs//5.6e-49:290.92//Hs.127298:H09155  
 F-HEM BB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//1.2e-83:672:81//Hs.82210:U47742  
 15 F-HEM BB1001910//EST, Weakly similar to albumin [H.sapiens]//0.047:206:62//Hs.159777:Z19955  
 F-HEM BB1001911  
 F-HEM BB1001915//ESTs//0.92:136:71//Hs.144465:R68882  
 F-HEM BB1001921//EST//2.0e-19:398.67//Hs.44789:N36113  
 20 F-HEM BB1001922//ESTs//4.3e-05:370.59//Hs.123669:AA805245  
 F-HEM BB1001925//ESTs//5.7e-27:329.71//Hs.141071:H16398  
 F-HEM BB1001930//EST//0.043:157:63//Hs.161927:AA483904  
 F-HEM BB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:80//Hs.154326:D42087  
 F-HEM BB1001945//ESTs//1.1e-19:142.88//Hs.7341:N57875  
 25 F-HEM BB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:66//Hs.40100:AB002390  
 F-HEM BB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:384:60//Hs.8546:U97669  
 F-HEM BB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101  
 F-HEM BB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//Hs.96:D90070  
 F-HEM BB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418  
 30 F-HEM BB1001962//Cytochrome P450, subfamily 1 (aromatic compound-inducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053  
 F-HEM BB1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969  
 F-HEM BB1001973//Myelin oligodendrocyte glycoprotein (alternative products)//1.2e-48:426:78//Hs.53217:Z48051  
 35 F-HEM BB1001983  
 F-HEM BB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051  
 F-HEM BB1001990//ESTs//0.25:171:64//Hs.7961:AA401205  
 F-HEM BB1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103  
 F-HEM BB1001997//EST//5.3e-33:294:76//Hs.161041:H82636  
 40 F-HEM BB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964  
 F-HEM BB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093  
 F-HEM BB1002009//ESTs//0.066:441:58//Hs.125313:AI201685  
 F-HEM BB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951  
 F-HEM BB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699  
 45 F-HEM BB1002043//ESTs, Weakly similar to T06E6.d [C.elegans]//1.0:217:60//Hs.3487:AA425553  
 F-HEM BB1002044  
 F-HEM BB1002045  
 F-HEM BB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.082:201:61//Hs.88756:AB018256  
 F-HEM BB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2557:Y00661  
 50 F-HEM BB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1e-07:402:61//Hs.112499:AB014512  
 F-HEM BB1002069  
 F-HEM BB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239  
 F-HEM BB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625  
 55 F-HEM BB1002115//EST//0.0083:244:64//Hs.125353:AA877080  
 F-HEM BB1002134//ESTs//1.7e-69:398.91//Hs.157492:AI361027  
 F-HEM BB1002139//ESTs//0.64:145:71//Hs.157821:AI362013  
 F-HEM BB1002142//ESTs//0.013:311:59//Hs.150037:AI292214

- F-HEMBB1002152//ESTs//8.4e-12:121.82//Hs.119540:T95254  
 F-HEMBB1002189//EST//0.26:81.70//Hs.147726:AI202208  
 F-HEMBB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.16:608.58//Hs.4:X03350  
 F-HEMBB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//Hs.301:U18934  
 5 F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:405:67//Hs.104115:X52332  
 F-HEMBB1002218//EST//0.015:24:61//Hs.105298:AA489813  
 F-HEMBB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs.155464:AF088219  
 F-HEMBB1002247  
 F-HEMBB1002249//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//  
 10 6.8e-47:418:77//Hs.125231:AF068006  
 F-HEMBB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0e-47:437:77//Hs.154872:  
 AB011166  
 F-HEMBB1002255//ESTs//0.017:255:61//Hs.126786:U74314  
 F-HEMBB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA, complete cds//0.17:511:57//  
 15 Hs.58169:AF017790  
 F-HEMBB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998  
 F-HEMBB1002300  
 F-HEMBB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.3e-14:228:72//Hs.  
 46468:U45984  
 20 F-HEMBB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083  
 F-HEMBB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:399:96//Hs.105837:AA536054  
 F-HEMBB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188  
 F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//1.4e-155:724:98//Hs.42644:  
 AJ010841  
 25 F-HEMBB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991  
 F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//1.7e-06:66:96//Hs.154762:  
 U00943  
 F-HEMBB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838  
 F-HEMBB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796  
 30 F-HEMBB1002381  
 F-HEMBB1002383//Vasoactive intestinal peptide receptor 2//0.98:190:63//Hs.2126:L36566  
 F-HEMBB1002387//EST//2.1e-07:253:61//Hs.145993:AI277784  
 F-HEMBB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456  
 F-HEMBB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.0e-32:371:73//Hs.  
 35 159897:AB007970  
 F-HEMBB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.54486:X54150  
 F-HEMBB1002442  
 F-HEMBB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:77//Hs.154326:D42087  
 F-HEMBB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101  
 40 F-HEMBB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274  
 F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds//6.0e-89:493:92//Hs.159605:U43885  
 F-HEMBB1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA, complete cds//0.019:228:63//  
 Hs.74304:AF001691  
 F-HEMBB1002492//EST//0.24:149:62//Hs.146790:AI149051  
 45 F-HEMBB1002495//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//1.3e-22:331:71//Hs.30:  
 M89796  
 F-HEMBB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494  
 F-HEMBB1002509//ESTs//0.017:220:63//Hs.155263:AI273725  
 F-HEMBB1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354  
 50 F-HEMBB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-50:580:72//Hs.23094:M19503  
 F-HEMBB1002522//EST//0.010:172:62//Hs.147224:AI205719  
 F-HEMBB1002531  
 F-HEMBB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs.155464:AF088219  
 F-HEMBB1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102  
 55 F-HEMBB1002550//Syntaxin 5A//0.17:235:59//Hs.154546:U26648  
 F-HEMBB1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191  
 F-HEMBB1002579//EST//1.0:77:68//Hs.147935:AI250286  
 F-HEMBB1002582//ESTs//0.00032:178:88//Hs.139163:AA226095

- F-HEMBB1002590//ESTs//0.64:132:63//Hs.155688:AI003657  
 F-HEMBB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336  
 F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-152:710:98//Hs.129826:AF089749
- 5 F-HEMBB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817  
 F-HEMBB1002603//EST//0.10:144:63//Hs.158180:AI367945  
 F-HEMBB1002607//ESTs//0.024:345:62//Hs.143304:AI084058  
 F-HEMBB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323  
 F-HEMBB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711
- 10 F-HEMBB1002614//ESTs//0.0048:136:71//Hs.106280:R13901  
 F-HEMBB1002617//EST//0.034:320:59//Hs.41223:H89127  
 F-HEMBB1002623//ESTs//0.88:222:60//Hs.129920:AA167217  
 F-HEMBB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs.151051:U07620  
 F-HEMBB1002664//EST//0.00013:203:61//Hs.117141:AA678811
- 15 F-HEMBB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680  
 F-HEMBB1002683//ESTs//0.23:224:61//Hs.128883:AI026679  
 F-HEMBB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124  
 F-HEMBB1002686//EST//0.25:189:62//Hs.132431:AA909674  
 F-HEMBB1002692//ESTs//0.00020:162:66//Hs.118180:N68504
- 20 F-HEMBB1002697//EST//7.2e-17:219:74//Hs.100459:T61992  
 F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor (TACI) mRNA, complete cds//0.059:297:62//Hs.158341:AF023614  
 F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588  
 F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SUI2-TDH2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0048:84:83//Hs.20814:AI242922
- 25 F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729  
 F-MAMMA1000009//Human c-yes-1mRNA//1.0e-48:447:77//Hs.75680:M15990  
 F-MAMMA1000019  
 F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750
- 30 F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945  
 F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739  
 F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461  
 F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//2.7e-18:330:63//Hs.59906:AA001281
- 35 F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.2e-50:367:75//Hs.133089:AF064019  
 F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:AI336840  
 F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067  
 F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:AB011174
- 40 F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//Hs.90357:U40705  
 F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:AB011792
- 45 F-MAMMA1000117  
 F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508  
 F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402  
 F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319  
 F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:AI383843
- 50 F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:AB014585  
 F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:219:87//Hs.129724:AF031924  
 F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050  
 F-MAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695
- 55 F-MAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:65//Hs.89434:D17530  
 F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657  
 F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763

- F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:AI091739  
 F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA9730035  
 F-MAMMA1000227//ESTs//0.010:268:60//Hs.16412:AA506926  
 F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913  
 5 F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873  
 F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:AI247587  
 F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:AI003543  
 F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015  
 F-MAMMA1000266//EST//0.14:270:60//Hs.132593:AI031874  
 10 F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087  
 F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726  
 F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:AI347361  
 F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505  
 F-MAMMA1000284  
 15 F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087  
 F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641  
 F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243  
 F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529  
 F-MAMMA1000312//EST//0.042:183:63//Hs.158928:AI379519  
 20 F-MAMMA1000313  
 F-MAMMA1000331  
 F-MAMMA1000339  
 F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC  
 REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//Hs.13096:AA180963  
 25 F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892  
 F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs.  
 158095:AB007953  
 F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-75:498:85//Hs.23094:M19503  
 F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:85//Hs.154326:D42087  
 30 F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569  
 F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344  
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710:  
 98//Hs.32170:AB015132  
 F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590  
 35 F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-58:834:68//Hs.23094:M19503  
 F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08:  
 117:84//Hs.83916:U53468  
 F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:AI200725  
 F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092  
 40 F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME  
 III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111  
 F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532  
 F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:  
 AF081573  
 45 F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459  
 F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:AI377641  
 F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102:  
 AF034546  
 F-MAMMA1000431//SLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830  
 50 F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872:  
 AB011166  
 F-MAMMA1000446  
 F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [C.elegans]//5.1e-08:58:  
 93//Hs.9043:W21827  
 55 F-MAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, complete  
 cds//0.58:311:63//Hs.66721:D49818  
 F-MAMMA1000472//SLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830  
 F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080

- F-MAMMA1000483//SLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400.75//Hs.51048:X68830  
 F-MAMMA1000490//ESTs//3.6e-52:331.88//Hs.163686:AA291948  
 F-MAMMA1000500//EST//9.7e-73:346.99//Hs.98812:AA434482  
 F-MAMMA1000501//Small inducible cytokine A5 (RANTES)/2.3e-50:325.86//Hs.155464:AF088219  
 5 F-MAMMA1000516//Oxytocin receptor//1.6e-29:660.64//Hs.2820:X64878  
 F-MAMMA1000522//ESTs//2.9e-23:328.70//Hs.125142:AA421352  
 F-MAMMA1000524//ESTs//1.1e-08:211.65//Hs.33467:R85497  
 F-MAMMA1000559//EST//4.7e-17:207.71//Hs.162733:AA614352  
 F-MAMMA1000565  
 10 F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//5.8e-51:404.80//Hs.125231:AF068006  
 F-MAMMA1000576//ESTs//3.8e-32:236.74//Hs.140039:AA047045  
 F-MAMMA1000583//ESTs//0.00099:123.70//Hs.135173:AI276780  
 F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//8.8e-45:390.78//Hs.159523:AF001622  
 15 F-MAMMA1000594//ESTs//8.3e-42:322.81//Hs.161660:AA167744  
 F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592.68//Hs.97476:AB007886  
 F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228.73//Hs.32567:AF073519  
 F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300.60//Hs.29207:AF071494  
 20 F-MAMMA1000616//EST//0.41:373.59//Hs.130699:AA621478  
 F-MAMMA1000621//EST//0.027:146.62//Hs.148305:AA909605  
 F-MAMMA1000623  
 F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428.56//Hs.98614:AF006751  
 F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//0.092:365.59//Hs.75474:AF023674  
 25 F-MAMMA1000664//ESTs//7.6e-07:259.64//Hs.140622:AA844353  
 F-MAMMA1000669//Human kpni repeat mrna (cdna clone pcd-kpni-4),3' end//9.0e-30:531.64//Hs.139107:K00629  
 F-MAMMA1000670//ESTs//6.6e-83:389.100//Hs.148595:AI244490  
 30 F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109.73//Hs.4316:U80743  
 F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//3.3e-07:249.62//Hs.44481:U13220  
 F-MAMMA1000696//Interleukin 10//5.6e-47:355.82//Hs.2180:M57627  
 F-MAMMA1000707//ESTs//1.4e-09:225.65//Hs.138722:N51081  
 35 F-MAMMA1000713//Acetylcholinesterase {I4-E5 domain} [human, tumor cell lines, Genomic, 847 nt]//0.16:84.72//Hs.157124:S71129  
 F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263.6//Hs.27414:U79275  
 F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210.66//Hs.71148:AA854648  
 F-MAMMA1000720//ESTs//1.4e-50:301.83//Hs.138852:AA284247  
 40 F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288.72//Hs.114685:AA700024  
 F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292.66//Hs.22670:AF006513  
 F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-40:288.78//Hs.158095:AB007953  
 45 F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467.58//Hs.1742:L33075  
 F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802.98//Hs.31575:AF100141  
 F-MAMMA1000738//EST//1.0:149.63//Hs.136928:AA812580  
 F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323.88//Hs.153468:AB011147  
 50 F-MAMMA1000746//ESTs//2.3e-42:409.76//Hs.61199:AA024494  
 F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285.68//Hs.162011:AA513663  
 F-MAMMA1000760//Myelin oligodendrocyte glycoprotein [alternative products]//6.2e-47:341.82//Hs.53217:Z48051  
 55 F-MAMMA1000761//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//9.8e-19:131.76//Hs.118972:AA761369  
 F-MAMMA1000775//EST//6.9e-32:424.69//Hs.44554:N34288  
 F-MAMMA1000776//ESTs//5.5e-43:154.84//Hs.141581:AA315361

- F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114  
 F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137  
 F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575  
 F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849  
 5 F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130  
 F-MAMMA1000831//ESTs//0.0061:194:60//Hs.150400:AI298089  
 F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e48:241:74//Hs.155464:AF088219  
 F-MAMMA1000841  
 10 F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//0.18:483:59//  
 Hs.82210:U47742  
 F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696  
 F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877  
 F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022  
 F-MAMMA1000855  
 15 F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:320:59//Hs.71388:AF032906  
 F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135  
 F-MAMMA1000862//EST//1.0:92:66//Hs.157599:AI357342  
 F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172  
 F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812  
 20 F-MAMMA1000867//EST//0.027:236:60//Hs.147156:AI191777  
 F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59//Hs.75850:D87459  
 F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147  
 F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-91:  
 484:94//Hs.138938:AA012894  
 25 F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812  
 F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465  
 F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3//2.6e-06:211:63//Hs.76716:  
 X67055  
 F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683  
 30 F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506  
 F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081  
 F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628  
 F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:AI125239  
 35 F-MAMMA1000931//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.0e-25:312:66//Hs.  
 116007:S79267  
 F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968  
 F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid  
 dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785  
 F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734  
 40 F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63//Hs.83790:AB002303  
 F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:64//Hs.25640:AB000714  
 F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474  
 F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-56:310:85//  
 Hs.129735:AF010144  
 45 F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814  
 F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096  
 F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802  
 F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062  
 F-MAMMA1000988//EST//2.0e-07:356:62//Hs.132467:AA922007  
 50 F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:AI003724  
 F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711  
 F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451:  
 Y15718  
 F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968  
 55 F-MAMMA1001030//Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete cds//3.6e-32:753:  
 61//Hs.98384:AF062006  
 F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857  
 F-MAMMA1001038

- F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//Hs.119000:M95178  
 F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:A1419882  
 F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs.135623:AA134719
- 5 F-MAMMA1001067//EST//0.30:166:60//Hs.148441:A198503  
 F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585  
 F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116  
 F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.135251:L09749
- 10 F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503  
 F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420  
 F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896  
 F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254
- 15 F-MAMMA1001092//Human kpni repeat mma (cdna clone pod-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:K00627  
 F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045  
 F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915
- 20 F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219  
 F-MAMMA1001133  
 F-MAMMA1001139  
 F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:A1091534  
 F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217
- 25 F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741  
 F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147  
 F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:A1014299  
 F-MAMMA1001181
- 30 F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47:313:81//Hs.97203:U83171  
 F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083  
 F-MAMMA1001198  
 F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348
- 35 F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974  
 F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.5e-25:275:75//Hs.105292:AA504776  
 F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200
- 40 F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:84//Hs.154326:D42087  
 F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898:AB014534  
 F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587  
 F-MAMMA1001244  
 F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:A1220476
- 45 F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:A160121  
 F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149  
 F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:AB014561
- 50 F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503  
 F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747  
 F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522  
 F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832  
 F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998  
 F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757426
- 55 F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305  
 F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//1.9e-58:295:97//Hs.102336:Z83838

- F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087  
 F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:745:73//Hs.93174:X57147  
 F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806  
 F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197  
 5 F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267  
 F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cds//0.94:89:75//Hs.109358:AB018258  
 F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.3e-49:273:80//Hs.42674:U61981  
 F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABEL CHAIN  
 PRECURSOR//4.6e-09:415:58//Hs.839:M86826  
 10 F-MAMMA1001397//Prostaglandin I2 (prostacyclin) synthase //1.3e-26:358:67//Hs.61333:D83402  
 F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763  
 F-MAMMA1001411//Autosomal dominant polycystic kidney disease type II//1.0:176:64//Hs.82001:U50928  
 F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:409:80//Hs.43681:AL022394  
 F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//0.00042:125:75//Hs.  
 15 46328:D87942  
 F-MAMMA1001435//Human HsLIM15 mRNA for HsLim15, complete cds//8.2e-43:543:71//Hs.37181:D64108  
 F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321  
 F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590  
 F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424040  
 20 F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053  
 F-MAMMA1001476//Human mRNA for 5'-terminal region of UMK, complete cds//2.0e-24:273:72//Hs.75939:  
 D78335  
 F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//3.2e-25:397:68//Hs.116874:  
 AA524909  
 25 F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366  
 F-MAMMA1001502//Human p120E4F transcription factor mRNA, complete cds//0.99:258:61//Hs.154196:U87269  
 F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795  
 F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AO18506  
 F-MAMMA1001547  
 30 F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds//7.5e-130:614:98//Hs.129937:  
 AB007931  
 F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//0.71:181:62//Hs.118866:  
 AI017072  
 F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150785:M61764  
 35 F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339  
 F-MAMMA1001600//EST//1.0e-08:81:87//Hs.149220:AI247132  
 F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375  
 F-MAMMA1001606//Human clone 23627 mRNA, complete cds//0.64:336:58//Hs.23642:U79266  
 F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152  
 40 F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58//Hs.158229:U28727  
 F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc  
 Finger protein (pseudogene, an unknown putative gene, a pseudogene with high similarity to part of antigen Ki-  
 67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger  
 protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and  
 45 DXS1055//1.4e-40:447:73//Hs.154353:AL022165  
 F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds//3.6e-44:617:67//Hs.57679:U57796  
 F-MAMMA1001635  
 F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524  
 F-MAMMA1001654//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.00069:140:  
 50 68//Hs.59829:AB014602  
 F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.015:135:71//Hs.27349:  
 AB007917  
 F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens]//0.064:472:60//Hs.110819:  
 AI027548  
 55 F-MAMMA1001671  
 F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA573317  
 F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA036889  
 F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI138765



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F-MAMMA1001692//ESTs//0.97:104:70//Hs. 27596:Al188549  
F-MAMMA1001711//Human G protein-coupled receptor (STRL22) mRNA, complete cds//8.0e-45:323:83//Hs. 46468:U45984  
5 F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs. 130815:AA936548  
F-MAMMA1001730//ESTs//0.048:198:65//Hs. 116412:AA506926  
F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//1.5e-111:725:84//Hs. 159154:U47634  
F-MAMMA1001740//EST//0.77:119:65//Hs. 148140:AA887098  
10 F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs. 163688:H48768  
F-MAMMA1001744//EST//0.00019:134:70//Hs. 146863:Al161245  
F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-67:822:69//Hs. 23094:M19503  
F-MAMMA1001751//Homo sapiens two P domain potassium channel subunit (HOHO1) mRNA, complete cds//1.0e-36:583:65//Hs. 79351:U33632  
F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs. 157928:AA775822  
15 F-MAMMA1001757//EST//0.0042:177:63//Hs. 144436:R07109  
F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense transcript, partial//6.6e-41:309:84//Hs. 102576:AJ010230  
F-MAMMA1001764//ESTs//0.0057:290:60//Hs. 68647:AA524072  
F-MAMMA1001768//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//2.2e-05:504:60//Hs. 96028:AF042832  
20 F-MAMMA1001769//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-85:686:79//Hs. 113283:AF018080  
F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete cds//0.00071:392:60//Hs. 32981:U38276  
F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs. 142524:H02940  
25 F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs. 61809:AA503549  
F-MAMMA1001788//Human kni repeat mma (cdna clone pod-kni-8), 3' end//6.7e-21:212:77//Hs. 103948:K00627  
F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:139:72//Hs. 5158:AB007869  
F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs. 105665:H78987  
30 F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs. 98613:D83884  
F-MAMMA1001815//EST//2.1e-56:374:85//Hs. 141488:N47096  
F-MAMMA1001817//EST//8.6e-39:336:78//Hs. 162236:AA551582  
F-MAMMA1001818//EST//0.32:375:58//Hs. 72729:AA167589  
F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA, complete cds//0.082:153:66//Hs. 114948:AF059293  
35 F-MAMMA1001824//EST//0.0013:195:63//Hs. 129275:AA992742  
F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs. 92290:R78691  
F-MAMMA1001837//Homo sapiens mRNA for zinc finger protein FPM315, complete cds//2.0e-29:641:62//Hs. 56808:D88827  
40 F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs. 116430:AA644665  
F-MAMMA1001851//ESTs//0.00050:251:64//Hs. 163776:Al393028  
F-MAMMA1001854  
F-MAMMA1001858//EST//1.0:113:68//Hs. 132482:AA922218  
F-MAMMA1001864//EST//1.3e-06:399:60//Hs. 161500:N69060  
45 F-MAMMA1001868//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.084:672:58//Hs. 152455:AF044209  
F-MAMMA1001874//ESTs//0.97:292:58//Hs. 24553:Al150687  
F-MAMMA1001878  
F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs. 15776:T91944  
50 F-MAMMA1001890//EST//1.7e-85:440:97//Hs. 128842:AA977576  
F-MAMMA1001907//EST//2.7e-26:294:74//Hs. 98794:AA434078  
F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs. 146145:Al391521  
F-MAMMA1001931//ESTs//1.0:108:67//Hs. 126624:AA768874  
F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs. 76260:M12529  
55 F-MAMMA1001963//ESTs//0.84:320:60//Hs. 6523:AA218859  
F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:423:81//Hs. 91916:AF035317  
F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs. 2820:X64878  
F-MAMMA1001992//EST, Weakly similar to reverse transcriptase [H.sapiens]//7.9e-09:150:72//Hs. 118222:

N91115

F-MAMMA1002009//ESTs//2.2e-18:234.69//Hs.21978:AA009633

F-MAMMA1002011//ESTs//0.91:276.59//Hs.141196:AA704826

F-MAMMA1002032//ESTs//7.8e-40:344.77//Hs.141658:N77915

5 F-MAMMA1002033//ESTs//2.5e-30:293.76//Hs.139158:AA226159

F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.2e-54:455.70//Hs.158095:AB007953

F-MAMMA1002042//ESTs//1.4e-20:199.79//Hs.140913:R44580

F-MAMMA1002047//EST//4.2e-14:170.75//Hs.124348:AA830225

10 F-MAMMA1002056//EST//2.1e-49:414.80//Hs.162335:AA564256

F-MAMMA1002058//EST//4.7e-26:268.78//Hs.140520:AA089305

F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-36:382.75//Hs.23094:M19503

F-MAMMA1002078

F-MAMMA1002082

15 F-MAMMA1002084//EST//0.37:351.59//Hs.46576:N46012

F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//0.54:388.57//Hs.99423:AJ010840

F-MAMMA1002108//Loricrin//0.00066:410.56//Hs.155657:M61120

F-MAMMA1002118//EST//0.50:202.64//Hs.126872:AA932932

20 F-MAMMA1002125//Small inducible cytokine A5 (RANTES)//2.4e-39:272.86//Hs.155464:AF088219

F-MAMMA1002132//EST//6.4e-05:245.60//Hs.149361:AI272963

F-MAMMA1002140//ESTs//5.8e-33:212.77//Hs.141203:H52638

F-MAMMA1002143//SERUM PROTEIN MSE55//1.9e-12:192.70//Hs.148101:M88338

F-MAMMA1002145//EST//0.12:204.60//Hs.160983:AI392837

25 F-MAMMA1002153

F-MAMMA1002155//ESTs, Weakly similar to p40 [H.sapiens]//3.6e-67:335.97//Hs.88424:AA281385

F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)//0.99:310.58//Hs.87149:M35999

F-MAMMA1002158//EST//0.015:278.58//Hs.162666:AA605196

F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573.82//Hs.119389:X17206

30 F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375.78//Hs.75859:U39400

F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:121.98//Hs.146354:Z22548

F-MAMMA1002209//ESTs//1.1e-84:409.98//Hs.139235:AA278362

F-MAMMA1002215//Loricrin//0.0024:369.57//Hs.155657:M61120

35 F-MAMMA1002219//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202.100//Hs.118849:AA215645

F-MAMMA1002230//ESTs//0.92:253.60//Hs.4222:AI024063

F-MAMMA1002236//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//4.6e-69:344.90//Hs.76822:AI359536

40 F-MAMMA1002243//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//0.99:454.56//Hs.122755:AF032986

F-MAMMA1002250//Human involucrin mRNA//0.0037:396.62//Hs.157091:M13903

F-MAMMA1002267//ESTs//2.0e-12:296.62//Hs.155686:AI308841

F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//1.2e-06:427.61//Hs.69949:M94172

45 F-MAMMA1002269

F-MAMMA1002282//ESTs//5.9e-65:342.95//Hs.13962:T72715

F-MAMMA1002292//EST//0.0050:346.58//Hs.97639:AA398440

F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.8e-60:387.75//Hs.133089:AF064019

50 F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//4.3e-07:349.64//Hs.92614:M62302

F-MAMMA1002297//EST//0.98:98.68//Hs.148207:AA897460

F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471.57//Hs.77234:AB001914

F-MAMMA1002299//ESTs//1.0:162.68//Hs.134132:AA205935

55 F-MAMMA1002308//ESTs, Weakly similar to !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! [H.sapiens]//6.9e-41:293.83//Hs.105292:AA504776

F-MAMMA1002310//Homo sapiens serine protease-like protease (nes1) mRNA, complete cds//0.0037:173.67//Hs.69423:AF055481

F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-41:473:65//Hs.92381:AB007956

F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA806291

F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908

5 F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:68//Hs.133342:AF070536

F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515

F-MAMMA1002329//Homo sapiens clone 24444 RaP2 interacting protein 8 (RPIP8) mRNA, complete cds//0.0079:143:67//Hs.6755:AF055026

10 F-MAMMA1002332//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//1.2e-26:342:72//Hs.103948:K00627

F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.8e-07:669:58//Hs.5333:AB018254

F-MAMMA1002339//H.sapiens mRNA for retrotransposon//3.2e-40:348:73//Hs.6940:Z48633

F-MAMMA1002347//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-14:146:81//Hs.163073:R02591

15 F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907

F-MAMMA1002352//EST//1.7e-09:198:68//Hs.149218:AI247086

F-MAMMA1002353//ESTs//7.4e-15:163:77//Hs.157253:AI357539

F-MAMMA1002355//Homo sapiens KIAA0441 mRNA, complete cds//7.7e-47:307:78//Hs.32511:AB007901

20 F-MAMMA1002356//ESTs//0.012:380:58//Hs.105349:AA779733

F-MAMMA1002359//EST//1.1e-44:264:77//Hs.141095:H23818

F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830

F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923

F-MAMMA1002362//EST//0.25:304:58//Hs.1.62427:AA576345

25 F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34677

F-MAMMA1002384//ESTs//1.1e-05:220:65//Hs.141388:R52022

F-MAMMA1002385//ESTs, Moderately similar to T11G6.8 [C.elegans]//8.4e-118:578:97//Hs.25516:AI086362

F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624

F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:AI142632

30 F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W85737

F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745

F-MAMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788

F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030

F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:83//Hs.154326:D42087

35 F-MAMMA1002446

F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809

F-MAMMA1002461//Human diacylglycerol kinase (DAGK) mRNA, complete cds//6.3e-06:595:59//Hs.99932:L38707

F-MAMMA1002470

40 F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, complete cds//0.018:417:58//Hs.75074:U12779

F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:N67059

F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//9.4e-120:560:98//Hs.155223:AF055460

45 F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628

F-MAMMA1002498//ESTs, Weakly similar to hypothetical protein [H.sapiens]//4.0e-07:257:63//Hs.133013:AA604920

F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391:L12392

50 F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//4.5e-162:775:97//Hs.18858:AF065214

F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788

F-MAMMA1002554

F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:187:62//Hs.62354:M83822

F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421

55 F-MAMMA1002571//EST//0.28:115:66//Hs.156768:AI351368

F-MAMMA1002573//ESTs//2.1e-4:8:265:94//Hs.155128:AI224516

F-MAMMA1002585

F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831

- F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:AI334107  
 F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:100//Hs.153:57958  
 F-MAMMA1002603//EST//0.070:99:71//Hs.122387:AA789220  
 5 F-MAMMA1002612//ESTs, Moderately similar to hCDC10 protein [H.sapiens]/8.3e-18:353:65//Hs.60895:AA428463  
 F-MAMMA1002617//B94 PROTEIN//0.0097:229:62//Hs.75522:M92357  
 F-MAMMA1002618  
 F-MAMMA1002619  
 10 F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//4.7e-22:157:90//Hs.47344:AF041449  
 F-MAMMA1002623//EST//1.5e-33:168:81//Hs.141526:N52300  
 F-MAMMA1002625  
 F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//1.1e-35:355:76//Hs.158241:AB007976  
 15 F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.9e-05:439:61//Hs.91400:AB006626  
 F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47:367:72//Hs.117977:L04733  
 F-MAMMA1002646//EST//1.2e-32:302:78//Hs.112540:AA601385  
 F-MAMMA1002650//TRICHOHYALIN//1.2e-08:570:63//Hs.82276:L09190  
 F-MAMMA1002655//EST//8.8e-40:198:100//Hs.159724:AI393335  
 20 F-MAMMA1002662//EST//0.99:95:63//Hs.144074:AI005489  
 F-MAMMA1002665//Lysosomal-associated membrane protein 2//1.8e-35:722:64//Hs.8262:U36336  
 F-MAMMA1002671//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//8.6e-06:272:64//Hs.106070:U22398  
 F-MAMMA1002673  
 25 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.2e-162:752:99//Hs.3363:D86987  
 F-MAMMA1002685//ESTs//7.5e-40:373:78//Hs.163937:N69915  
 F-MAMMA1002698//EST//2.5e-09:190:68//Hs.138292:AI220397  
 F-MAMMA1002699//Homo sapiens epsin 2b mRNA, complete cds//4.7e-56:398:81//Hs.22396:AF062085  
 F-MAMMA1002701//ESTs//4.3e-10:110:80//Hs.156041:AI274697  
 30 F-MAMMA1002708//Homo sapiens mRNA for alpha1,2-fucosyltransferase, complete cds//1.1e-51:307:79//Hs.46328:D87942  
 F-MAMMA1002711//EST//3.6e-38:186:77//Hs.139715:N25041  
 F-MAMMA1002721//EST//3.9e-06:110:71//Hs.136758:AA714692  
 F-MAMMA1002727//EST//0.97:137:63//Hs.145153:AI150165  
 35 F-MAMMA1002728//ESTs, Highly similar to PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE [Saccharomyces cerevisiae]/2.6e-12:129:81//Hs.154181:AA193502  
 F-MAMMA1002744//ESTs//0.0026:420:58//Hs.95793:AA617853  
 F-MAMMA1002746//ESTs//0.28:117:69//Hs.12925:T66312  
 F-MAMMA1002748  
 40 F-MAMMA1002754//ESTs//1.1e-34:340:77//Hs.163641:R61848  
 F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//1.1e-27:151:98//Hs.32168:AB007902  
 F-MAMMA1002764//ESTs//1.7e-45:323:84//Hs.155243:N70293  
 F-MAMMA1002765//EST//3.2e-11:145:73//Hs.162551:AA584782  
 F-MAMMA1002769  
 45 F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met.protein (M8604 Met) gene//7.6e-84:417:97//Hs.77705:U07563  
 F-MAMMA1002780//EST//0.78:210:63//Hs.149413:AI273988  
 F-MAMMA1002782  
 F-MAMMA1002796//ESTs//0.021:122:65//Hs.132221:AI380710  
 50 F-MAMMA1002807//EST//1.0e-31:184:71//Hs.161497:N66919  
 F-MAMMA1002820//ESTs//0.21:292:59//Hs.132513:AI778514  
 F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-57:286:88//Hs.15731:AB011135  
 F-MAMMA1002833//Human mRNA for KIAA0033 gene, partial cds//9.1e-52:583:72//Hs.22271:D26067  
 55 F-MAMMA1002835  
 F-MAMMA1002838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 [Locusta migratoria]/7.7e-38:179:78//Hs.141344:H29951  
 F-MAMMA1002842//ESTs//1.7e-19:134:89//Hs.111583:AA463590

- F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//5.4e-137:635.99//Hs.7531:AB018353
- F-MAMMA1002844//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.6e-07:329.58//Hs.107747:AI357868
- F-MAMMA1002858
- 5 F-MAMMA1002868//EST//4.1e-23:180.77//Hs.163196:AA767643
- F-MAMMA1002869//Human PINCH protein mRNA, complete cds//7.0e-88:696.78//Hs.83987:U09284
- F-MAMMA1002871//ESTs//3.4e-93:466.98//Hs.11873:T68423
- F-MAMMA1002880//EST//2.0e-09:364.59//Hs.14518:AI183632
- 10 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds//3.8e-30:680.61//Hs.129732:D45027
- F-MAMMA1002886//Long (electrocardiographic) QT syndrome 2//0.00075:504.60//Hs.19944:U04270
- F-MAMMA1002887//ESTs//0.044:144.68//Hs.133152:H91657
- F-MAMMA1002890//EST//1.7e-05:74.86//Hs.116013:AA612666
- F-MAMMA1002892//EST//2.1e-67:383.93//Hs.22815:R44265
- 15 F-MAMMA1002895//Human transcription factor ERF-1 mRNA, complete cds//0.00053:382.57//Hs.61796:U85658
- F-MAMMA1002908//EST//0.0022:132.68//Hs.161697:AA224952
- F-MAMMA1002909//ESTs//9.1e-21:343.70//Hs.142068:AA176125
- F-MAMMA1002930//ESTs//0.55:72.72//Hs.132440:AA923730
- F-MAMMA1002937//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.9e-103:485.99//Hs.102928:AI346344
- 20 F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//1.6e-194:910.98//Hs.31720:AB014598
- F-MAMMA1002941//ESTs//9.5e-19:196.67//Hs.137945:AI423389
- F-MAMMA1002947//ESTs//1.2e-96:460.99//Hs.156001:AI313418
- 25 F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial cds//0.48:250.60//Hs.54697:AB007884
- F-MAMMA1002970//EST//2.0e-16:132.84//Hs.136518:AA601400
- F-MAMMA1002972
- F-MAMMA1002973//ESTs//3.2e-43:225.74//Hs.155179:AA223932
- F-MAMMA1002982//ESTs//0.0017:162.66//Hs.152669:AA604944
- 30 F-MAMMA1002987//EST//0.044:254.59//Hs.135014:AI095645
- F-MAMMA1003003//Coagulation factor III (thromboplastin, tissue factor)//3.9e-22:185.83//Hs.62192:J02931
- F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.0e-16:343.61//Hs.159897:AB007970
- F-MAMMA1003007//EST//6.6e-10:265.66//Hs.144389:AA530979
- 35 F-MAMMA1003011//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.2e-51:620.69//Hs.75258:AF054174
- F-MAMMA1003013//Human HOX4C mRNA for a homeobox protein//0.73:347.58//Hs.74061:X59372
- F-MAMMA1003015//EST//2.5e-11:137.77//Hs.141312:H73062
- F-MAMMA1003019//ESTs//0.0099:182.65//Hs.60787:AI374951
- 40 F-MAMMA1003026//EST//1.0:136.67//Hs.9123:T50137
- F-MAMMA1003031//EST//1.3e-11:244.67//Hs.136611:AA669549
- F-MAMMA1003035
- F-MAMMA1003039//ESTs//1.4e-23:265.74//Hs.33393:R83391
- F-MAMMA1003040//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.5e-93:339.85//Hs.5247:AF029750
- 45 F-MAMMA1003044//Cyclin D2//1.0:234.61//Hs.75586:D13639
- F-MAMMA1003047//H.sapiens mRNA for F25B3.3 kinase like protein from C.elegans//1.0:209.60//Hs.99491:Y12336
- F-MAMMA1003049//EST//0.99:126.67//Hs.162634:AA601742
- F-MAMMA1003055//ESTs//0.00011:130.70//Hs.130539:R68518
- 50 F-MAMMA1003056
- F-MAMMA1003057//ESTs, Moderately similar to hypothetical protein MD6 [M.musculus]//1.3e-88:334.97//Hs.96500:AI206781
- F-MAMMA1003066//ESTs//0.77:88.71//Hs.143618:AI022618
- F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 protein, partial cds//4.5e-51:329.71//Hs.75154:AB014531
- 55 F-MAMMA1003099//Homo sapiens actin-binding protein homolog ABP-278 mRNA, complete cds//8.5e-44:288.88//Hs.81008:AF043045
- F-MAMMA1003104//H.sapiens mRNA for ASM-like phosphodiesterase 3a//1.0:213.60//Hs.42945:Y08136

- F-MAMMA1003113//Homo sapiens mRNA for hair keratin acidic 3-II//0.99:200:64//Hs.32950:X82634  
 F-MAMMA1003127//Homo sapiens brush border myosin I (BBM) mRNA, complete cds//5.4e-27:421:66//Hs.5394:  
 AF105424  
 F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786  
 5 F-MAMMA1003140  
 F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein//7.2e-82:397:97//Hs.151344:Y15062  
 F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cds//0.00019:297:61//Hs.108945:  
 AB011087  
 10 F-MAMMA1003166//Glycoprotein Ib (platelet), beta polypeptide//1.2e-31:487:65//Hs.3847:U59632  
 F-NT2RM1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:244:63//Hs.79706:U53204  
 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-66:385:92//Hs.82510:D31886  
 F-NT2RM1000032  
 F-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-110:849:81//Hs.78442:D83782  
 15 F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.5e-108:542:95//Hs.60103:  
 AB014590  
 F-NT2RM1000039//Human plectin (PLEC1) mRNA, complete cds//0.11:545:57//Hs.79706:U53204  
 F-NT2RM1000055//ESTs, Highly similar to TIP120 [R.norvegicus]//3.2e-69:353:96//Hs.154980:AA948067  
 F-NT2RM1000059//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.029:281:59//  
 Hs.46465:U45285  
 20 F-NT2RM1000062//ESTs//0.30:368:59//Hs.131675:AA843210  
 F-NT2RM1000080//Homo sapiens chromosome 9, P1 clone 11659//2.8e-102:493:97//Hs.3439:AC004472  
 F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//5.8e-116:550:97//Hs.65238:  
 AB014561  
 F-NT2RM1000092//Murine leukemia viral (bmi-1) oncogene homolog//0.42:190:63//Hs.431:L13689  
 25 F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00086:126:70//Hs.92693:  
 AF007155  
 F-NT2RM1000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:Z48054  
 F-NT2RM1000127  
 F-NT2RM1000131  
 30 F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene en-  
 coding mitochondrial protein, complete cds//3.7e-92:448:97//Hs.49767:AF044959  
 F-NT2RM1000153//Homo sapiens mRNA for MTG8-related protein MTG16a, complete cds//1.0:456:58//Hs.  
 110099:AB010419  
 35 F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00081:126:70//Hs.92693:  
 AF007155  
 F-NT2RM1000187//ESTs//3.4e-79:400:96//Hs.54971:AI424382  
 F-NT2RM1000199//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.87:454:59//Hs.47061:AF045458  
 F-NT2RM1000242  
 40 F-NT2RM1000244//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.97:  
 135:66//Hs.27910:AF049105  
 F-NT2RM1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L08190  
 F-NT2RM1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-13:248:69//Hs.1674:M90516  
 F-NT2RM1000257//ESTs, Highly similar to similar to mago nashi [H.sapiens]//2.9e-98:530:93//Hs.104650:  
 AI037879  
 45 F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-58:460:80//Hs.23106:D50920  
 F-NT2RM1000271//ESTs//0.93:224:60//Hs.91226:AA649047  
 F-NT2RM1000272  
 F-NT2RM1000280//ESTs, Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]//1.3e-21:308:  
 73//Hs.15071:AA781144  
 50 F-NT2RM1000300  
 F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-128:708:92//Hs.5719:D63880  
 F-NT2RM1000318//Human mRNA for ribosomal protein L39, complete cds//1.8e-35:182:99//Hs.9837:D79205  
 F-NT2RM1000341//ESTs//2.3e-72:381:95//Hs.23070:AA631976  
 F-NT2RM1000354//EST//5.2e-27:202:84//Hs.151186:AI125798  
 55 F-NT2RM1000355//ESTs, Weakly similar to putative [M.musculus]//7.7e-75:387:95//Hs.108619:W28608  
 F-NT2RM1000365//ESTs//1.7e-99:495:97//Hs.103926:AA165691  
 F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase [H.sapiens]//7.4e-91:481:95//Hs.  
 163707:AA137181

- F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.8939:X80507  
 F-NT2RM1000394//HISTONE H3.3//8.5e-91:474:93//Hs.118838:M11353  
 F-NT2RM1000399  
 F-NT2RM1000421
- 5 F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.2e-85:418:97//Hs.20815:AF084928  
 F-NT2RM1000499//ESTs. Weakly similar to KIAA0167 protein [H.sapiens]//1.6e-38:201:97//Hs.106262:A052382  
 F-NT2RM1000539//EST//0.070:145:62//Hs.149711:A1284660  
 F-NT2RM1000553//EST//2.2e-48:265:95//Hs.99230:AA449847
- 10 F-NT2RM1000555//ESTs//0.82:193:61//Hs.96944:A1359957  
 F-NT2RM1000563//Human plectin (PLEC1) mRNA, complete cds//1.0:336:58//Hs.79706:U53204  
 F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gene, partial cds//0.98:226:61//Hs.17931:AB006625  
 F-NT2RM1000648//ESTs. Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.ele-gans]//6.2e-51:254:98//Hs.132096:AA314601
- 15 F-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds//8.5e-55:276:97//Hs.19122:AF038957  
 F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete cds//0.87:274:60//Hs.113936:AB005297  
 F-NT2RM1000669//ESTs//5.5e-63:481:85//Hs.90527:A1188279  
 F-NT2RM1000672
- 20 F-NT2RM1000691//Homo sapiens mRNA for HRIHFB2060, partial cds//7.0e-121:582:98//Hs.146282:AB015348  
 F-NT2RM1000699//ESTs//1.1e-89:435:97//Hs.28964:AA715101  
 F-NT2RM1000702//ESTs//5.4e-90:429:99//Hs.151001:AA564706  
 F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase//1.5e-66:435:85//Hs.5038:AJ004832  
 F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds//2.6e-127:690:92//Hs.147946:
- 25 AB011139  
 F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds//8.2e-68:524:83//Hs.112360:AF027208  
 F-NT2RM1000746//ESTs//2.6e-37:231:89//Hs.94446:AA845465  
 F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, complete cds//3.3e-09:321:63//Hs.150390:AB007885  
 F-NT2RM1000772//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.053:271:60//Hs.139745 :U39067
- 30 F-NT2RM1000780//Human Line-1 repeat mRNA with 2 open reading frames//6.9e-20:128:94//Hs.23094:M19503  
 F-NT2RM1000781//ESTs//4.4e-60:346:92//Hs.35089:N50845  
 F-NT2RM1000800  
 F-NT2RM1000802
- 35 F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds//1.2e-64:490:84//Hs.112360:AF027208  
 F-NT2RM1000826//ESTs//0.82:193:61//Hs.96944:A1359957  
 F-NT2RM1000829//Mannose-binding lectin, soluble (opsonic defect)//0.92:283:58//Hs.2314:X15422  
 F-NT2RM1000833//Hydroxysteroid (11-beta) dehydrogenase 2//0.022:178:67//Hs.1376:U26726
- 40 F-NT2RM1000850//Human protein tyrosine kinase related mRNA sequence//3.8e-06:384:59//Hs.90314:L05148  
 F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//3.0e-149:726:97//Hs.99423:AJ010840  
 F-NT2RM1000857//ESTs//0.52:274:60//Hs.112095:AA447643  
 F-NT2RM1000867//ESTs. Highly similar to signal peptidase:SUBUNIT//5.3e-54:277:96//Hs.11125:A015619  
 F-NT2RM1000874//ESTs//0.032:185:64//Hs.97713:AA442239
- 45 F-NT2RM1000882//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.0e-155:750:97//Hs.132898:AC004770  
 F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//8.8e-158:762:97//Hs.26285:AF082516  
 F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds//6.3e-19:310:67//Hs.65238:AB014561
- 50 F-NT2RM1000894  
 F-NT2RM1000898  
 F-NT2RM1000905//EST//4.8e-07:77:84//Hs.148017:A1268701  
 F-NT2RM1000924//HOMEOBOX PROTEIN HOX-A5//0.00051:458:59//Hs.37034:M26679
- 55 F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 protein, partial cds//0.084:386:58//Hs.101474:AB018350  
 F-NT2RM1000962//Human mRNA for KIAA0252 gene, partial cds//0.98:299:59//Hs.83419:D87440  
 F-NT2RM1000978  
 F-NT2RM1001003//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.3e-161:760:98//

- Hs. 58488:U97067  
 F-NT2RM1001008//ESTs//1.3e-12:144.75//Hs.133122:AI025200  
 F-NT2RM1001043//EST//0.24:117.64//Hs.161536:N80395  
 F-NT2RM1001044//ESTs. Weakly similar to C43E11.9[C.elegans]//3.0e-98:491.96//Hs.102173:AA045270  
 5 F-NT2RM1001059//Human plectin (PLEC1) mRNA, complete cds//0.52:533.57//Hs.79706:U53204  
 F-NT2RM1001066//ESTs//1.2e-114:538.99//Hs.129020:AI380703  
 F-NT2RM1001072//Human beige-like protein (BGL) mRNA, partial cds//0.69:586.56//Hs.62354:M83822  
 F-NT2RM1001074//Macrophage stimulating 1 (hepatocyte growth factor-like)/0.0019:294.64//Hs.30223:X90846  
 F-NT2RM1001082//Archain//3.9e-37:290.81//Hs.33642:X81198  
 10 F-NT2RM1001085  
 F-NT2RM1001092//Zinc finger protein 43 (HTF6)//1.9e-57:770.68//Hs.74107:X59244  
 F-NT2RM1001102//ESTs//1.2e-35:638.63//Hs.131737:AI343331  
 F-NT2RM1001105//WEE1-LIKE PROTEIN KINASE//0.0024:246.63//Hs.75188:U10564  
 F-NT2RM1001121//ESTs//8.9e-82:437.93//Hs.6330:H38495  
 15 F-NT2RM1001115  
 F-NT2RM1001139//Keratin 9//1.5e-05:518.59//Hs.2783:Z29074  
 F-NT2RM2000006//ESTs//3.9e-16:96.98//Hs.101117:AA576113  
 F-NT2RM2000013//RNA polymerase II polypeptide B (140 kD)/6.3e-13:640.59//Hs.148027:X63563  
 F-NT2RM2000030  
 20 F-NT2RM2000032//ESTs//7.1e-18:138.68//Hs.114031:AA700958  
 F-NT2RM2000042//ESTs//0.0091:241.61//Hs.147895:AI286243  
 F-NT2RM2000092  
 F-NT2RM2000093//ESTs//2.6e-40:226.94//Hs.163521:H42085  
 F-NT2RM2000101//ESTs//1.0.235.61//Hs.48860:N27428  
 25 F-NT2RM2000124//Protein kinase, cAMP-dependent, catalytic, alpha//5.8e-46:287.88//Hs.77271:X07767  
 F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//3.0e-139:566.97//Hs.18953:AF067223  
 F-NT2RM2000192//EST//3.5e-07:168.65//Hs.163122:AA756999  
 F-NT2RM2000239//ESTs. Weakly similar to K04G2.6 [C.elegans]//3.6e-93:489.95//Hs.143499:R72672  
 30 F-ntnnnnnnnnnn//ESTs//1.0e-70:269.97//Hs.156175:AI334328  
 F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.0e-129:615.98//Hs.111862:AB011162  
 F-NT2RM2000259//ESTs//6.1e-30:172.85//Hs.116406:AA209520  
 F-NT2RM2000260//ESTs//2.5e-25:133.93//Hs.14169:AA203500  
 35 F-NT2RM2000287//ESTs//6.2e-13:97.83//Hs.118523:H98981  
 F-NT2RM2000322//Interferon regulatory factor 5//0.84:208.61//Hs.54434:U51127  
 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds//2.8e-176:805.99//Hs.129952:AB011132  
 F-NT2RM2000363//ESTs//1.2e-24:139.96//Hs.48818:N63543  
 40 F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds//3.7e-96:599.86//Hs.75871:U48251  
 F-NT2RM2000371  
 F-NT2RM2000374//ESTs//3.2e-13:98.91//Hs.65853:AI050866  
 F-NT2RM2000395//Growth arrest-specific 1//0.80:129.67//Hs.65029:L13698  
 45 F-NT2RM2000402//Human p76 mRNA, complete cds//7.2e-23:714.59//Hs.28757:U81006  
 F-NT2RM2000407//ESTs//9.4e-92:458.96//Hs.148873:T33582  
 F-NT2RM2000420//EST//1.8e-61:296.99//Hs.147186:AI193053  
 F-NT2RM2000422//Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4//1.5e-06:260.61//Hs.553:L05568  
 50 F-NT2RM2000452//ESTs//1.0:132.62//Hs.110004:AI097379  
 F-NT2RM2000469//ESTs//0.34:249.60//Hs.149575:AI261807  
 F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.4e-16:386.63//Hs.8309:AB018290  
 F-NT2RM2000502//Human nicotinamide N-methyltransferase (NNMT) mRNA, complete cds//0.99:272.61//Hs.76669:U08021  
 55 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//1.6e-172:824.97//Hs.4812:AF061243  
 F-NT2RM2000522//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.18:313.60//Hs.129725:AF047487  
 F-NT2RM2000540//ESTs. Weakly similar to C27F2.7 gene product [C.elegans]//2.7e-41:231.94//Hs.7049:



- AI141736  
 F-NT2RM2000556//ESTs//3.1e-33:183.96//Hs.136990:AA769220  
 F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751.97//Hs.74369:AF032108  
 F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689.59//Hs.89631:U48508  
 5 F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128  
 F-NT2RM2000577//ESTs. Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214.92//Hs.55609:W37993  
 F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.8e-175:820.98//Hs.3363:D86987  
 10 F-NT2RM2000588//ESTs//1.5e-33:183.97//Hs.136990:AA769220  
 F-NT2RM2000594  
 F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.017:253.65//Hs.102402:AF040963  
 F-NT2RM2000609//ESTs//1.0:220.59//Hs.110155:AA007313  
 15 F-NT2RM2000612//ESTs//0.97:208.59//Hs.73217:AA846548  
 F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.024:326.59//Hs.6150:AB011093  
 F-NT2RM2000624//ESTs//2.3e-118:557.99//Hs.145904:AA203258  
 F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0e-143:664.98//Hs.19542:AB018272  
 20 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4e-139:664.98//Hs.7278:AB014558  
 F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:AI189702  
 F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4e-169:518.99//Hs.115763:AB014576  
 F-NT2RM2000669//ESTs//1.3e-56:283.98//Hs.156342:AI337371  
 25 F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds//6.7e-86:746.74//Hs.5321:AF06083  
 F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748.64//Hs.7938:D86984  
 F-NT2RM2000718//Homo sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:594.98//Hs.136058:AB015342  
 F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756.82//Hs.74107:X59244  
 30 F-NT2RM2000740//ESTs. Highly similar to HYPOTHETICAL 132.7 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION [Saccharomyces cerevisiae]//4.2e-85:464.91//Hs.161551:W24286  
 F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-82:640.81//Hs.5247:AF029750  
 F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679.59//Hs.105919:AB002338  
 F-NT2RM2000837//ESTs//2.3e-105:501.98//Hs.101514:AI346701  
 35 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//2.8e-185:847.99//Hs.137580:AB015046  
 F-NT2RM2000952//ESTs. Weakly similar to lethal(2)denticleless [D.melanogaster]//6.2e-94:441.99//Hs.59075:AI023761  
 F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351.62//Hs.84753:D87433  
 40 F-NT2RM2001004//ESTs//5.0e-10:247.64//Hs.36049:AA436831  
 F-NT2RM2001035//ESTs. Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//2.9e-48:282.93//Hs.17035:AI080471  
 F-NT2RM2001065  
 F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449:62//Hs.75111:D87258  
 45 F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.00079:274.59//Hs.102732:U88153  
 F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684.62//Hs.82276:L09190  
 F-NT2RM2001141  
 50 F-NT2RM2001152//ESTs//0.53:333.58//Hs.153087:AA649042  
 F-NT2RM2001177  
 F-NT2RM2001194//ESTs. Weakly similar to T2H10.2 [C.elegans]//2.4e-23:149.93//Hs.10618:AI288739  
 F-NT2RM2001196//ESTs//4.0e-98:486.97//Hs.59628:W91959  
 F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554.69//Hs.155291:D13630  
 55 F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165.64//Hs.24279:AB018349  
 F-NT2RM2001238//EST//6.8e-67:420.89//Hs.130586:AI004766  
 F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125.64//Hs.75889:U65928  
 F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321.61//Hs.132206:

AF039694  
 F-NT2RM2001256  
 F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845  
 F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601  
 5 F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615  
 F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.elegans]//5.2e-30:277:77//Hs.25347:AI138605  
 F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567  
 F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706  
 10 F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905  
 F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61//Hs.82925:U70322  
 F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:U68382  
 F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378  
 F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-97:453:99//Hs.155218:AJ007509  
 15 F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X57303  
 F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328:60//Hs.68900:AF016903  
 F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969  
 F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459  
 20 F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262  
 F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//6.9e-28:582:64//Hs.1042:M62800  
 F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:57:89//Hs.114722:AA448077  
 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65//Hs.32168:AB007902  
 25 F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:AI391729  
 F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//Hs.76272:S66431  
 F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073  
 F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:AI393918  
 30 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.0e-154:740:98//Hs.15832:AB014518  
 F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952  
 F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]//3.5e-13:94:92//Hs.22142:AA814725  
 35 F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073  
 F-NT2RM2001652//ESTs//2.5e-08:82:80//Hs.128203:AA972301  
 F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287  
 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-173:802:99//Hs.31323:AF044195  
 40 F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATCH REPAIR PROTEIN MSH6 [H.sapiens]//1.1e-136:671:97//Hs.27721:U17907  
 F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414:AB011129  
 45 F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:AI365356  
 F-NT2RM2001675  
 F-NT2RM2001681//ESTs//0.16:197:63//Hs.20585:R10305  
 F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211  
 F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216  
 50 F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//5.8e-16:144:84//Hs.14671:T79937  
 F-NT2RM2001698//ESTs//0.14:164:63//Hs.148080:AI277415  
 F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:AI003817  
 F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//0.95:270:61//Hs.15791:AF027826  
 55 F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788  
 F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650  
 F-NT2RM2001718  
 F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//Hs.12457:AF052123

- F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0e-112:530:98//Hs.129937:AB007931
- F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269:58//Hs.129952:AB011132
- 5 F-NT2RM2001743
- F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:AB011399
- F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073
- 10 F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:A1222742
- F-NT2RM2001771//Zinc finger protein 10 (KOX 1)//1.1e-66:669:71//Hs.2479:X78933
- F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698
- F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:A193595
- F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770
- 15 F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481:72//Hs.70617:D31763
- F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142:66//Hs.78202:U29175
- F-NT2RM2001803//Homo sapiens IkkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195
- 20 F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341
- F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068
- F-NT2RM2001823//H.sapiens mRNA for 218kD Mi-2 protein//9.7e-21:554:60//Hs.74441:X86691
- F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//1.2e-132:738:90//Hs.7753:AF013759
- F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:329:86//Hs.113283:AF018080
- 25 F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M57567
- F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-28:421:66//Hs.8763:W30741
- F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723
- F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.1e-189:866:97//Hs.4198:AB014610
- 30 F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLC1101133Q7 (RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892
- F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4e-178:859:97//Hs.129937:AB007931
- F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.2e-08:481:59//Hs.27621:U52840
- 35 F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//0.37:424:60//Hs.118634:U66688
- F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//2.2e-139:653:98//Hs.21811:AF091080
- 40 F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392
- F-NT2RM2001982
- F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds//1.2e-21:123:98//Hs.6454:AF089816
- F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//Hs.104135:AJ006778
- 45 F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538
- F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//0.99:271:60//Hs.63888:AA203398
- F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5e-37:509:65//Hs.6214:AB018274
- F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:429:58//Hs.79090:D89729
- F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822:73//Hs.1674:M90516
- 50 F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427
- F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:AI382154
- F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:AI198377
- F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//Hs.89631:U48508
- F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.5e-165:776:98//Hs.99423:AJ010840
- 55 F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435
- F-NT2RM2002128

- F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA575274
- F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.4e-144:800:92//Hs.20815:AF084928
- 5 F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds//1.7e-165:787:97//Hs.11147:AB007936
- F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//0.064:291:61//Hs.99936:X14487
- F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:610:59//Hs.148027:X63563
- 10 F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074
- F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:A1391464
- F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:A094674
- F-NT2RM4000061//ESTs//0.89:207:60//Hs.98445:A1038511
- F-NT2RM4000085//ESTs. Weakly similar to The KIAA0134 gene product is related to human RNA helicase A. [H. sapiens]//1.6e-30:369:70//Hs.114623:A1204280
- 15 F-NT2RM4000086
- F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds//1.3e-24:345:69//Hs.13128:AF060865
- F-NT2RM4000139
- F-NT2RM4000155
- 20 F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632
- F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, complete cds//9.8e-30:676:61//Hs.159228:AF041853
- F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044
- F-NT2RM4000191//TRICHOHYALIN//0.011:324:60//Hs.82276:L09190
- 25 F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744
- F-NT2RM4000199//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.13:322:61//Hs.145088:A1221147
- F-NT2RM4000200
- F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.0027:424:60//Hs.91400:AB006626
- 30 F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//4.4e-184:856:98//Hs.111138:AB018255
- F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//0.0013:358:60//Hs.75055:M93651
- F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.65:572:60//Hs.47061:AF045458
- 35 F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582
- F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439
- F-NT2RM4000251//ESTs. Weakly similar to CUT1 PROTEIN [Schizosaccharomyces pombe]//1.1e-16:112:92//Hs.93841:AA442297
- 40 F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.8e-48:229:83//Hs.46328:D87942
- F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds//2.5e-154:609:93//Hs.31305:M99438
- F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complete cds//0.070:460:59//Hs.5372:AB000712
- 45 F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:A1240707
- F-NT2RM4000344//ESTs. Highly similar to YME1 PROTEIN [Saccharomyces cerevisiae]//2.7e-83:432:95//Hs.12796:W27884
- F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-53:666:68//Hs.155291:D13630
- 50 F-NT2RM4000354//ESTs. Weakly similar to lethal(2)denticleless [D.melanogaster]//0.0078:55:92//Hs.59075:M023761
- F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:A1418425
- F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//5.3e-135:628:99//Hs.8152:AB014542
- F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745
- F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//2.0e-72:843:68//Hs.23796:AL022718
- 55 F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)//0.63:166:65//Hs.946:X73029

- F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds//4.9e-17.114.94//Hs.137580:AB015046
- F-NT2RM4000421
- 5 F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42.432.74//Hs.154872:AB011166
- F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.023:543.58//Hs.2175:M59820
- F-NT2RM4000457
- F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:178.631//Hs.66369:U95040
- 10 F-NT2RM4000486//ESTs//9.2e-48:237.99//Hs.160685:AI280004
- F-NT2RM4000496//ESTs//0.069:252.61//Hs.155958:AA573632
- F-NT2RM4000511//EST//0.92:191.58//Hs.61517:AA028915
- F-NT2RM4000514
- F-NT2RM4000515//ESTs//7.3e-93.450.98//Hs.120975:AA034409
- 15 F-NT2RM4000520//ESTs//0.13:183.65//Hs.144828:AI221305
- F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.8e-153.756.96//Hs.125870:AI364967
- F-NT2RM4000532//ESTs//7.7e-43:388.78//Hs.105665:H78987
- F-NT2RM4000534
- 20 F-NT2RM4000585
- F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593.62//Hs.7764:AB007938
- F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//3.1e-104.532.96//Hs.6092:T75227
- 25 F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305.68//Hs.40100:AB002390
- F-NT2RM4000611//EST//0.76:268.58//Hs.150031:AI292068
- F-NT2RM4000616
- F-NT2RM4000674
- F-NT2RM4000689
- 30 F-NT2RM4000698//Apolipoprotein E//1.0:290.59//Hs.76260:M12529
- F-NT2RM4000700
- F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.5e-91:744.77//Hs.42400:AF022789
- F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.6e-163.771.97//Hs.6823:W18181
- 35 F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257.60//Hs.957:M84605
- F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-159:743.98//Hs.137168:AB018303
- F-NT2RM4000741
- 40 F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.1e-75:388.96//Hs.112361:R99396
- F-NT2RM4000764//ESTs//3.8e-104.539.95//Hs.24739:H67815
- F-NT2RM4000778//ESTs//1.5e-85.419.97//Hs.99838:AA204731
- F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.8e-173.810.98//Hs.18586:AB007920
- 45 F-NT2RM4000787//EST//0.011:182.65//Hs.159928:AA969186
- F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156.736.98//Hs.25817:AC005306
- F-NT2RM4000795//ESTs, Highly similar to LIVER CARBOXYLESTERASE PRECURSOR [Homo sapiens]//6.7e-19:160.80//Hs.124902:AI337820
- 50 F-NT2RM4000796//Human K<sup>+</sup> channel subunit gene, complete cds//0.96:292.62//Hs.124212:M64676
- F-NT2RM4000798//ESTs//1.9e-34:271.82//Hs.128203:AA972301
- F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//0.052:238.64//Hs.113265:AF032387
- F-NT2RM4000820//ESTs//0.053:274.61//Hs.23748:H16568
- 55 F-NT2RM4000833
- F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374.61//Hs.7841:AB002322
- F-NT2RM4000852//EST//1.0:222.60//Hs.120354:AA718934
- F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 [Homo sapiens]

- ensj//4.4e-29:164:95//Hs.115095:AI392943  
F-NT2RM40000887
- 5 F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds//6.8e-22:407:64//Hs.21293:AB011004  
F-NT2RM40000950  
F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:AI014546  
F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571:77//Hs.7289:AB007875  
F-NT2RM4000996//Zinc finger protein 3 (AB-51)//8.7e-34:381:67//Hs.2481:X78926
- 10 F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.6e-171:803:98//Hs.19542:AB018272  
F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//1.1e-126:584:99//Hs.15711:AB014539  
F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete cds//4.8e-05:469:58//Hs.5333:AB018254
- 15 F-NT2RM4001047//ESTs, Moderately similar to MO25 PROTEIN [M.musculus]//7.0e-56:340:92//Hs.87310:AI247543  
F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM" PRECURSOR//0.79:142:69//Hs.77424:M63835  
F-NT2RM4001084
- 20 F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235:62//Hs.108947:D30758  
F-NT2RM4001116  
F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225:61//Hs.134989:L12701  
F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730  
F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:AI004145
- 25 F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351  
F-NT2RM4001187  
F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220  
F-NT2RM4001200//Zinc finger protein 10 (KOX 1)//4.0e-68:799:69//Hs.2479:X78933  
F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.4e-153:707:99//Hs.14934:AF004828
- 30 F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]//0.19:291:62//Hs.31582:AA877205  
F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds//7.0e-63:715:70//Hs.104925:AF059611
- 35 F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-67:208:96//Hs.26676:AA033997  
F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete cds//0.0019:435:59//Hs.6360:AB007950
- 40 F-NT2RM4001309//Human Chromosome 16 BAC clone CIT987SK-254P9//0.019:356:59//Hs.26971:AC003003  
F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-79:474:89//Hs.32971:Z46973  
F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335  
F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642:66//Hs.87435:D89016  
F-NT2RM4001340//EST//0.40:135:70//Hs.161198:AA18988
- 45 F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PM140-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0096:284:58//Hs.120997:R56714  
F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.7e-52:252:100//Hs.15301:AA167818  
F-NT2RM4001371//EST//0.52:262:59//Hs.145991:AI277656
- 50 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-169:790:98//Hs.5151:AF098799  
F-NT2RM4001384  
F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575  
F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475:64//Hs.105052:AB000520  
F-NT2RM4001412
- 55 F-NT2RM4001414//ESTs, Moderately similar to 18547\_1 [H.sapiens]//5.2e-18:133:87//Hs.28209:AI073817  
F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:70//Hs.154326:D42087  
F-NT2RM4001444  
F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658

- F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914  
 F-NT2RM4001483//ESTs. Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sapiens]//1.1e-71:313:99//Hs.163754:AA587784  
 5 F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.9e-157:724:99//Hs.153121:AB014585  
 F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619  
 F-NT2RM4001522//ESTs. Weakly similar to D9481.12 gene product [S.cerevisiae]//1.3e-114:536:99//Hs.88820:AA456247  
 F-NT2RM4001557  
 10 F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487  
 F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//1.0:255:60//Hs.14207:U86453  
 F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:AI198859  
 F-NT2RM4001582  
 15 F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566  
 F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0072:484:60//Hs.129892:AB011094  
 F-NT2RM4001597//ESTs. Moderately similar to red-1 [M.musculus]//2.3e-72:387:95//Hs.114722:AA448077  
 20 F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.1e-163:750:99//Hs.23255:AB018334  
 F-NT2RM4001611//ESTs. Weakly similar to F25H9.6 [C.elegans]//8.6e-05:91:79//Hs.24647:W19739  
 F-NT2RM4001629//ESTs. Moderately similar to 55 KD ERYTHROCYTE MEMBRANE PROTEIN [Homo sapiens]//0.0042:153:68//Hs.114832:AI147946  
 F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339  
 25 F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320  
 F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323  
 F-NT2RM4001682//EST//0.027:145:70//Hs.133253:AI052638  
 F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA76384  
 F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957  
 30 F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:AI332905  
 F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903  
 F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318  
 F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306  
 F-NT2RM4001754//ESTs. Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//2.0e-27:205:83//Hs.110601:AA206719  
 35 F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:X97630  
 F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4e-175:803:99//Hs.39871:AB018270  
 40 F-NT2RM4001783//ESTs. Weakly similar to T12D8.1 [C.elegans]//3.1e-71:376:95//Hs.108396:AA160677  
 F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.99:446:58//Hs.27910:AF049105  
 F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547  
 F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712  
 45 F-NT2RM4001823//ESTs. Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.3e-40:252:90//Hs.119294:AI379442  
 F-NT2RM4001828//Zinc finger protein 157 (HZF22)//1.8e-75:688:72//Hs.89897:U28687  
 F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953:M96824  
 F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:AI214204  
 50 F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814  
 F-NT2RM4001856  
 F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250  
 F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.3e-150:704:98//Hs.61628:Y17711  
 55 F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:66//Hs.7938:D86984  
 F-NT2RM4001880  
 F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:AI204212

- F-NT2RM4001922//ESTs//2.5e-51:291.93//Hs.26660:AI312633  
 F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, partial cds//0.98:359:57//Hs.155356:AJ224875  
 F-NT2RM4001938  
 5 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808:98//Hs.118631:AF098162  
 F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:83//Hs.154326:D42087  
 F-NT2RM4001965//ESTs. Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//1.8e-65:337:96//Hs.130135:AA905493  
 10 F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:AI312862  
 F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527:76//Hs.159277:AB018341  
 F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082  
 F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181:65//Hs.11147:AB007936  
 15 F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:AI302271  
 F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601  
 F-NT2RM4002034  
 F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048  
 F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912  
 20 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:AB014540  
 F-NT2RM4002062//ESTs. Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus] //7.0e-94:396:94//Hs.59346:AI126802  
 F-NT2RM4002063  
 25 F-NT2RM4002068//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:AF071309  
 F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040  
 F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302  
 F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.122967:AF059569  
 30 F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) [alternative products]//9.2e-34:532:65//Hs.146459:X66975  
 F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.69360:U63743  
 35 F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542  
 F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877  
 F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158  
 F-NT2RM4002146//ESTs. Highly similar to similar to mago nashi [H.sapiens]//1.6e-135:646:97//Hs.104650:AI037879  
 40 F-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535  
 F-NT2RM4002174  
 F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L21998  
 F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454:60//Hs.32981:U38276  
 45 F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454  
 F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313:61//Hs.118087:AB011182  
 F-NT2RM4002226//ESTs. Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster] //8.4e-125:588:98//Hs.23900:U82984  
 50 F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966  
 F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:AI205764  
 F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502:57//Hs.77783:AF014118  
 F-NT2RM4002278//EST//0.33:138:63//Hs.144096:AI032180  
 F-NT2RM4002281  
 F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979  
 55 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:72//Hs.31463:D87457  
 F-NT2RM4002301  
 F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:AI343331  
 F-NT2RM4002339



- F-NT2RM4002344//EST//0.16:166.64//Hs.128600:AA906454  
 F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.1e-151:708.98//Hs.26163:AB014549
- 5 F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0040:303.63//Hs.23741:AB018263  
 F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:N70293  
 F-NT2RM4002390  
 F-NT2RM4002398  
 F-NT2RM4002409
- 10 F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-55:282.96//Hs.26676:AA033997  
 F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339.60//Hs.18686:AF052151  
 F-NT2RM4002452  
 F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228.81//Hs.115263:D30783  
 F-NT2RM4002460//EST//1.0:142.65//Hs.145370:AI252780
- 15 F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//8.9e-165:777.98//Hs.8765:AF083255  
 F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464.97//Hs.94781:AB014591  
 F-NT2RM4002493
- 20 F-NT2RM4002499//ESTs//1.3e-44:653.67//Hs.23790:N99347  
 F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225.83//Hs.155646:AF088219  
 F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290.60//Hs.154968:U02020  
 F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232.61//Hs.82042:D87075
- 25 F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor AII/AVP mRNA, complete cds//1.0:100.70//Hs.159483:AF054176  
 F-NT2RM4002558//Homo sapiens amphiphysin II mRNA, complete cds//0.17:393.61//Hs.6619:U84004  
 F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226.60//Hs.84043:D84273
- 30 F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C.elegans]//3.3e-88:484.93//Hs.105837:AA536054  
 F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetyltransferase [H.sapiens]//0.059:121.70//Hs.155413:AA429394  
 F-NT2RM4002593//ESTs//1.0e-15:103.95//Hs.108920:W28151
- 35 F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:499.59//Hs.79357:D78275  
 F-NT2RM4002623//ESTs//1.2e-11:92.92//Hs.164046:T97402  
 F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746.81//Hs.3628:AB014587  
 F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747.96//Hs.159597:AJ012449
- 40 F-NT2RP1000040//ESTs//1.3e-58:338.92//Hs.17534:H16907  
 F-NT2RP1000063//ESTs//0.0013:72.83//Hs.108196:W81647  
 F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548.91//Hs.79971:X98834  
 F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247.61//Hs.30792:AF044924
- 45 F-NT2RP1000111  
 F-NT2RP1000112//TTK protein kinase//3.2e-40:324.81//Hs.2052:M86699  
 F-NT2RP1000124//ESTs//2.4e-42:268.89//Hs.146078:AI084025  
 F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens]//1.4e-71:382.94//Hs.127842:W38901
- 50 F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77.90//Hs.3760:AF0111792  
 F-NT2RP1000170//EST//0.68:130.63//Hs.146994:AI184430  
 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679.97//Hs.78019:AF070535  
 F-NT2RP1000191//ESTs//1.3e-71:405.93//Hs.24054:N46499
- 55 F-NT2RP1000202//H.sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591.58//Hs.74019:X83703  
 F-NT2RP1000243  
 F-NT2RP1000259  
 F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528.97//Hs.

- 4214:AF067730  
F-NT2RP1000324//ESTs//3.4e-98.499.96//Hs.42530:N41661  
F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148.693.98//Hs.31584:AF053551
- 5 F-NT2RP1000333//Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28:328.60//Hs.22405:AF004231  
F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337.62//Hs.79706:U53204  
F-NT2RP1000357  
F-NT2RP1000358//DYNAMIN-1//0.96:273.59//Hs.126:L07807
- 10 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497.86//Hs.77864:AB014538  
F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178:877:96//Hs.120360:AF064594  
F-NT2RP1000409//ESTs//5.4e-59.415.83//Hs.140578:AA828031
- 15 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.0e-179:710.98//Hs.21862:AB011159  
F-NT2RP1000416//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus] //7.3e-177:857.97//Hs.6823:W18181  
F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.46:222:60//Hs.89230:AF031815
- 20 F-NT2RP1000439//EST//0.98:339.56//Hs.137377:AA101603  
F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356.59//Hs.58435:AF001862  
F-NT2RP1000460  
F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence//3.7e-134:665.96//Hs.143187:AC002985
- 25 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440.80//Hs.159154:U47634  
F-NT2RP1000481//ESTs//4.8e-21:154.87//Hs.17392:AA535102  
F-NT2RP1000493  
F-NT2RP1000513//ESTs//2.2e-71:409.91//Hs.121029:AA480977
- 30 F-NT2RP1000522//Homo sapiens clone DT1P1A11 mRNA, CAG repeat region//0.21:255.62//Hs.98834:U92992  
F-NT2RP1000547//H.sapiens mRNA for transmembrane protein mp24//1.9e-06:337.63//Hs.75914:X92098  
F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82:295.92//Hs.104105:AF017418
- 35 F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235.65//Hs.121552:J05213  
F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223.89//Hs.110802:X04385  
F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//2.2e-49:506.73//Hs.132898:AC004770  
F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556.62//Hs.152936:D63475
- 40 F-NT2RP1000630  
F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389.59//Hs.3844:U24576  
F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43:232.95//Hs.3487:AA425553
- 45 F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312.90//Hs.7049:AI141736  
F-NT2RP1000701//Myogenic factor 3//0.81:186.63//Hs.2834:AF027148  
F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.0e-33:278.78//Hs.58167:D30612  
F-NT2RP1000730//ESTs, Weakly similar to putative p150 [H.sapiens]//6.2e-40:297.84//Hs.18122:A1338045
- 50 F-NT2RP1000733//G1 to S phase transition 1//1.4e-31:286.78//Hs.2707:X17644  
F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//2.6e-123:604.96//Hs.21771:AF101434  
F-NT2RP1000746  
F-NT2RP1000767
- 55 F-NT2RP1000782//Human globin gene//3.6e-21:140.91//Hs.100090:M69023  
F-NT2RP1000796//H.sapiens mRNA for ROX protein//0.17:404.57//Hs.25497:X96401  
F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein, ribosomal protein L6 pseudogene, ESTs and CA repeat//

- 2.7e-23;147.91//Hs.102336:Z83838  
 F-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143;424:96//Hs.18953:AF067223  
 F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:AI332903  
 5 F-NT2RP1000836//EST//0.60:103:66//Hs.145708:AI267990  
 F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:AI288838  
 F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875  
 F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023  
 F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//Hs.125156:AF064094  
 10 F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:AI218663  
 F-NT2RP1000915//ESTs//8.1e-11:102:81//Hs.163740:AI248847  
 F-NT2RP1000916//ESTs, Weakly similar to coded for by C. elegans cDNA cm04e9 [C.elegans]//2.2e-27:159:94//Hs.122153:AA780270  
 F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U76248  
 15 F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400  
 F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds//2.7e-26:185:87//Hs.108332:U39317  
 F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.154276:AB002803  
 F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:AI248847  
 20 F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M17885  
 F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858  
 F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:N28866  
 F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//Hs.82837:L13435  
 F-NT2RP1001011  
 25 F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:AI089163  
 F-NT2RP1001014  
 F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M61764  
 F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901  
 F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:AI360531  
 30 F-NT2RP1001080//Homo sapiens forkhead protein (FKHRL1) mRNA, complete cds//0.57:215:64//Hs.14845:AF032886  
 F-NT2RP1001113//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//1.4e-65:293:95//Hs.32751:H38087  
 F-NT2RP1001173  
 35 F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-26:259:74//Hs.75258:AF054174  
 F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524  
 F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:AI022150  
 F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.25195:U81523  
 40 F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:AI337094  
 F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:AJ002231  
 F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724  
 45 F-NT2RP1001294  
 F-NT2RP1001302  
 F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341  
 F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:H67815  
 F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//3.1e-87:437:97//Hs.132898:AC004770  
 50 F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bostaurus]//6.8e-101:480:94//Hs.75017:AA166853  
 F-NT2RP1001385//EST//0.86:127:65//Hs.156304:AI336859  
 F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673  
 55 F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081  
 F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700  
 F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700  
 F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:AF052149

F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104  
 F-NT2RP1001466  
 F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742  
 F-NT2RP1001482  
 5 F-NT2RP1001494  
 F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI016400  
 F-NT2RP1001548//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:254:64//Hs.75814:AB000277  
 F-NT2RP1001569  
 10 F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds//2.5e-41:496:74//Hs.12956:U90913  
 F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420  
 F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//4.7e-137:685:96//Hs.93677:AF091081  
 F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C. elegans]//8.2e-47:300:89//Hs.6473:AA853955  
 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:68//Hs.40100:AB002390  
 15 F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:66//Hs.70617:D31763  
 F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.0e-26:214:82//Hs.140385:AA773359  
 F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:AI038867  
 F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1e-78:383:97//Hs.8309:AB018290  
 20 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//7.8e-97:467:97//Hs.6216:AF061749  
 F-NT2RP2000054//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:L20433  
 F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosphatase epsilon//1.2e-27:146:100//Hs.155991:X54134  
 25 F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//8.1e-41:767:61//Hs.23796:AL022718 F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609  
 30 F-NT2RP2000076//H.sapiens mRNA for TFIIIAI.0.00023:356:62//Hs.121686:D14887  
 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.54877:AF050078  
 F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879  
 F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:AB018338  
 35 F-NT2RP2000091  
 F-NT2RP2000097  
 F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:AI371963  
 F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390  
 40 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-115:551:97//Hs.17706:AB018356  
 F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22670  
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:607:96//Hs.159273:AF054177  
 45 F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195  
 F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs.152936:D63475  
 F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910  
 50 F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291  
 F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:AI188190  
 F-NT2RP2000173  
 F-NT2RP2000175  
 F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.0018:324:58//Hs.100058:AB006713  
 55 F-NT2RP2000195//ESTs, Weakly similar to C37E2.2 [C. elegans]//3.6e-37:233:90//Hs.56750:AI148761  
 F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050  
 F-NT2RP2000208

- F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.0071:243.61//Hs.143641:AB009462
- F-NT2RP2000232//EST//0.0087:187.62//Hs.151024:Z39990
- F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:342.59//Hs.8546:U97669
- 5 F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227.60//Hs.47822:AB002378
- F-NT2RP2000248//EST//0.49:117.70//Hs.61016:AA019719
- F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.51:227.60//Hs.30223:X90846
- F-NT2RP2000258//ESTs//3.1e-48:261.94//Hs.128230:AA972691
- 10 F-NT2RP2000270//ESTs//2.9e-38:357.75//Hs.140329:AA714011
- F-NT2RP2000274//ESTs//1.1e-106:508.98//Hs.47646:AA307599
- F-NT2RP2000283//EST//1.0:139.63//Hs.128256:AA972910
- F-NT2RP2000288
- F-NT2RP2000289
- 15 F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.2e-60:744.70//Hs.37138:U35376
- F-NT2RP2000298//ESTs//6.1e-46:322.85//Hs.159490:AI123467
- F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//4.3e-13:140:80//Hs.58218:U82381
- F-NT2RP2000327//ESTs//4.3e-18:108.98//Hs.126212:AI417006
- 20 F-NT2RP2000328//ESTs//6.3e-88:437.96//Hs.127336:AI332905
- F-NT2RP2000329//GTP.AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607.66//Hs.101642:X60673
- F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:126.69//Hs.153706:AF026547
- 25 F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.2e-130:627:97//Hs.76556:U83981
- F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.56:464.57//Hs.12259:AB014530
- F-NT2RP2000412//ESTs//1.0:214.60//Hs.91226:AA649047
- F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67:375.93//Hs.808:L28010
- 30 F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.sapiens]//3.9e-75:413.92//Hs.36779:AA626790
- F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//6.7e-128:609:96//Hs.5819:AF102265
- F-NT2RP2000438//ESTs//1.3e-05:50.98//Hs.156532:AA913381
- F-NT2RP2000448//EST//1.1e-24:136.98//Hs.160402:AI393918
- 35 F-NT2RP2000459//H.sapiens mRNA for Imogen 38//1.9e-22:158.87//Hs.154655:Z68747
- F-NT2RP2000498//ESTs//1.0e-17:181.79//Hs.155243:N70293
- F-NT2RP2000503//ESTs//4.5e-41:205.100//Hs.62751:AA765702
- F-NT2RP2000510
- F-NT2RP2000516
- 40 F-NT2RP2000523//ESTs, Highly similar to APOLIPOPROTEIN B MRNA EDITING PROTEIN [Rattus norvegicus]//3.2e-15:167.75//Hs.10984:AA806768
- F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6e-38:196.98//Hs.14409:AB011144
- F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//1.0:242.57//Hs.114001:Z20656
- 45 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2e-151:732.97//Hs.7314:AB014514
- F-NT2RP2000644//ESTs//0.035:276.60//Hs.43660:N33174
- F-NT2RP2000656
- F-NT2RP2000658//ESTs//0.032:281.59//Hs.124853:AA20602
- F-NT2RP2000668
- 50 F-NT2RP2000678//ESTs//2.9e-16:310.65//Hs.126867:AI093453
- F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//2.4e-31:233.78//Hs.114905:AA088442
- F-NT2RP2000710
- F-NT2RP2000715
- 55 F-NT2RP2000731
- F-NT2RP2000758//EST//1.0e-14:199.71//Hs.162409:AA573242
- F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.6e-74:445.89//Hs.21421:AA911739

F-NT2RP2000809//ESTs//1.2e-36:235.89//Hs.154580:N34101  
 F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351.58//Hs.159275:AF030880  
 F-NT2RP2000814  
 F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.0:311:61//Hs.118087:AB011182  
 5 F-NT2RP2000819  
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390.70//Hs.20695:AB002292  
 F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds//9.5e-29:167.94//Hs.75794:U80811  
 F-NT2RP2000845//ESTs//1.0e-83:403.98//Hs.156828:AI336850  
 10 F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]//6.4e-34:207.92//Hs.135235:AI081880  
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.7e-142:732.94//Hs.3615:AB018284  
 F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.50:189.65//Hs.46146:AA418097  
 15 F-NT2RP2000931//MATRIN3//1.1e-130:610.98//Hs.78825:AB018266  
 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21//5.5e-66:326.97//Hs.15144:AC005014  
 F-NT2RP2000938//ESTs//1.8e-28:296.75//Hs.22822:H06408  
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.9e-113:533.98//Hs.19822:AB018298  
 20 F-NT2RP2000965//ESTs//5.3e-59:328.94//Hs.35575:R96494  
 F-NT2RP2000970  
 F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [Saccharomyces cerevisiae]//7.3e-76:385.96//Hs.21875:AA243700  
 25 F-NT2RP2000987//ESTs//5.6e-11:177.72//Hs.15776:T91944  
 F-NT2RP2001036//ESTs//2.0e-55:352.88//Hs.122131:AA789292  
 F-NT2RP2001044//EST//0.069:267.60//Hs.102808:N67117  
 F-NT2RP2001058//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-145:696.97//Hs.67619:AB007957  
 30 F-NT2RP2001065  
 F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313  
 F-NT2RP2001081  
 F-NT2RP2001094//ESTs//0.0071:262.64//Hs.128115:AI356560  
 F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311.78//Hs.155464:AF088219  
 35 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519.63//Hs.80358:U52191  
 F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR ALPHA [Bos taurus]//6.4e-34:201.91//Hs.118470:AI336362  
 F-NT2RP2001149//EST//3.9e-27:244.78//Hs.162236:AA551582  
 F-NT2RP2001168//ESTs//0.0023:216.62//Hs.134938:AI091361  
 40 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567.96//Hs.26247:AB007949  
 F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256.59//Hs.104020:X68011  
 F-NT2RP2001196  
 F-NT2RP2001218//ESTs//1.1e-65:337.96//Hs.115710:AA524598  
 45 F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395.59//Hs.2685:Z50053  
 F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656.70//Hs.69740:U09367  
 F-NT2RP2001245//EST//0.018:228.62//Hs.116798:AA633813  
 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514.97//Hs.7531:AB018353  
 F-NT2RP2001277//EST//0.42:127.66//Hs.42834:N20277  
 50 F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527.76//Hs.75848:U39412  
 F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287  
 F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:AI146387  
 F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359.71//Hs.76090:M80783  
 F-NT2RP2001328//ESTs//5.2e-103:532.94//Hs.69476:AA628522  
 55 F-NT2RP2001347//ESTs//4.3e-28:217.82//Hs.31775:H41883  
 F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:418.91//Hs.107039:W27244  
 F-NT2RP2001378  
 F-NT2RP2001381//ESTs//0.59:235.62//Hs.118569:AI377558

- F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203c13 (LBNL H155), complete sequence//0.28:225:62//Hs.159402.AC005609
- F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:AI189767
- F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088
- 5 F-NT2RP2001420
- F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H.sapiens]//0.030:443:59//Hs.140506:AA308018
- F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:AI032875
- F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966
- 10 F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide//9.8e-56:603:72//Hs.75544:Z82248
- F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218
- F-NT2RP2001449
- F-NT2RP2001450
- F-NT2RP2001467
- 15 F-NT2RP2001506
- F-NT2RP2001511//ESTs, Weakly similar to F48F7.1 [C.elegans]//3.2e-83:409:98//Hs.156161:AI333779
- F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.4e-138:657:97//Hs.4277:Y14494
- F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134
- 20 F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//5.2e-105:384:94//Hs.99742:AF035586
- F-NT2RP2001560
- F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.4e-124:590:98//Hs.67619:AB007957
- 25 F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:521:60//Hs.75936:U28389
- F-NT2RP2001581//EST//1.0:28:96//Hs.148002:AI264876
- F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:165:65//Hs.82201:M55268
- F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-138:647:98//Hs.27197:AB018340
- 30 F-NT2RP2001613
- F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:AI082229
- F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//4.9e-124:604:96//Hs.58488:U97067
- 35 F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds//1.3e-145:687:97//Hs.159558:AF058718
- F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74//Hs.675:M14328
- F-NT2RP2001675//X-LINKED HELICASE III//0.040:454:58//Hs.96264:U72936
- F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.028:285:63//Hs.6162:AB018314
- 40 F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.7e-34:328:76//Hs.27621:U52840
- F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091
- F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.musculus]//1.0:173:62//Hs.107361:AI197870
- F-NT2RP2001721
- 45 F-NT2RP2001740//Homo sapiens Rigui (RIGUI) mRNA, complete cds//0.58:403:57//Hs.8114:AF022991
- F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//1.2e-19:151:86//Hs.77393:D14697
- F-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete\_cds//5.2e-34:191:96//Hs.47504:AF091754
- 50 F-NT2RP2001813//EST//0.46:183:57//Hs.144096:AI032180
- F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:AI052250
- F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610
- F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//0.0013:174:62//Hs.9443:AF027219
- 55 F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768
- F-NT2RP2001883
- F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR//3.0e-113:633:90//Hs.142189:M74161

- F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650  
 F-NT2RP2001907//ESTs. Weakly similar to ankryrin 3, long form [H.sapiens]//0.37:263:62//Hs.106377:H29757  
 F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:AI393754  
 F-NT2RP2001936  
 5 F-NT2RP2001943  
 F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797  
 F-NT2RP2001947  
 F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489  
 F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//Hs.155174:AB007892  
 10 F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4e-05:235:62//Hs.129943:AB011117  
 F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196  
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314:97//Hs.116604:AB018299  
 15 F-NT2RP2002032  
 F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:AI003543  
 F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336  
 F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R51509  
 F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:AI284198  
 20 F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137:71//Hs.3615:AB018284  
 F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:66//Hs.44553:AF055634  
 F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241  
 F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:96//Hs.11039:AF052183  
 25 F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014  
 F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:AI313156  
 F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//3.2e-112:533:97//Hs.155218:AJ007509  
 F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//6.1e-07:408:60//Hs.122755:AF032986  
 30 F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286  
 F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319:59//Hs.995:M83363  
 F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.100217:AJ008112  
 F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:AI085314  
 35 F-NT2RP2002185//ESTs. Weakly similar to ubiquitin S6(1) [D.melanogaster]//6.8e-61:354:91//Hs.109966:C06057  
 F-NT2RP2002192//Human 75-kD autoantigen (PM-Sc1) mRNA, complete cds//3.7e-37:194:97//Hs.91728:M58460  
 F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT protein PIASX-alpha mRNA, complete cds//6.8e-15:228:67//Hs.111323:AF077954  
 40 F-NT2RP2002208  
 F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628  
 F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:AI394318  
 F-NT2RP2002235//H.sapiens mRNA for PHAPI2b protein//0.86:67:82//Hs.84264:U70439  
 45 F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cds//0.79:264:59//Hs.129748:AB011099  
 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//2.1e-51:315:89//Hs.150595:AF005418  
 F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:343:71//Hs.92137:M19720  
 F-NT2RP2002270//ESTs. Weakly similar to AF-9 PROTEIN [H.sapiens]//1.3e-31:206:88//Hs.4029:Z78373  
 50 F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23079  
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//5.0e-95:467:96//Hs.24812:AF069532  
 F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445  
 F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.3e-124:640:95//Hs.31034:AB015594  
 55 F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257:60//Hs.75516:X54637  
 F-NT2RP2002373  
 F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//3.1e-139:673:



- 97//Hs.109051:AF038958  
 F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.90798:U79289  
 F-NT2RP2002408//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//0.00069:265:65//Hs.74095:L20433  
 F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:AI269098  
 5 F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326  
 F-NT2RP2002442//ESTs. Weakly similar to similar to molybdopterin biosynthesis MOEB proteins [C.elegans]//5.6e-26:169:89//Hs.25198:AA904265  
 F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:AI091436  
 F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013:207:63//Hs.1560:D42045  
 10 F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:AI139929  
 F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//7.6e-125:607:96//Hs.125856:AB005289  
 F-NT2RP2002498  
 F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.2e-89:314:87//Hs.102681:U95044  
 15 F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.8e-159:761:97//Hs.23255:AB018334  
 F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs.107563:M28212  
 F-NT2RP2002537  
 F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096  
 20 F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979  
 F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.9e-33:285:78//Hs.159277:AB018341  
 F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:Z35309  
 F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4e-24:144:95//Hs.23094:M19503  
 25 F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1) mRNA, complete cds//1.0:120:68//Hs.334:U02082  
 F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp//4.3e-28:460:63//Hs.20521:Y10805  
 F-NT2RP2002621  
 30 F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0022:210:64//Hs.155302:U57317  
 F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs.94694:W52493  
 F-NT2RP2002701//ESTs. Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:278:97//Hs.109857:AA088385  
 35 F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58583  
 F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.0e-42:631:65//Hs.6336:AB014572  
 F-NT2RP2002727  
 F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217  
 40 F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:AI150297  
 F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30:628:62//Hs.87435:D89016  
 F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29:285:75//Hs.146395:AB002329  
 F-NT2RP2002752//EST//2.2e-06:126:74//Hs.159913:AA862709  
 F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705  
 45 F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:507:57//Hs.79706:U53204  
 F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:AI216407  
 F-NT2RP2002800  
 F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763  
 F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:AI382142  
 50 F-NT2RP2002862  
 F-NT2RP2002880  
 F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0:237:62//Hs.106487:AB014573  
 F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:W22606  
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds//3.9e-136:623:99//Hs.116674:AF038392  
 55 F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24:158:65//Hs.108447:AJ000517  
 F-NT2RP2002939  
 F-NT2RP2002954

- F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//6.4e-21:135.91//Hs.108332:U39317  
 F-NT2RP2002979  
 F-NT2RP2002980
- 5 F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272.61//Hs.122967:AF059569  
 F-NT2RP2002987//ESTs//8.2e-20:99.82//Hs.138965:AI004740  
 F-NT2RP2002993
- 10 F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353.81//Hs.155464:AF088219  
 F-NT2RP2003034//ESTs//1.6e-08:263.66//Hs.164048:AA811741  
 F-NT2RP2003073//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.6e-43:381:78//Hs.159176:U92019  
 F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190  
 F-NT2RP2003108//H. sapiens nek2 mRNA for protein kinase//0.025:185.67//Hs.153704:U11050
- 15 F-NT2RP2003117//ESTs//7.1e-30:219.88//Hs.153408:AA416633  
 F-NT2RP2003121//ESTs//1.9e-13:158.73//Hs.129998:AI291379  
 F-NT2RP2003125//Serum response factor (c-fos serum response element-binding transcription factor)//4.5e-06:556.57//Hs.155321:J03161  
 F-NT2RP2003129//ESTs//0.095:218.63//Hs.70836:AA121544
- 20 F-NT2RP2003137  
 F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.40:227.61//Hs.105958:AB014520  
 F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds//5.7e-113:581.93//Hs.9736:D67025  
 F-NT2RP2003161//ESTs//0.0095:120.65//Hs.163532:AI424170
- 25 F-NT2RP2003164//EST//0.11:179.63//Hs.163299:AA853944  
 F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342.79//Hs.153014:AB002353  
 F-NT2RP2003177//ESTs//3.6e-80:414.96//Hs.4767:N91123  
 F-NT2RP2003194//ESTs//5.4e-20:119.95//Hs.149531:AI393223  
 F-NT2RP2003206//EST//0.095:182.60//Hs.88461:AA278594
- 30 F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726.93//Hs.154443:X74794  
 F-NT2RP2003230//ESTs//3.0e-10:239.62//Hs.163720:AA526947  
 F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543.77//Hs.108966:U48696  
 F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.52:200.62//Hs.102732:U88153
- 35 F-NT2RP2003265  
 F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//5.8e-57:313.93//Hs.109966:C06057  
 F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9e-147:714.96//Hs.154919:AB014525
- 40 F-NT2RP2003280  
 F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.0097:243.65//Hs.21862:AB011159  
 F-NT2RP2003293//ESTs//5.5e-28:418.70//Hs.146227:AI269334
- 45 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meiding protein, complete cds//2.0e-86:416.97//Hs.7943:AB006572  
 F-NT2RP2003297//EST//0.99:240.60//Hs.133228:AI052312  
 F-NT2RP2003307//ESTs//5.6e-15:137.81//Hs.90020:AA442752  
 F-NT2RP2003308
- 50 F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//1.8e-102:532.95//Hs.6092:T75227  
 F-NT2RP2003339//ESTs//0.13:166.63//Hs.149649:AI346765  
 F-NT2RP2003347//ESTs//0.96:185.59//Hs.125003:H85963  
 F-NT2RP2003367//Human HsLIM15 mRNA for HsLIM15, complete cds//0.99:243.60//Hs.37181:D64108
- 55 F-NT2RP2003391  
 F-NT2RP2003393  
 F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416.57//Hs.4976:AF039023  
 F-NT2RP2003401

- F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]/3.7e-33.303.77//Hs.14038:R06800  
 F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893  
 F-NT2RP2003446//Prostaglandin receptor, ep1 subtype//0.81:273.61//Hs.159360:L22647  
 5 F-NT2RP2003456//EST//0.17:95:65//Hs.147190:AI193320  
 F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.3e-53.339.78//Hs.132874:AC004770  
 F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04106  
 10 F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481:60//Hs.80220:U96136  
 F-NT2RP2003506  
 F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.107164:M96803  
 F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403:94//Hs.78482:Y16270  
 F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)/1.3e-24:151:95//Hs.1976:M12783  
 15 F-NT2RP2003522//Zinc finger protein 148 (pH-Z2)//1.1e-17:512:60//Hs.112180:AF039019  
 F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:AI138765  
 F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010  
 F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:AI356513  
 20 F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800  
 F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114:541:98//Hs.129937:AB007931  
 F-NT2RP2003581//EST//1.0:59:76//Hs.158575:AI368947  
 F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]/1.3e-63:224:95//Hs.34627:AA126463  
 25 F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124:585:98//Hs.58488:U97067  
 F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166  
 F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M97252  
 30 F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//9.4e-47:371:80//Hs.125231:AF068006  
 F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:AI032875  
 F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247  
 F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61//Hs.18366:L09561  
 35 F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]/5.1e-44:269:91//Hs.139757:N95271  
 F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494:AB011097  
 F-NT2RP2003713  
 F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:252:83//Hs.86371:AF054180  
 40 F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879  
 F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds//4.0e-55:584:71//Hs.118797:U93918  
 F-NT2RP2003751  
 45 F-NT2RP2003760  
 F-NT2RP2003764  
 F-NT2RP2003769  
 F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:U47677  
 F-NT2RP2003777  
 50 F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]/3.7e-63:356:92//Hs.16131:AA568689  
 F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955  
 F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742  
 F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300:59//Hs.77768:X63368  
 F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425  
 55 F-NT2RP2003859  
 F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780  
 F-NT2RP2003885  
 F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA [Emmericella nidulans]/2.2e-

- 113.632:92//Hs. 50072:AI378221  
 F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H.sapiens]/1.0:146:67//Hs. 156920:AA489296  
 F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//6.8e-30:165:96//Hs. 35086:AB014458  
 5 F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.9e-116:610:94//Hs.7302: AB007916  
 F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2e-161:783:96//Hs.7316:AB018347  
 F-NT2RP2003984  
 10 F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs. 152482:AI050036  
 F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs. 51124:AF019369  
 F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]/7.0e-104:556:93// Hs.111081:AI380378  
 F-NT2RP2004014  
 15 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs. 10116:AC004780  
 F-NT2RP2004042  
 F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147: AF011573  
 F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs. 102296:AI217942  
 20 F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2) mRNA, complete cds//0.15:199: 60//Hs. 104315:AF054828  
 F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs. 158306:AJ007292  
 F-NT2RP2004142  
 F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs. 98977:AA625872  
 25 F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs. 78353:U88666  
 F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs. 143748:AI419966  
 F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs. 157031:AI343501  
 F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapiens]/1.7e-16:276:67//Hs. 36779: AA626790  
 30 F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs. 155302: U57317  
 F-NT2RP2004196  
 F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs. 22678:AA604756  
 F-NT2RP2004226//ESTs, Weakly Similar to teg292 protein [M.musculus]/1.8e-80:386:98//Hs. 68791:AA527270  
 35 F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs. 2891:X75756  
 F-NT2RP2004239//ESTs//0.12:196:61//Hs. 127209:AA976680  
 F-NT2RP2004240//EST//1.0:134:63//Hs. 104466:AA282536  
 F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs. 129725:AF047487  
 40 F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.elegans]/8.2e-51:474:74//Hs. 108990: N25951  
 F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:60//Hs. 12432:AC005263  
 F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35: 157:67//Hs. 37121:Z37544  
 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs. 61152: AF000416  
 45 F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs. 133128:W27735  
 F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs. 145091:AA814510  
 F-NT2RP2004347//ESTs//1.0:184:61//Hs. 134469:AA731632  
 F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs. 14928:AA256202  
 50 F-NT2RP2004365  
 F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.60:295:57//Hs. 39163: AF000986  
 F-NT2RP2004373  
 F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]/3.3e-97:477:98//Hs. 30490:AA146916  
 55 F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs. 43100:AA186588  
 F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from Tq21//1.4e-174:875:95//Hs. 152759:AC005164  
 F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans]/1.2e-92:519:91//Hs. 13275:AI341468

- F-NT2RP2004400//EST//0.018:150:65//Hs.158739:AI375367  
F-NT2RP2004412  
F-NT2RP2004425//EST//0.049:145:64//Hs.160759:R36944  
F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687  
5 F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K<sup>+</sup> channel (TASK) mRNA, complete cds//0.45:208:61//Hs.24040:AF006823  
F-NT2RP2004490  
F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:AI091203  
10 F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.3e-29:270:79//Hs.73614:U83460  
F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6e-139:687:96//Hs.129908:AB011163  
F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:AI346891  
F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-06:291:61//Hs.132206:AF039694  
15 F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:82//Hs.155464:AF088219  
F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.98:136:64//Hs.28020:AB018309  
F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.0:104:68//Hs.125729:N99898  
F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:60//Hs.24756:U43895  
20 F-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-59:273:93//Hs.12845:N28835  
F-NT2RP2004614//EST//0.99:103:68//Hs.148738:AI224908  
F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496:98//Hs.5198:AJ006291  
F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2e-155:728:98//Hs.29956:AB007929  
25 F-NT2RP2004675//EST//0.65:151:62//Hs.130504:AI003839  
F-NT2RP2004681  
F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1e-61:327:94//Hs.154919:AB014525  
30 F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942  
F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780  
F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.1e-118:582:96//Hs.4236:AB007947  
F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA090242  
35 F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183  
F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]//3.7e-110:548:96//Hs.85768:W16504  
F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA, complete cds//0.025:547:57//Hs.107474:AF045451  
40 F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete cds//0.99:121:64//Hs.2864:L40157  
F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//4.9e-118:594:95//Hs.40820:AF058953  
F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043  
45 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495:97//Hs.67052:AF054179  
F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83//Hs.84775:M23161  
F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:AI290258  
F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111  
50 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418:95//Hs.25619:AB007144  
F-NT2RP2004936  
F-NT2RP2004959  
F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456:66//Hs.70617:D31763  
F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:AI149478  
F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:AI239735  
55 F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218:61//Hs.7414:AB007927  
F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260:60//Hs.41723:U37426

F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478  
 F-NT2RP2004999  
 F-NT2RP2005012//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58//  
 Hs.124161:AF065164  
 5 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972:  
 AB014515  
 F-NT2RP2005003//H.sapiens Staf50 mRNA//9.4e-44:430:75//Hs.68054:X82200  
 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5e-100:501:96//Hs.31575:AF100141  
 10 F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:J03600  
 F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433  
 F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.095:271:60//Hs.139745:U39067  
 F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:338:61//Hs.112743:D67035  
 F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial cds//0.098:217:60//Hs.58167:D30612  
 15 F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, complete cds//0.22:498:59//Hs.137574:  
 AF055917  
 F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838  
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//6.4e-105:495:98//Hs.22616:  
 AB014564  
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//9.2e-29:157:98//Hs.  
 20 100555:X98743  
 F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803  
 F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947  
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//8.3e-91:447:96//Hs.132226:  
 AF045583  
 25 F-NT2RP2005147  
 F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:AI357582  
 F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.97:80:73//Hs.107747:AI357868  
 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//4.4e-127:633:96//Hs.155218:  
 AJ007509  
 30 F-NT2RP2005204//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.0034:187:66//Hs.82128:AJ012159  
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-66:340:95//Hs.8173:AC005189  
 F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783  
 F-NT2RP2005254//H.sapiens mRNA for PHAPI2b protein//1.0:101:71//Hs.84264:U07439  
 F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete cds//0.56:114:68//Hs.154503:U36341  
 35 F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds//1.2e-40:594:65//Hs.  
 81452:AF030555  
 F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:AI383932  
 F-NT2RP2005288//Homo sapiens RCC 1-like G exchanging factor RLG mRNA, complete cds//2.3e-123:604:96//  
 Hs.27007:AF060219  
 40 F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:98//Hs.44766:AJ007590  
 F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833  
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.6e-97:483:96//Hs.115763:  
 AB014576  
 45 F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.6e-23:166:90//Hs.  
 1569:U11701  
 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete  
 cds//0.016:353:62//Hs.113265:AF032387  
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//2.8e-30:456:66//Hs.44697:AB011138  
 50 F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958  
 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-100:  
 489:96//Hs.107254:AC005943  
 F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122  
 F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mRNA, complete cds//0.87:244:59//Hs.  
 113252:U80761  
 55 F-NT2RP2005407  
 F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cds//0.28:338:57//Hs.6189:AB011133  
 F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068  
 F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI091164

- F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos tau-  
rus]/8.5e-48:295.90//Hs.75017:AA166853
- F-NT2RP2005464//ESTs/2.0e-99:495.96//Hs.3530:AA808243
- F-NT2RP2005465//V-ck avian sarcoma virus CT10 oncogene homolog/0.032:176.64//Hs.16:D10656
- 5 F-NT2RP2005472//ESTs/1.4e-34:180.98//Hs.158892:AD78412
- F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds/9.9e-48:432.77//Hs.15519:  
AB018315
- F-NT2RP2005490//ESTs/4.5e-19:165.84//Hs.134382:AA083573
- F-NT2RP2005491
- 10 F-NT2RP2005495//ESTs/5.6e-96:452.99//Hs.145417:AI084164
- F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds/4.4e-48:621.68//Hs.6833:AB002324
- F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, complete cds/1.6e-63:503.78//Hs.7688:  
M64930
- F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds/0.56:139.66//Hs.8546:U97669
- 15 F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)/1.0:  
291.59//Hs.89709:L35546
- F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds/1.2e-82:  
444.92//Hs.119023:AF092563
- F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds/2.2e-19:112.99//Hs.6232:  
AB018307
- 20 F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1 [H.sapiens]/3.5e-50:366.83//Hs.  
61833:AA036735
- F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)/9.4e-155:747.97//Hs.159597:  
AJ012449
- 25 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds/1.9e-131:618.98//Hs.62515:  
AB007963
- F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME  
III [C.elegans]/2.5e-51:292.93//Hs.105684:H24407
- F-NT2RP2005555//EST/0.046:308.57//Hs.145962:AI276822
- 30 F-NT2RP2005557//ESTs/4.6e-48:382.79//Hs.125014:AI422839
- F-NT2RP2005581//ESTs/6.3e-28:166.93//Hs.87803:AA034436
- F-NT2RP2005600//ESTs/1.6e-40:228.93//Hs.160085:AI218627
- F-NT2RP2005605//ESTs/5.7e-13:115.86//Hs.37718:H60071
- F-NT2RP2005620//Homo sapiens epsilon 2b mRNA, complete cds/3.1e-92:447.97//Hs.22396:AF062085
- 35 F-NT2RP2005622//ESTs/0.16:242.63//Hs.136395:AA523702
- F-NT2RP2005635
- F-NT2RP2005637//ESTs/0.055:96.69//Hs.105998:R90905
- F-NT2RP2005640//ESTs/4.5e-16:107.92//Hs.150823:AI292145
- F-NT2RP2005645//ESTs/2.7e-29:181.90//Hs.121653:AI375440
- 40 F-NT2RP2005651//Oxysterol binding protein/0.00011:122.69//Hs.1433065:M86917
- F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds/1.5e-08:351.62//Hs.91400:  
AB006626
- F-NT2RP2005669//ESTs/0.016:185.64//Hs.97713:AA442239
- F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds/7.7e-96:462.98//  
Hs.25664:AF089814
- 45 F-NT2RP2005683//ESTs/0.83:242.62//Hs.136395:AA523702
- F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE/2.5e-11:328.61//Hs.79217:M77836
- F-NT2RP2005694
- F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA, complete cds/0.15:496:  
55//Hs.79326:L76703
- 50 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds/5.1e-126:599.97//Hs.61638:  
AB018342
- F-NT2RP2005719//ESTs/0.58:326.60//Hs.157209:N57527
- F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)/8.2e-46:415.77//Hs.69740:U09367
- 55 F-NT2RP2005723//ESTs/1.0e-15:141.81//Hs.163747:AA174017
- F-NT2RP2005726//EST/3.4e-15:96.95//Hs.156170:AI334191
- F-NT2RP2005732//ESTs/0.99:162.62//Hs.154914:AA721086
- F-NT2RP2005741//Homo sapiens chondroadherin gene, 5'flanking region and/0.80:362.58//Hs.97220:U96769

- F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688  
 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//Hs.159651:AF068868  
 5 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.26285:AF082516  
 F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425:56//Hs.79768:D21853  
 F-NT2RP2005767//Homolog 2 of Drosophila large discs//0.085:262:61//Hs.23205:X82895  
 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:M77836  
 10 F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:Z50115  
 F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556  
 F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs.34853:U28368  
 F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820  
 15 F-NT2RP2005812  
 F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595  
 F-NT2RP2005835  
 F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.94:148:65//Hs.59829:AB014602  
 20 F-NT2RP2005853  
 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//5.4e-176:829:98//Hs.50758:AF092564  
 F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567  
 F-NT2RP2005868  
 25 F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.240:L16782  
 F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943  
 F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360  
 F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399  
 30 F-NT2RP2005933//ESTs. Highly similar to nucleoporin p54 [R.nonvegicus]//7.9e-90:326:98//Hs.156882:AA292186  
 F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770  
 F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339  
 F-NT2RP2006023  
 35 F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382  
 F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.51:271:59//Hs.37035:U07664  
 F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093  
 F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58//Hs.57652:D87469  
 F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI337416  
 40 F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970  
 F-NT2RP2006100  
 F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135  
 F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349  
 F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.126677:AA649240  
 45 F-NT2RP2006166  
 F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73//Hs.74368:X69910  
 F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-114:567:96//Hs.109299:AB014554  
 F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-23:187:85//Hs.15519:AB018315  
 50 F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503  
 F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//4.4e-118:618:93//Hs.153910:X96484  
 F-NT2RP2006237  
 F-NT2RP2006238  
 55 F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI269970  
 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//0.019:111:71//Hs.157199:X97630  
 F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//2.4e-05:388:60//Hs.75111:D87258



- F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:598:97//Hs.3404:AF035262  
F-NT2RP2006320//ESTs. Moderately similar to maternal transcript Maid [M.musculus]/1.9e-29:151:100//Hs.36794:AI038407
- 5 F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371  
F-NT2RP2006323//Homo sapiens mRNA for NBPhox, complete cds//4.7e-06:170:70//Hs.87202:D82344  
F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0.11:43:100//Hs.6892:AF076974
- F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1e-05:233:65//Hs.37656:AB011174  
10 F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501  
F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341  
F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs.95838:AF059734
- F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934  
F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI380509
- 15 F-NT2RP2006456  
F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein/1.1e-149:545:98//Hs.72160:AJ006266  
F-NT2RP2006467  
F-NT2RP2006472
- F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048  
20 F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134  
F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds//2.1e-115:669:90//Hs.31218:AF038966  
F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.73864:U22029
- 25 F-NT2RP2006573  
F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223  
F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180  
F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)/1.9e-137:637:98//Hs.6764:AJ011972
- 30 F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531:AF000560  
F-NT2RP3000047  
F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs.37138:U35376
- 35 F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961  
F-NT2RP3000068  
F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769  
F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353:78//Hs.108287:L27670
- F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//Hs.80741:X14608  
40 F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140  
F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595  
F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:438:100//Hs.8173:AC005189  
F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9e-182:849:98//Hs.13273:AB011164
- 45 F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-20:133:94//Hs.23094:M19503  
F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//6.6e-08:152:71//Hs.127338:AB007961  
F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779  
F-NT2RP3000207
- 50 F-NT2RP3000220  
F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.6e-20:509:58//Hs.122967:AF059569  
F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740  
F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691:86//Hs.75863:D86972
- 55 F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733  
F-NT2RP3000252  
F-NT2RP3000255  
F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568

- F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//1.7e-13:214.67//Hs.80261:L43821
- F-NT2RP3000312//ESTs//2.6e-50:255.97//Hs.146263:AA255863
- 5 F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.0088:236.63//Hs.102732:U88153
- F-NT2RP3000324//ESTs//3.8e-10:102.83//Hs.55495:AI091242
- F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.57:189.65//Hs.46146:AA418097
- 10 F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442.78//Hs.40100:AB002390
- F-NT2RP3000348
- F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164.59//Hs.78582:X80754
- F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649.66//Hs.101642:X60673
- 15 F-NT2RP3000361//ESTs//2.6e-112:531.98//Hs.17672:AA305921
- F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Lymnaea stagnalis]//4.0e-116:596.95//Hs.21094:AI337016
- F-NT2RP3000393//ESTs//2.6e-18:137.89//Hs.115600:AA351639
- F-NT2RP3000397//ESTs//8.7e-44:355.73//Hs.121961:AA777873
- 20 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.6e-175:841.97//Hs.28307:AF071185
- F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-33:610.65//Hs.23094:M19503
- F-NT2RP3000433//ESTs//1.5e-32:246.69//Hs.120892:AA724948
- F-NT2RP3000439//Adenosine A2b receptor//0.44:210.62//Hs.45743:X68487
- F-NT2RP3000441
- 25 F-NT2RP3000449//ESTs//0.60:177.64//Hs.132605:AI051562
- F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315.58//Hs.75562:U48705
- F-NT2RP3000456//ESTs//7.5e-23:140.92//Hs.5209:AA780068
- F-NT2RP3000484//EST//2.5e-06:166.67//Hs.149950:AI289822
- F-NT2RP3000487//ESTs//1.2e-63:311.98//Hs.143304:AI084058
- 30 F-NT2RP3000512//Homeo box B3//3.1e-18:109.97//Hs.49931:X16667
- F-NT2RP3000526//ESTs//3.7e-74:424.93//Hs.42991:N21379
- F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706.63//Hs.79347:D86966
- F-NT2RP3000531//ESTs//9.6e-75:392.95//Hs.144148:H08308
- F-NT2RP3000542//ESTs//3.2e-88:448.96//Hs.30622:AA486412
- 35 F-NT2RP3000561//EST//0.88:92.64//Hs.148290:AA908404
- F-NT2RP3000562//ESTs//1.1e-112:522.99//Hs.125153:AA453723
- F-NT2RP3000578
- F-NT2RP3000582//ESTs//2.1e-82:413.97//Hs.118544:R17277
- F-NT2RP3000584
- 40 F-NT2RP3000590//ESTs//1.0:134.64//Hs.12969:N56904
- F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502.57//Hs.77234:AB001914
- F-NT2RP3000596//ESTs//6.8e-71:361.95//Hs.118741:AA179811
- F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]//9.3e-61:355.92//Hs.114622:AA693492
- F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553.59//Hs.79170:D66980
- 45 F-NT2RP3000605//ESTs//5.8e-51:283.94//Hs.127152:AI421203
- F-NT2RP3000622//ESTs//1.7e-10:72.98//Hs.155360:AA984683
- F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194.61//Hs.79386:X54162
- F-NT2RP3000628//ESTs//0.96:221.61//Hs.131161:AI017333
- F-NT2RP3000632//ESTs//4.4e-53:244.77//Hs.143010:AA767904
- 50 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343.84//Hs.155464:AF088219
- F-NT2RP3000661
- F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305.59//Hs.13063:AF017789
- F-NT2RP3000685
- 55 F-NT2RP3000690//EST//1.0:149.64//Hs.140263:AA709001
- F-NT2RP3000736//ESTs//5.3e-26:146.97//Hs.98613:D83884
- F-NT2RP3000739//ESTs//0.0046:66.87//Hs.6880:V26854
- F-NT2RP3000742//ESTs//5.5e-08:311.61//Hs.152224:AI369426

- F-NT2RP3000753//ESTs//2.6e-63.318.97//Hs.153000:AA777765  
 F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP), complete cds//1.6e-38.245.91//Hs.2427:D89937  
 F-NT2RP3000815  
 5 F-NT2RP3000825//EST//1.0.220.61//Hs.135944:N45132  
 F-NT2RP3000826//Homo sapiens dellex (Dx) mRNA, complete cds//0.00040:263.65//Hs.124024:AF053700  
 F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 [H.sapiens]//1.1e-71:363.96//Hs.23803:AA126476  
 F-NT2RP3000841//EST//0.36.224.60//Hs.162094:AA524012  
 10 F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593.68//Hs.157199:X97630  
 F-NT2RP3000847//ESTs//0.0028:56.92//Hs.116406:AA209520  
 F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323.86//Hs.155464:AF088219  
 F-NT2RP3000852  
 15 F-NT2RP3000859//ESTs//0.39:169.62//Hs.148948:AA699918  
 F-NT2RP3000865//EST//0.15.236.62//Hs.123366:AA811476  
 F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//6.4e-31:766.60//Hs.15432:U53445  
 F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701.60//Hs.79706:U53204  
 20 F-NT2RP3000875  
 F-NT2RP3000901//ESTs//8.2e-26:191.87//Hs.18793:R99101  
 F-NT2RP3000904//EST//2.4e-49:240.100//Hs.160842:AI348374  
 F-NT2RP3000917  
 F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19.340.60//Hs.109895:X68277  
 25 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351.83//Hs.2953:X84407  
 F-NT2RP3000980//ESTs//6.5e-10:102.81//Hs.86950:AI204212  
 F-NT2RP3000994//ESTs//4.1e-120:571.98//Hs.127295:AA918411  
 F-NT2RP3001004//ESTs//1.1e-76:438.88//Hs.144554:N92198  
 F-NT2RP3001007  
 30 F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//2.9e-121:588.98//Hs.128781:AA160707  
 F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-54:282.97//Hs.30303:AI244662  
 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.7e-51:534.74//Hs.27007:AF060219  
 35 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474.60//Hs.21264:AB018325  
 F-NT2RP3001096//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.4e-16:428.60//Hs.155481:AJ006470  
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712.64//Hs.82292:D86969  
 40 F-NT2RP3001109//ESTs//1.2e-67:323.99//Hs.134734:AI337050  
 F-NT2RP3001111  
 F-NT2RP3001113//EST//1.1e-33:173.99//Hs.112640:AA609088  
 F-NT2RP3001115//EST//1.3e-22:122.100//Hs.162990:AA688023  
 F-NT2RP3001116//ESTs//1.1e-15:93.98//Hs.58412:W47479  
 45 F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258.61//Hs.12107:AF042384  
 F-NT2RP3001120//Zinc finger protein 136 (clone pHZ-20)//2.4e-77:687.75//Hs.69740:U09367  
 F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341.60//Hs.94790:AB018318  
 F-NT2RP3001133//Homeo box A4//0.00011:484.59//Hs.77637:M74297  
 50 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851.98//Hs.5378:AB018305  
 F-NT2RP3001147  
 F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257.59//Hs.957:M84605  
 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891.98//Hs.72160:AJ006266  
 F-NT2RP3001176  
 55 F-NT2RP3001214//EST//0.88:218.60//Hs.161147:AI417859  
 F-NT2RP3001216//ESTs//1.5e-66:340.96//Hs.105994:W19981  
 F-NT2RP3001221//ESTs, Weakly similar to M05D6.7 [C.elegans]//1.7e-97:512.95//Hs.103816:AA130866  
 F-NT2RP3001232//EST//0.0016:116.71//Hs.136498:AA594010

- F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:AI362756  
 F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62//Hs.103042:L06237  
 F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132  
 F-NT2RP3001253//Human prepromltmerin mRNA, complete cds//0.99:293:60//Hs.32934:U27109  
 5 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds//1.2e-48:761:64//Hs.107809:AB018269  
 F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.2e-42:454:72//Hs.41728:L75847  
 F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566  
 10 F-NT2RP3001274  
 F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811  
 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-48:544:69//Hs.31463:D87457  
 F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0.72:151:68//Hs.159437:U44060  
 15 F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.012:522:56//Hs.904:U84010  
 F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731  
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-30:345:73//Hs.79347:D86966  
 F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//6.3e-67:559:80//Hs.18586:AB007920  
 20 F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.00019:473:61//Hs.124161:AF085164  
 F-NT2RP3001355//ESTs, Weakly similar to ADP/ATP CARRIER PROTEIN, LIVER ISOFORM T2 [H.sapiens]//1.1e-81:421:96//Hs.32508:H29831  
 25 F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.15:313:60//Hs.129725:AF047487  
 F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022  
 F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.30965:AB001451  
 F-NT2RP3001384//Homo sapiens mRNA for HRIHF2018, partial cds//2.1e-158:743:98//Hs.146214:AB015332  
 F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595  
 30 F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783  
 F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.0e-05:189:66//Hs.41728:L75847  
 F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CTP) mRNA, 3' end//0.77:132:66//Hs.111024:L77567  
 35 F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658  
 F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047  
 F-NT2RP3001426  
 F-NT2RP3001427  
 F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.8e-73:431:91//Hs.85844:X66397  
 40 F-NT2RP3001432//ESTs, Moderately similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//6.9e-05:195:65//Hs.115868:AA568393  
 F-NT2RP3001447  
 F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:68//Hs.89631:U48508  
 F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212  
 45 F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323  
 F-NT2RP3001459  
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds//4.2e-10:168:70//Hs.32317:AF072836  
 F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877  
 50 F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231  
 F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//2.8e-172:804:98//Hs.28285:AF064801  
 F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds//9.4e-139:743:91//Hs.85283:U36500  
 55 F-NT2RP3001529//ESTs, Moderately similar to topoisomerase IC-terminal fragment [H.sapiens]//0.28:224:65//Hs.105912:AI431328  
 F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074  
 F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//Hs.147918:U38291

- F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302  
 F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11 (Cq class)//0.049:185:65//Hs.1686:M69013  
 5 F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)/9.6e-51:345:82//Hs.144563:AF057280  
 F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688  
 F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI091349  
 F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435  
 F-NT2RP3001629  
 10 F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4e-62:276:97//Hs.9899:AF099149  
 F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173  
 F-NT2RP3001646  
 F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.1e-172:816:98//Hs.159597:AJ012449  
 15 F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027  
 F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [*Pseudomonas fluorescens*]/9.0e-53:375:85//Hs.41127:AA555184  
 F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65//Hs.79077:D87071  
 F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [*Caenorhabditis elegans*]/4.0e-111:518:99//Hs.20364:AI420022  
 20 F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63//Hs.7486:D83198  
 F-NT2RP3001690//EST//0.5:291:59//Hs.162336:AA564329  
 F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219  
 F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRECURSOR [D.melanogaster]/1.4e-31:191:94//Hs.131279:AA486291  
 25 F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41:259:59//Hs.58435:AF001862  
 F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]/1.7e-159:747:98//Hs.6823:W18181  
 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//4.4e-161:565:97//Hs.159273:AF054177  
 30 F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III [*Caenorhabditis elegans*]/3.5e-116:554:98//Hs.144332:AA046836  
 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:78//Hs.90998:D50918  
 F-NT2RP3001739  
 35 F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.116549:AL009172  
 F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//0.10:528:56//Hs.22138:U49250  
 F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2.4e-47:725:64//Hs.41688:U27193  
 40 F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds//0.42:198:61//Hs.57783:U78525  
 F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1e-153:710:98//Hs.28169:AB007928  
 F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.79024:L03532  
 45 F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361  
 F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.53563:L41162  
 F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-III//0.90:379:58//Hs.32950:X82634  
 F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729  
 F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.8e-35:481:67//Hs.158225:U68727  
 50 F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706  
 F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [*C.elegans*]/2.9e-94:452:98//Hs.54952:AA872675  
 F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6139:AL022326  
 55 F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896  
 F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185  
 F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247  
 F-NT2RP3001931

F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//0.0022:268:61//Hs.106070:U23298  
 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.8e-167:815:96//Hs.15869:AB014575  
 F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335  
 5 F-NT2RP3001969  
 F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180  
 F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:83//Hs.155464:AF088219  
 F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//Hs.75087:X86779  
 F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946  
 10 F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821  
 F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67//Hs.147189:D88153  
 F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]//3.8e-48:353:81//Hs.127507:AA993745  
 F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0e-25:212:83//Hs.71622:AA195155  
 15 F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PROTEIN 1 [Homo sapiens]//4.2e-82:407:97//Hs.131888:AI091806  
 F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-21:168:85//Hs.23094:M19503  
 F-NT2RP3002062//EST//0.46:198:62//Hs.157711:AI359710  
 F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//0.91:194:65//Hs.1298:J03779  
 20 F-NT2RP3002081  
 F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA partial cds//0.073:297:61//Hs.102732:U88153  
 F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256  
 25 F-NT2RP3002108  
 F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018  
 F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260  
 F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009  
 30 F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644  
 F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985  
 F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]//3.0e-61:340:93//Hs.11379:AA594140  
 35 F-NT2RP3002168//EST//0.039:114:69//Hs.140335:AA737046  
 F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141429:AA631915  
 F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA30643  
 F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic)//0.98:242:57//Hs.114001:Z20656  
 40 F-NT2RP3002248  
 F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261  
 F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds//0.42:189:62//Hs.110637:AC004080  
 45 F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139  
 F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386  
 F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//1.3e-05:496:60//Hs.21537:X80910  
 F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871  
 F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:462:56//Hs.143624:AF033383  
 50 F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1.6e-65:588:75//Hs.154672:X16396  
 F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//4.2e-166:770:98//Hs.6483:Y16355  
 F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5e-161:911:89//Hs.2397:Z70200  
 55 F-NT2RP3002399  
 F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233:94//Hs.22880:AA056274  
 F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9e-140:649:99//Hs.12707:AB014578

- F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:AI291310  
 F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108  
 F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0:173:61//Hs.81234:AB007935  
 5 F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//4.4e-146:763:93//Hs.57738:U35246  
 F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9e-180:833:98//Hs.19542:AB018272  
 F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sapiens]//1.3e-42:510:70//Hs.96759:AA469984  
 10 F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X78706  
 F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054  
 F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:AI187919  
 F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.89631:U48508  
 F-NT2RP3002603  
 15 F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:61//Hs.3845:AB014888  
 F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.121287:AF029900  
 F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP)/2.6e-13:441:63//Hs.155481:AJ006470  
 F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, complete cds//1.7e-05:615:58//Hs.151518:U38847  
 20 F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:AA584308  
 F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo sapiens]//4.1e-38:493:70//Hs.41086:AI337400  
 F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:AI421991  
 25 F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans]//1.6e-61:294:100//Hs.128750:AI367584  
 F-NT2RP3002687  
 F-NT2RP3002688//EST//1.0:312:58//Hs.156800:AI352200  
 F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:AI393657  
 F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:AI279514  
 30 F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291  
 F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6) gene, partial cds//0.91:161:62//Hs.129736:AF040753  
 F-NT2RP3002785  
 F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713  
 35 F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens]//1.4e-76:423:93//Hs.41068:AA844350  
 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds//2.2e-55:615:70//Hs.105940:AF004715  
 F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA524070  
 F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T33582  
 40 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88//Hs.123090:AB001895  
 F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA626040  
 F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8e-181:853:98//Hs.6162:AB018314  
 F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:AI138765  
 F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//1.4e-133:645:97//Hs.3826:U69560  
 45 F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.2e-13:594:57//Hs.74599:AB011160  
 F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.76:412:57//Hs.21198:AB018262  
 F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870  
 50 F-NT2RP3002972//Homo sapiens PAC clone DJ1130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997  
 F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:AI287703  
 F-NT2RP3002985//Human TFIIIB related factor hBRF (HBRF) mRNA, complete cds//0.071:550:58//Hs.32935:U28838  
 F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:AI218308  
 55 F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:M91083  
 F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C06446  
 F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749  
 F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609

- F-NT2RP3003068//EST//0.00014:80.83//Hs.121993:AA777928  
 F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079  
 F-NT2RP3003078  
 F-NT2RP3003101
- 5 F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//0.98:88.68//Hs.99715:AA292700  
 F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:AI090740  
 F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1) mRNA, complete cds//0.013:438:57//Hs.101299:AF017061
- 10 F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975  
 F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA, complete cds//2.2e-20:430:63//Hs.118397:AF053944  
 F-NT2RP3003150  
 F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.37138:U35376
- 15 F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.045:410:59//Hs.6150:AB011093  
 F-NT2RP3003193//Zinc finger protein 10 (KOX 1)/2.4e-74:737:71//Hs.2479:X78933  
 F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211  
 F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854
- 20 F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308  
 F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325  
 F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525  
 F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//6.0e-55:587:70//Hs.109606:D44497
- 25 F-NT2RP3003242//Homo sapiens stannocalcin-2 (STC-2) mRNA, complete cds//1.2e-129:617:98//Hs.155223:AF055460  
 F-NT2RP3003251//H.sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200  
 F-NT2RP3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59//Hs.620:M69225
- 30 F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.98:261:59//Hs.30792:AF044924  
 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:694:93//Hs.11702:L36983  
 F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953  
 F-NT2RP3003301//EST//1.0:58:74//Hs.158575:AI368947
- 35 F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1e-91:681:80//Hs.23094:M19503  
 F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947  
 F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:AI084058  
 F-NT2RP3003327//H.sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200  
 F-NT2RP3003330  
 F-NT2RP3003344
- 40 F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//1.2e-42:644:66//Hs.2638:Z28339  
 F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L78833  
 F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//Hs.148090:D83542  
 F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791  
 F-NT2RP3003385//ESTs. Highly similar to SKD3 [M.musculus]//7.0e-74:384:96//Hs.21263:H16363
- 45 F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850  
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//3.2e-22:430:63//Hs.113272:U90653  
 F-NT2RP3003411//Human metallothionein-le gene (hMT-le)//0.99:116:62//Hs.74170:M10942
- 50 F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:AI422830  
 F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:243:61//Hs.62:M93425  
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.7e-182:853:98//Hs.14934:AF004828  
 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2e-175:826:98//Hs.26450:AB018268
- 55 F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X96330  
 F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302  
 F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete cds//0.64:626:58//Hs.150828:



- AF038169  
F-NT2RP3003552  
F-NT2RP3003555/ESTs//1.4e-12.81.98//Hs.144487:AI418322  
F-NT2RP3003564/EST//4.5e-08.186.69//Hs.116769:AA630365  
5 F-NT2RP3003572/EST//0.27-105.69//Hs.162134:AA526311  
F-NT2RP3003576/ESTs//1.2e-57.277.84//Hs.138852:AA284247  
F-NT2RP3003589/RAS-RELATED PROTEIN RAB-8//6.3e-38.373.73//Hs.123109:X56741  
F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09.564.61//Hs.104:  
D14012  
10 F-NT2RP3003625  
F-NT2RP3003656  
F-NT2RP3003659  
F-NT2RP3003665/ESTs//0.015:221.62//Hs.153705:AA527586  
F-NT2RP3003672/ESTs//0.70:351.57//Hs.27633:N78184  
15 F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds//0.013:190:  
63//Hs.44585:U58334  
F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69:246.62//Hs.118463:AF055000  
F-NT2RP3003701/EST//0.93:79.69//Hs.145285:AI249848  
F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478.61//Hs.48998:AB007865  
20 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.4e-150:700.98//Hs.48513:  
AB018300  
F-NT2RP3003746  
F-NT2RP3003795/ESTs//7.1e-20:228.74//Hs.159571:AA454230  
F-NT2RP3003799  
25 F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-igr) oncogene homolog/4.7e-41:432.73//Hs.1422:  
M19722  
F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:  
242.57//Hs.114001:Z20656  
F-NT2RP3003809//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//  
30 5.1e-07:624.59//Hs.96028:AF042832  
F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//0.84:171.63//Hs.  
102877:U41315  
F-NT2RP3003825  
F-NT2RP3003828/ESTs//2.1e-12:434.61//Hs.156864:AI346481  
35 F-NT2RP3003831  
F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242.98//Hs.25300:  
AF070811  
F-NT2RP3003842//Integrin, beta 8//1.0:345.60//Hs.832:M73780  
F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335.68//Hs.26450:AB018268  
40 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805.99//Hs.118738:  
AB018343  
F-NT2RP3003876/ESTs, Highly similar to Rabin3 [R.norvegicus]//6.8e-39:243.90//Hs.124832:AA846576  
F-NT2RP3003914/ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE  
PRECURSOR [D.melanogaster]//1.1e-107:499.99//Hs.105794:AA701659  
45 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//8.3e-49:  
404.77//Hs.9006:AF057358  
F-NT2RP3003932/ESTs//0.94:278.58//Hs.15661:W02396  
F-NT2RP3003989/ESTs//1.0:174.64//Hs.8095:AI359006  
F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)//0.00070:433.58//Hs.  
50 93909:AF042498  
F-NT2RP3004013/ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//2.8e-127:617.97//Hs.  
142151:AA984061  
F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283.62//Hs.  
155302:U57317  
55 F-NT2RP3004041/EST//0.98:264.58//Hs.127552:AA953234  
F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774.67//Hs.26441:AB002317  
F-NT2RP3004070/EST//6.8e-22:163.85//Hs.132635:AI032875  
F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression)//5.3e-90:520.90//Hs.

- 100007:X76091  
F-NT2RP3004093  
F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372.69//Hs.81281:U97258  
F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211.77//Hs.40100:AB002390  
5 F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCOF7.1 [Xenopus laevis]//1.0e-126:590.99//Hs.129888:AI096509  
F-NT2RP3004145  
F-NT2RP3004148  
F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578.98//Hs.157113:AF032900  
10 F-NT2RP3004189//ESTs//1.3e-80:409.97//Hs.151001:AA564706  
F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245.60//Hs.56045:D86640  
F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281:62//Hs.101047:M31523  
15 F-NT2RP3004209//ESTs//5.8e-87:458.94//Hs.155303:AI221835  
F-NT2RP3004215//ESTs//0.074:56.80//Hs.163590:H43361  
F-NT2RP3004242  
F-NT2RP3004246//EST//0.20:219.63//Hs.161920:AA483240  
F-NT2RP3004253//ESTs//1.2e-36:204.96//Hs.143588:AI149140  
20 F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369.59//Hs.71346:Y00067  
F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733.98//Hs.158471:AF089882  
F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:597.61//Hs.19261:AF007871  
F-NT2RP3004332  
25 F-NT2RP3004334//ESTs//8.8e-27:142.99//Hs.28068:H06285  
F-NT2RP3004341//EST//0.0068:213.64//Hs.153208:X98426  
F-NT2RP3004348//ESTs//1.2e-18:126.93//Hs.58595:AA830999  
F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-45:337.63//Hs.141429:AA631915  
30 F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//4.3e-125:608.98//Hs.128781:AA160707  
F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1//2.3e-141:804.90//Hs.123122:X97249  
F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-122:609.96//Hs.20132:AA203113  
35 F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458.60//Hs.153638:AF010403  
F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.00023:357.59//Hs.99948:M97016  
F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.0e-124:583.99//Hs.27349:AB007917  
F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.48:399.58//Hs.22616:AB014564  
40 F-NT2RP3004470//EST//1.3e-56:331.91//Hs.136830:AA769219  
F-NT2RP3004472  
F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8e-152:715.98//Hs.5003:AB007925  
F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//4.6e-118:547.99//Hs.124768:AA307735  
45 F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:752.97//Hs.158311:AB012851  
F-NT2RP3004498//ESTs, Moderately similar to ROSA26AS [M.musculus]//3.5e-89:425.99//Hs.126082:AI077718  
F-NT2RP3004503//EST//5.3e-49:399.81//Hs.162335:AA564256  
F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0:370.59//Hs.158244:AB007948  
F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129.66//Hs.7647:M94046  
50 F-NT2RP3004527//EST//0.053:260.62//Hs.123314:AA810110  
F-NT2RP3004534//ESTs//3.5e-78:370.99//Hs.132808:AI031571  
F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7e-146:679.98//Hs.75970:AB014532  
F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1e-171:793.98//Hs.74750:AB011126  
55 F-NT2RP3004566//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//2.2e-66:362.94//Hs.125870:AI364967  
F-NT2RP3004569

- F-NT2RP3004572//Homo sapiens cofactor of initiator function (Clf50) mRNA, complete cds//3.3e-181:860:97//  
Hs.122752:AF026445
- F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0e-85:422:97//Hs.129928:  
AB007923
- 5 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs.72160:AJ006266
- F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger protein, efp [H.sapiens]//6.4e-13:356:64//  
Hs.124138:AI266336
- F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA090232
- 10 F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56//Hs.79706:U53204
- F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436
- F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//8.0e-177:827:98//  
Hs.118991:AA675919
- F-NT2RP4000023//ESTs//1.4e-33:182:96//Hs.122722:AA455668
- 15 F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495
- F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556:85//Hs.129844:AF029761
- F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.9e-13:441:62//Hs.155481:  
AJ006470
- F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e-151:720:97//Hs.159597:  
AJ012449
- 20 F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743
- F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:99//Hs.57929:AB011538
- F-NT2RP4000111
- F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548:98//Hs.64691:  
AB007952
- 25 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:63//Hs.75520:D26069
- F-NT2RP4000150
- F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3386:AF053356
- F-NT2RP4000159
- 30 F-NT2RP4000167
- F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946
- F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825:98//Hs.13999:  
AB014600
- F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA422006
- 35 F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731
- F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425:71//Hs.  
46468:U45984
- F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.6e-158:771:97//Hs.155481:  
AJ006470
- 40 F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus]//1.9e-62:  
384:89//Hs.115498:AA436298
- F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728:  
AF091092
- F-NT2RP4000263
- F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580
- 45 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481
- F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.  
143648:AB000732
- F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112
- F-NT2RP4000355
- 50 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:  
AB018281
- F-NT2RP4000367//Homo sapiens ikappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-  
137:649:97//Hs.31323:AF044195
- F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECUR-  
SOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:AI382073
- 55 F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//  
0.098:291:59//Hs.994:M95678
- F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965

- F-NT2RP4000398//Zinc finger protein 140 (clone PHZ-39)//4.9e-60:469:68//Hs.154205:U09368  
F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688  
F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156
- 5 F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete cds//2.0e-34:431:73//Hs.46468:U45984  
F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087  
F-NT2RP4000449//EST//0.84:113:65//Hs.145274:A1249468  
F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853
- 10 F-NT2RP4000457//H. sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)//1.1e-05:532:57//Hs.78683:Z72499  
F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151:AB001535  
F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//Hs.78862:D87742  
F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.94:133:69//Hs.159234:U89995
- 15 F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2//0.60:335:61//Hs.74605:X13293  
F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594  
F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904  
F-NT2RP4440518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.0e-34:203:93//Hs.99423:AJ010840
- 20 F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66//Hs.100837:AB002372  
F-NT2RP4000524  
F-NT2RP4000528  
F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:A1348154  
F-NT2RP4000556//ESTs. Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//1.1e-27:162:93//Hs.25597:H93026
- 25 F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351  
F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053  
F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.4214:AF067730
- 30 F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513  
F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396  
F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367:60//Hs.144626:AF100907
- 35 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//8.0e-167:676:98//Hs.50748:AB004484  
F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783  
F-NT2RP4000724//ESTs. Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:78//Hs.11817:T80622
- 40 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178  
F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440  
F-NT2RP4000739//DESMOPLAKIN I AND II//0.99:192:63//Hs.74316:AL031058  
F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162  
F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123
- 45 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:AB007939  
F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:99//Hs.8173:AC005189  
F-NT2RP4000837//Homo sapiens SALL 1 gene, partial//5.9e-05:470:59//Hs.123094:X98833  
F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:W27603
- 50 F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs.75875:U49278  
F-NT2RP4000865//Zinc finger protein 136 (clone PHZ-20)//2.0e-96:415:78//Hs.69740:U09367  
F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:A1206803  
F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843
- 55 F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142  
F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901  
F-NT2RP4000918  
F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865

- F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:Al341503  
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//  
 Hs.24812:AF069532
- 5 F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:Al281371  
 F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542  
 F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888  
 F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:Al084058  
 F-NT2RP4000979  
 F-NT2RP4000984
- 10 F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U09013  
 F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068  
 F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204  
 F-NT2RP4001004  
 F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:Al077718  
 F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.  
 113287:AF009204
- 15 F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494  
 F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:  
 L40157
- 20 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157  
 F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP) //7.2e-13:441:63//Hs.155481:  
 AJ006470  
 F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497  
 F-NT2RP4001079//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//1.4e-131:634:98//Hs.  
 106778:AJ010953
- 25 F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) (alternative products)//0.025:166:66//Hs.  
 146459:X66975  
 F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164  
 F-NT2RP4001095
- 30 F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:448:98//Hs.105837:AA536054  
 F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRAPSTOR PROTEIN SEC61 ALPHA SUBUNIT [Canis  
 familiaris]//2.2e-26:171:92//Hs.14038:R06800  
 F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//Hs.109804:D64142  
 F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//5.8e-37:185:  
 100//Hs.126925:AA931237
- 35 F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.1433 82:AA476266  
 F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:Al358261  
 F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207  
 F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171
- 40 F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734  
 F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324  
 F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264  
 F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324  
 F-NT2RP4001207
- 45 F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:Al017636  
 F-NT2RP4001213//KRAB zinc finger protein (alternative products)//1.1e-45:187:74//Hs.22556:U37251  
 F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262  
 F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.  
 122967:AF059569
- 50 F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs.106387:AF029778  
 F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:D67463  
 F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A1, 59kD, acidic component)//0.015:246:62//  
 Hs.31121:U40571
- 55 F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578  
 F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs.110826:U80736  
 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding  
 mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250  
 F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:Al375917

- F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110  
 F-NT2RP4001339  
 F-NT2RP4001343  
 F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39;686.64//Hs.112125:M12625  
 5 F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//2.0e-31;784:62//Hs.15432:U53445  
 F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356  
 F-NT2RP4001372  
 10 F-NT2RP4001373//Homo sapiens clone Dt1P1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101.Z50194  
 F-NT2RP4001375  
 F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190  
 F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI393918  
 F-NT2RP4001407//Homo sapiens mRNA for RGS5, complete cds//0.93:218:58//Hs.24950:AB008109  
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957  
 15 F-NT2RP4001433//Zinc finger protein 10 (KOX 1)//1.1e-88:839:73//Hs.2479:X78933  
 F-NT2RP4001442  
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153:AB018326  
 F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//2.1e-90:460:96//Hs.26676:AA033997  
 20 F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//Hs.75533:D10523  
 F-NT2RP4001498//ESTs, Weakly similar to GABINDING PROTEIN BETA-2 CHAIN [H.sapiens]//0.25:216:60//Hs.63220:AA522707  
 F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395  
 25 F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:281:61//Hs.5923:X82260  
 F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:173:94//Hs.5570:AI377863  
 F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-35:329:76//Hs.154970:U03494  
 F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//0.0015:221:65//Hs.44481:U13220  
 30 F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs.30649:U05034  
 F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174  
 F-NT2RP4001567  
 F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN MET30-CBR5 INTERGENIC REGION [Saccharomyces cerevisiae]//1.1e-54:252:83//Hs.158208:AA167836  
 35 F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410  
 F-NT2RP4001574  
 F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98//Hs.108826:AL031228  
 F-NT2RP4001592  
 40 F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903  
 F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952  
 F-NT2RP4001634  
 F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN FKHI-STH1 INTERGENIC REGION [S.cerevisiae]//8.6e-57:287:97//Hs.117439:C18436  
 F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.5591:AB000409  
 45 F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.0:311:59//Hs.57969:AA203629  
 F-NT2RP4001677//Homo sapiens short form transcription factor C-Maf (C-maf) mRNA, complete cds//0.19:162:67//Hs.30250:AF055376  
 F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:332:86//Hs.113283:AF018080  
 50 F-NT2RP4001696  
 F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927  
 F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs.92614:M62302  
 F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198  
 55 F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M27878  
 F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656  
 F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-34:400:68//Hs.154212:AC004522

F-NT2RP4001803//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L36069

F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131

5 F-NT2RP4001823//Human facio-genital dysplasia (FGD1) mRNA, complete cds//3.1e-07:509:59//Hs.1572:U11690

F-NT2RP4001828

F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:73//Hs.78398:D31888

F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749

10 F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-57:813:65//Hs.6336:AB014572

F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.8e-12:84:94//Hs.140232:AA705170

F-NT2RP4001889

15 F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from T2p21//4.4e-108:535:97//Hs.15144:AC005014

F-NT2RP4001896

F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848

F-NT2RP4001927

F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.8e-54:375:84//Hs.119294:AI379442

20 F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894

F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063

F-NT2RP4001953//ESTs//0.018:206:65//Hs.130105:AA904868

F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//1.7e-54:788:65//Hs.23796:AL022718 F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete cds//0.0019:279:65//Hs.159439:AF092047

25 F-NT2RP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//0.58:463:55//Hs.3826:U69560

30 F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139

F-NT2RP4002052

F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873

F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA, complete cds//0.97:227:60//Hs.100030:AF002999

35 F-NT2RP4002075

F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.0e-38:243:90//Hs.139115:AA325104

F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654

F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152:70//Hs.25180:M96684

40 F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0e-10:401:59//Hs.89616:M55284

F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204

F-NT2RP4002888

F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960

F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96//Hs.74456:U34995

45 F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071

F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.18:271:60//Hs.139745:U39067

F-NT2RP5003492

F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase, complete cds//6.1e-56:750:69//Hs.132884:AB006179

50 F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-14:348:62//Hs.154050:AC004131

F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.94:202:63//Hs.8152:AB014542

F-NT2RP5003522

F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:AI308943

55 F-NT2RP5003534

F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0e-69:373:94//Hs.108258:AB007934

F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729

- F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairnia moschata]/4.4e-75:355:99//Hs.36727:AI051983
- F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304
- F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-171:815:98//Hs.81449:AF058922
- 5 F-OVARC1000017//Homo sapiens mRNA for NTAk, complete cds//0.50:482:58//Hs.113264:AB005060
- F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2e-37:238:89//Hs.69469:AF064603
- F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549
- F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor [H.sapiens]/6.7e-60:305:97//Hs.31696:H50008
- 10 F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798
- F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543
- F-OVARC1000085
- F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442
- F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete cds//0.00017:414:59//Hs.106387:AF029778
- 15 F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600
- F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans]/2.9e-73:406:92//Hs.109463:AI205174
- F-OVARC1000109
- F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.3e-135:663:96//Hs.3688:AF069250
- 20 F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete cds//3.4e-43:532:72//Hs.118401:AB011134
- F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:AI384010
- F-OVARC1000139
- F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293
- 25 F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414
- F-OVARC1000151
- F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305
- F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)//0.10:504:59//Hs.154083:U70136
- 30 F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:AI249131
- F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840
- F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834
- F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//2.7e-31:264:79//Hs.151895:AA196379
- 35 F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:466:68//Hs.8136:U81984
- F-OVARC1000288//ESTs, Weakly similar to Y53C12A.3 [C.elegans]/0.00084:170:65//Hs.107747:AI357868
- F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306
- F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287
- 40 F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECURSOR [Felis catus]/0.51:193:66//Hs.6194:AI378579
- F-OVARC1000321
- F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds//0.0018:507:60//Hs.122359:AF051946
- F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444
- 45 F-OVARC1000347
- F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds//3.4e-06:353:62//Hs.121895:AF001450
- F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:231:64//Hs.156016:D50930
- F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162
- 50 F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682
- F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:231:58//Hs.156016:D50930
- F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]/1.7e-25:190:84//Hs.139513:AA259082
- F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615
- F-OVARC1000437//Filamin 1 (actin-binding protein-280)/0.93:281:60//Hs.76279:X53416
- 55 F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:116:99//Hs.83987:U09284
- F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:AI377423
- F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.2e-140:566:99//Hs.12334:AB014583



- F-OVARC1000461//ESTs//1.0e-39.215.95//Hs.131532:AI024524  
 F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252.58//Hs.108112:AF070640  
 F-OVARC1000466//ESTs//3.6e-14:189.71//Hs.164041:R51854  
 F-OVARC1000473//ESTs//0.00012:77.85//Hs.29173:AA134926  
 F-OVARC1000479  
 F-OVARC1000486//ESTs//4.2e-07:409.60//Hs.99280:AA453036  
 F-OVARC1000496//ESTs//6.0e-14:240.69//Hs.131900:AI023327  
 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115.539.99//Hs.111285:AF051850  
 F-OVARC1000526//ESTs//2.9e-08:368.611//Hs.42771:N26740  
 F-OVARC1000533//EST//3.4e-14:137.82//Hs.123405:AA813492  
 F-OVARC1000543//ESTs//0.13:278.61//Hs.54894:N96475  
 F-OVARC1000556//ESTs//1.4e-31:217.90//Hs.106385:W26667  
 F-OVARC1000557//ESTs//3.8e-20:208.76//Hs.138919:AA827410  
 F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA, complete cds//0.87:135.66//Hs.85302:U76421  
 F-OVARC1000573//ESTs//2.1e-22:268.76//Hs.121852:AA776358  
 F-OVARC1000576//ESTs//9.4e-22:124.98//Hs.24220:W22200  
 F-OVARC1000578//EST//4.7e-31:335.74//Hs.162881:AA652729  
 F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263.63//Hs.3080:U29725  
 F-OVARC1000605//EST//0.1:148.62//Hs.163346:AA883722  
 F-OVARC1000622//EST//4.3e-50:313.88//Hs.149580:AI281881  
 F-OVARC1000640//ESTs//2.6e-55:441.80//Hs.105319:AA470097  
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds//1.6e-78:424.93//Hs.86859:D43772  
 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536.94//Hs.111862:AB011162  
 F-OVARC1000678//EST//1.3e-08:131.77//Hs.145970:AI277106  
 F-OVARC1000679//ESTs//0.66:223.61//Hs.134782:H74279  
 F-OVARC1000681//EST//0.017:315.61//Hs.147799:AI221639  
 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.8e-153:549.99//Hs.125315:AF027156  
 F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479.57//Hs.4764:AB018306  
 F-OVARC1000700  
 F-OVARC1000703//ESTs//0.41:100.68//Hs.160699:AI284320  
 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds//1.2e-110:451.91//Hs.13476:AF038661  
 F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318.91//Hs.7049:AI141736  
 F-OVARC1000746//ESTs//3.2e-123:570.99//Hs.127295:AA918411  
 F-OVARC1000769//ESTs//0.072:177.67//Hs.142573:AA601196  
 F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-2 [H.sapiens]//1.2e-38:194.99//Hs.157059:W28130  
 F-OVARC1000781//ESTs//4.0e-14:113.89//Hs.41972:AA626793  
 F-OVARC1000787//EST//0.92:91.64//Hs.163258:AA828835  
 F-OVARC1000800//ESTs//1.6e-44:193.81//Hs.163971:N27584  
 F-OVARC1000802//ESTs//4.6e-43:395.80//Hs.115401:AA400032  
 F-OVARC1000834//ESTs//1.9e-91:431.99//Hs.154450:AA069390  
 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432.100//Hs.155995:AB014543  
 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632.99//Hs.18910:AF045584  
 F-OVARC1000862//ESTs, Highly similar to gene Fir protein [M.musculus]//6.1e-31:183.93//Hs.108620:AA418155  
 F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.54:133.69//Hs.159234:U89995  
 F-OVARC1000883//ESTs//0.44:154.63//Hs.98183:AA471143  
 F-OVARC1000885//EST//0.91:152.63//Hs.160765:AI313323  
 F-OVARC1000886//ESTs//4.6e-08:375.61//Hs.131653:AI025777  
 F-OVARC1000890  
 F-OVARC1000891

- F-OVARC1000897//ESTs//1.1e-07:145.69//Hs.119878:AA706818  
 F-OVARC1000912//EST//3.6e-08:376.61//Hs.158782:Al376601  
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3e-85:419:97//Hs.9028:AF039691  
 F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA424456  
 5 F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//4.3e-64:623:72//Hs.114440: M11119  
 F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078  
 F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.sapiens]//2.4e-29:157:97//Hs. 136243:AA307843  
 10 F-OVARC 1000948  
 F-OVARC1000959//EST//0.65:293:55//Hs.134725:Al088986  
 F-OVARC1000960//Ley L-L//1.4e-41:425:72//Hs.37062:AC005952  
 F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288  
 F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:Al283069  
 15 F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2557:Y00661  
 F-OVARC1000986//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//6.8e-10:312:65//Hs. 155302:U57317  
 F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete cds//0.0056:209:62//Hs.10458: AF088219  
 20 F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114  
 F-OVARC1001004  
 F-OVARC1001010  
 F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus]//3.8e-47:234:99//Hs.110327:AA205866  
 F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.0076: 624:57//Hs.75063:Al023584  
 25 F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus]//3.9e-97:578:89//Hs.111974:Al050735  
 F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//8.6e-152:733:97//Hs.9899:AF099149  
 F-OVARC 1001040//ESTs//2.2e-38:204:96//Hs.128927:Al168074  
 F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017385  
 30 F-OVARC1001051  
 F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//1.1e-46:381:81//Hs. 154968:U02020  
 F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:Al312873  
 F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans]//1.4e-21:183:84//Hs.46680:AA809451  
 35 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//6.6e-132:620:98//Hs. 3426:AF082657  
 F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA709013  
 F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001937  
 F-OVARC1001085//H.sapiens mRNA for sortilin//0.99:142:67//Hs.104247:X98248  
 40 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F185707 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.3e-75:289:95//Hs.21753:AJ005897  
 F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds//1.2e-73:351:86//Hs.12912:AF015913  
 F-OVARC1001113//Homo sapiens diaphanous 1 (HDI1) mRNA, complete cds//2.1e-151:710:98//Hs.26584: AF051782  
 45 F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA813102  
 F-OVARC1001118  
 F-OVARC1001129  
 F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.75451:AF055008  
 F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA621725  
 50 F-OVARC1001162  
 F-OVARC1001167  
 F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:Al078279  
 F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA813287  
 F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA226159  
 55 F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1 PRECURSOR [Homo sapi- ens]//1.8e-11:192:69//Hs.130020:AA867581  
 F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:58//Hs.91103:AC005551  
 F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//1.5e-13:199:71//Hs.109966:

C06057

F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]/1.4e-52:324:90//Hs.114673:W72675

F-OVARC1001200//ESTs/3.9e-16:104:94//Hs.125520:AA883889

F-OVARC1001232//Cyclin A/0.95:124:67//Hs.85137:X51688

F-OVARC1001240//EST/0.017:351:60//Hs.120655:AA745676

F-OVARC1001243//ESTs/0.78:291:59//Hs.132458:AI424825

F-OVARC1001244//RING3 PROTEIN/2.8e-19:118:95//Hs.75243:D42040

F-OVARC1001261//EST/1.9e-42:225:96//Hs.158854:AI377837

F-OVARC1001268//ESTs/0.66:239:61//Hs.132525:AA576821

F-OVARC1001270//ESTs/0.99:204:60//Hs.144647:AA625224

F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds/6.8e-144:644:96//Hs.155995:AB014543

F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]/0.11:355:60//Hs.108812:AA044835

F-OVARC1001296//ESTs/1.1e-46:237:98//Hs.33746:N78172

F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds/0.20:188:64//Hs.152455:AF044209

F-OVARC1001329//ESTs/1.4e-97:486:97//Hs.125886:AA884264

F-OVARC1001330

F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)/0.021:232:62//Hs.79410:U62531

F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]/2.5e-76:363:99//Hs.105837:AA536054

F-OVARC1001342//EST/0.98:97:65//Hs.148210:AA897493

F-OVARC1001344//EST/5.3e-10:241:64//Hs.138777:N67251

F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete cds/0.64:198:61//Hs.105940:AF004715

F-OVARC1001360//ESTs/4.9e-87:429:97//Hs.130145:AI264633

F-OVARC1001369//ESTs/6.3e-07:371:62//Hs.131653:AI025777

F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds/1.4e-69:533:74//Hs.109299:AB014554

F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds/2.5e-49:365:73//Hs.129735:AF010144

F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL/4.1e-149:683:99//Hs.151428:AJ224819

F-OVARC1001391//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds/0.097:235:65//Hs.25674:AF072242

F-OVARC1001399//ESTs/1.1e-35:264:83//Hs.59379:W28225

F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds/1.3e-150:707:98//Hs.21586:AB006651

F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds/1.6e-49:586:69//Hs.74597:U52426

F-OVARC1001425//ESTs/2.4e-11:258:67//Hs.119197:T83651

F-OVARC1001436

F-OVARC1001442

F-OVARC1001453

F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631-KRE11 INTERGENIC REGION [S.cerevisiae]/1.9e-125:581:99//Hs.110950:AI041823

F-OVARC1001480//ESTs/0.95:125:72//Hs.152584:AA584568

F-OVARC1001489//EST/4.9e-72:341:100//Hs.148191:AA897343

F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds/2.6e-86:479:92//Hs.6534:AF016507

F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)/1.1e-97:538:92//Hs.75813:L33243

F-OVARC1001525

F-OVARC1001542//Envoplakin/0.34:258:60//Hs.25482:U53786

F-OVARC1001547//EST/0.0046:237:62//Hs.54638:N90595

F-OVARC1001555

F-OVARC1001577//Homo sapiens SRP46 splicing factor retropseudogene mRNA/6.8e-57:275:98//Hs.155160:AF031166

F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]/0.0035:271:60//Hs.108465:AI144299

- F-OVARC1001610//ESTs, Weakly similar to F22E10.5 [C.elegans]//1.4e-43:216:99//Hs.120002:AI038398  
F-OVARC1001611
- F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500
- F-OVARC1001668//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3e-37:217:94//Hs.14409:AB011144
- 5 F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e-49:393:81//Hs.95582:AB006867
- F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229
- F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.428:U03858
- 10 F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807
- F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863
- F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80//Hs.155652:X06825
- F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI148588
- F-OVARC1001762
- 15 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//1.4e-150:706:98//Hs.155377:U97670
- F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.8e-117:580:96//Hs.15869:AB014575
- F-OVARC 1001768//ESTs//0.035:179:64//Hs.87279:AI218697
- F-OVARC1001791
- 20 F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830
- F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:AI005102
- F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.77:362:58//Hs.116753:AB018287
- F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.69949:M94172
- 25 F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825
- F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453
- F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567
- F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537
- 30 F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973
- F-OVARC1001861
- F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:AF070611
- F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel sub-unit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709
- 35 F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127
- F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.158095:AB007953
- 40 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//2.6e-57:300:96//Hs.6216:AF061749
- F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:AI263834
- F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261
- F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263
- F-OVARC1001928
- 45 F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204
- F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III [C.elegans]//0.2:3e-119:565:98//Hs.5392:AA313794
- F-OVARC1001949//KRAB zinc finger protein (alternative products)//1.8e-17:294:67//Hs.22556:U37251
- 50 F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228
- F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639
- F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-23:213:78//Hs.105292:AA504776
- F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417
- 55 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6e-160:739:98//Hs.108258:AB007934
- F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:AI375865
- F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063
- F-OVARC1002107

- F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7e-101:498:96//Hs.75258:AF054174
- F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913
- F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399:62//Hs.112725:AF056022
- 5 F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795
- F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097
- F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:329:58//Hs.107747:AI357868
- F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.00010:300:64//Hs.118929:X79568
- 10 F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:178:64//Hs.108447:AJ000517
- F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230
- F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:AI378928
- F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//1.2e-52:550:72//Hs.42400:AF022789
- 15 F-PLACE1000014
- F-PLACE1000031
- F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088
- F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494
- F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:AI076755
- 20 F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:106499
- F-PLACE1000068//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-47:266:93//Hs.30026:AI356771
- F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-15:203:70//Hs.157422:R85366
- 25 F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30:324:60//Hs.76460:U49082
- F-PLACE1000094
- F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//6.2e-82:476:92//Hs.111081:AI380378
- F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//7.7e-27:205:85//Hs.9670:AA632135
- 30 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//2.5e-151:737:97//Hs.151017:AF058291
- F-PLACE1000185
- F-PLACE1000213
- 35 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:AI167255
- F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226
- F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022
- F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:AI278202
- F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294
- 40 F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047
- F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675
- F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:M37197
- F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:262:58//Hs.102732:U88153
- 45 F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024
- F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:47:1:58//Hs.6051:AB014516
- F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR [Homo sapiens]//8.7e-63:346:93//Hs.19501:AA742260
- 50 F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174
- F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:U33053
- F-PLACE1000424
- F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590
- 55 F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included) //2.7e-52:421:80//Hs.69747:M35531
- F-PLACE1000453//Human mRNA for MTG8a protein, complete cds//0.026:240:60//Hs.31551:D43638
- F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878

F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60//Hs.153014:AB002353  
 F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573  
 F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds//0.0046:223:65//Hs.75578:M85289  
 5 F-PLACE1000562  
 F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538  
 F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:525:72//Hs.21838:AF038179  
 F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD//2.3e-85:503:88//Hs.62661:M55542  
 10 F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e-165:798:97//Hs.159597:AJ012449  
 F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA578571  
 F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.98:215:60//Hs.8152:AB014542  
 F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986  
 F-PLACE1000636  
 15 F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.0e-154:747:96//Hs.5819:AF102265  
 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//7.5e-158:775:97//Hs.29595:AJ005896  
 F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//1.0e-57:675:69//Hs.128763:AF009353  
 20 F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949  
 F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:70//Hs.47313:D87447  
 F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288  
 F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//0.72:331:57//Hs.37110:U10694  
 25 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858  
 F-PLACE1000769  
 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.1e-139:663:98//Hs.31921:AB014548  
 F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:362:59//Hs.44782:Z82215  
 30 F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079  
 F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189  
 F-PLACE1000841//EST//0.47:143:61//Hs.144096:A032180  
 F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:63//Hs.110826:U80736  
 F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000  
 35 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428  
 F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455  
 F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201  
 F-PLACE1000948  
 F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//7.9e-10:294:66//Hs.80261:L43821  
 40 F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cDNA yk28h2.5 [C.elegans]//9.3e-45:309:88//Hs.13531:R61789  
 F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:62//Hs.8597:L11672  
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds//2.6e-141:694:96//Hs.158497:AB018267  
 45 F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913  
 F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//0.050:338:61//Hs.1974:M92432  
 F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80//Hs.6940:Z48633  
 F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876  
 50 F-PLACE1001024  
 F-PLACE1001036//EST//1.0:133:65//Hs.161424:A1424741  
 F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:284:59//Hs.79706:U53204  
 F-PLACE1001062  
 F-PLACE1001076//EST//0.84:223:59//Hs.161147:A1417859  
 55 F-PLACE1001088  
 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//1.0e-96:489:96//Hs.95448:AF065485  
 F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817  
 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//8.2e-66:676:

- 71//Hs.150406:AF022158  
 F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//1.5e-16:122:91//Hs.1257:M30704  
 F-PLACE1001168  
 F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135  
 5 F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-28:421:66//Hs.8763:W30741  
 F-PLACE1001238  
 F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494  
 F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929  
 F-PLACE1001272//COATOMER BETA'SUBUNIT//0.012:50:96//Hs.75724:X70476  
 10 F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:N51283  
 F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.2e-08:586:58//Hs.124161:AF065164  
 F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.91:221:61//Hs.16533:D87930  
 15 F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6e-08:370:60//Hs.42672:AF016052  
 F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385  
 F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591  
 F-PLACE1001351  
 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds//2.8e-26:155:95//Hs.61638:AB018342  
 20 F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//3.4e-44:393:79//Hs.152005:AF009615  
 F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748  
 F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//2.6e-09:117:84//Hs.21301:AF093419  
 25 F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 [H.sapiens]//0.00083:187:64//Hs.5399:N30646  
 F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, complete CDS//0.0038:496:57//Hs.97681:AJ233333  
 F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mRNA//7.0e-45:456:75//Hs.154069:U06452  
 30 F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//6.5e-71:365:96//Hs.110404:AF091087  
 F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232  
 F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987  
 35 F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510  
 F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:AJ379455  
 F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716  
 F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529  
 F-PLACE1001503  
 40 F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914  
 F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753  
 F-PLACE1001545  
 F-PLACE1001551  
 F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835  
 45 F-PLACE1001602//Human POJ domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266:U06233  
 F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406:AF069987  
 F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:AJ342230  
 F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005  
 F-PLACE1001611//Human facio-genital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572:U11690  
 50 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.4e-76:702:75//Hs.159277:AB018341  
 F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198  
 F-PLACE1001640  
 F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927  
 55 F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//2.8e-148:726:96//Hs.3688:AF069250  
 F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//1.1e-95:481:92//Hs.24309:AI125696

- F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete cds//6.0e-30:347:76//Hs.101555:U93869
- F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:73//Hs.12413:D83776
- F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686
- 5 F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0064:484:60//Hs.129892:AB011094
- F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.1480:M60052
- F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159
- F-PLACE1001745
- F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361
- 10 F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//2.8e-160:773:97//Hs.4812:AF061243
- F-PLACE1001756//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.7e-35:269:83//Hs.5247:AF029750
- F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283
- F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, complete cds//3.4e-52:548:72//Hs.150981:U47050
- 15 F-PLACE1001781
- F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115
- F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138
- F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//
- 20 3.6e-110:546:96//Hs.40820:AF058953
- F-PLACE1001821
- F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494
- F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214
- F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906
- 25 F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343257
- F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220
- F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//4.0e-153:685:95//Hs.17839:AF099936
- F-PLACE1001928//H. sapiens HUMM9 mRNA//0.063:196:66//Hs.2750:X74837
- 30 F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58//Hs.106387:AF029778
- F-PLACE1001989
- F-PLACE1002004
- F-PLACE1002046
- F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465:58//Hs.153322:D42108
- 35 F-PLACE1002068//EST//0.49:307:61//Hs.150652:AA908555
- F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707
- F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2e-39:635:64//Hs.38176:AB011178
- F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA, complete cds//4.3e-83:388:99//Hs.5171:AF069765
- 40 F-PLACE1002115//EST//0.18:215:62//Hs.135747:AI002637
- F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.2e-13:384:61//Hs.737:M62831
- F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSOR [Homo sapiens]//0.89:60:75//Hs.144290:T61747
- F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631
- 45 F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:79//Hs.40100:AB002390
- F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366891
- F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627
- F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674
- F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.90798:U79289
- 50 F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA399989
- F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127862:AI024442
- F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935
- F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-75:434:83//Hs.23094:M19503
- F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675
- 55 F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279
- F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291
- F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710
- F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067



- F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//2.6e-23:458.66//Hs.40993:AF000148
- F-PLACE1002438//EST//0.81:48:77//Hs.158575:AI368947
- 5 F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//7.1e-07:270:66//Hs.150406:AF022158
- F-PLACE1002465
- F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369:63//Hs.129361:AJ007581
- F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523
- 10 F-PLACE1002493
- F-PLACE1002499
- F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708:59//Hs.111967:U76010
- F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482
- 15 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583:95//Hs.88756:AB018256
- F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//3.1e-115:566:96//Hs.99348:AC004774
- F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198:86//Hs.51124:AF019369
- F-PLACE1002571//Homo sapiens mRNA for TP53, complete cds//0.99:274:59//Hs.138202:AF027866
- 20 F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627
- F-PLACE1002583//EST//0.0028:348:61//Hs.160396:AI393725
- F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279:74//Hs.109606:D44497
- F-PLACE1002598//EST//0.011:209:62//Hs.131470:AI024187
- 25 F-PLACE1002604//EST//0.47:220:61//Hs.145434:AI198915
- F-PLACE1002625
- F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693:62//Hs.80562:X04412
- F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706
- F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:804:97//Hs.124903:AF068180
- 30 F-PLACE1002714//Human involucrin mRNA//3.6e-08:509:60//Hs.157091:M13903
- F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230:58//Hs.159196:U92971
- F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080
- 35 F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728
- F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:AI049827
- F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0031:298:62//Hs.26285:AF082516
- F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:AI368926
- 40 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567:70//Hs.77546:D79994
- F-PLACE1002815
- F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687:73//Hs.9028:AF039691
- F-PLACE1002834//ESTs//2.6e-41:393:74//Hs.120206:AI089163
- F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:AI334167
- 45 F-PLACE1002851//EST//0.0034:102:72//Hs.129630:AI000405
- F-PLACE1002853//ESTs//1.1e-20:136:90//Hs.125895:AA889024
- F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627
- F-PLACE1002908//ESTs//3.8e-48:325:88//Hs.54702:AI040029
- F-PLACE1002941//ESTs//5.0e-18:128:88//Hs.17376:AA855056
- 50 F-PLACE1002962
- F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus]//0.031:372:59//Hs.8021:AI041815
- F-PLACE1002991
- F-PLACE1002993
- F-PLACE1002996//ESTs, Weakly similar to T20D3.3 [C.elegans]//1.3e-12:104:86//Hs.124808:T86959
- 55 F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510//0.99:192:64//Hs.92660:AB007979
- F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0e-131:632:97//Hs.129872:AB011088

- F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7e-14:555:58//Hs.154740:AB014567  
F-PLACE1003045  
F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491
- 5 F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//Hs.102137:U31875  
F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419  
F-PLACE1003136  
F-PLACE1003145
- 10 F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590  
F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:W01997  
F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797  
F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransferase mRNA, complete cds//0.98:221:60//Hs.139756:U59209  
F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532
- 15 F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:AI208770  
F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208  
F-PLACE1003249//Insulin-like growth factor 1 (somatomedins C)/0.99:175:62//Hs.85112:X57025  
F-PLACE1003256  
F-PLACE1003258//H.sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.29285:X99802
- 20 F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106  
F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.3e-51:700:67//Hs.37138:U35376  
F-PLACE1003334  
F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:AI023308
- 25 F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568  
F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//2.6e-144:773:92//Hs.6564:U92715  
F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]//8.9e-35:332:78//Hs.163820:H71277
- 30 F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:57//Hs.143897:AF075575  
F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858  
F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:AI343009  
F-PLACE1003375//EST//0.75:119:68//Hs.160270:AI149069  
F-PLACE1003383
- 35 F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]//8.9e-113:590:94//Hs.125175:AI124546  
F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178  
F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)/0.40:206:62//Hs.30223:X90846  
F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912
- 40 F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874  
F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635  
F-PLACE1003516//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//3.4e-85:357:86//Hs.103948:K00627  
F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145  
F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6940:Z48633
- 45 F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248  
F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans]//3.6e-110:543:97//Hs.120416:AA057428  
F-PLACE1003553  
F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780
- 50 F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:499:58//Hs.65993:AF000367  
F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932  
F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194  
F-PLACE1003592//ESTs, Moderately similar to !!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//1.4e-50:287:93//Hs.154799:AA130620
- 55 F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965  
F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.89650:L38961  
F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97//Hs.56851:D83200  
F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00065:236:64//Hs.22116:AF064104